

Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val Ser Glu Thr Arg
 225 230 235 240

Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp Gly Trp Phe Asp
 245 250 255

Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn Ala Phe Val His
 260 265 270

Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr Tyr
 275 280 285

Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val Thr Asn Trp Ala
 290 295 300

Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Leu
 305 310 315 320

Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr Val Pro Ser Leu
 325 330 335

Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro
 340 345 350

Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala
 355 360 365

Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu
 370 375 380

Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln
 385 390 395 400

His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His
 405 410 415

Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
 420 425

<210> 97

<211> 980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA00499

<400> 97

ggt aat gat att ttg gaa aaa ccc aca gca gaa gta gtg gag tac tta 48
 Gly Asn Asp Ile Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu
 1 5 10 15

tcc cac ctg cgc gca gat ggc att gtg cga gat gct gaa gcc ctg cgt 96
 Ser His Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg
 20 25 30

aag cat ttg ggt gtg aat cag tgg aac ctt tta ggc cag tcc ttc gga 144
 Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly

35					40					45						
ggt	ttc	acc	acc	ctg	cat	tac	ttg	tcc	cgg	cac	gcc	gat	tcc	ttg	gac	192
Gly	Phe	Thr	Thr	Leu	His	Tyr	Leu	Ser	Arg	His	Ala	Asp	Ser	Leu	Asp	
50					55					60						
aac	gtg	ttt	att	acc	ggc	ggt	ctc	agc	gct	att	gat	cgc	cca	gca	gaa	240
Asn	Val	Phe	Ile	Thr	Gly	Gly	Leu	Ser	Ala	Ile	Asp	Arg	Pro	Ala	Glu	80
65					70					75						
gac	gtg	tat	gcc	aac	tgt	tac	aac	cgc	atg	cgc	cga	aac	tct	gag	gaa	288
Asp	Val	Tyr	Ala	Asn	Cys	Tyr	Asn	Arg	Met	Arg	Arg	Asn	Ser	Glu	Glu	
85					90					95						
ttc	tac	cgt	cgc	ttc	ccg	caa	tta	cgg	gaa	act	ttc	cga	ggg	ttg	gtt	336
Phe	Tyr	Arg	Arg	Phe	Pro	Gln	Leu	Arg	Glu	Thr	Phe	Arg	Gly	Leu	Val	
100					105					110						
aat	cgt	gct	cgc	gcc	ggg	gag	att	gtg	ctt	ccc	acc	ggc	gaa	gtt	gtg	384
Asn	Arg	Ala	Arg	Ala	Gly	Glu	Ile	Val	Leu	Pro	Thr	Gly	Glu	Val	Val	
115					120					125						
tca	gaa	acc	agg	ctg	cga	tcc	ctt	ggt	cac	ttg	ttg	ggt	agc	aat	gac	432
Ser	Glu	Thr	Arg	Leu	Arg	Ser	Leu	Gly	His	Leu	Leu	Gly	Ser	Asn	Asp	
130					135					140						
ggc	tgg	ttt	gat	ctg	tac	aac	ctg	ctg	gaa	tta	gat	ccc	acc	tcc	aac	480
Gly	Trp	Phe	Asp	Leu	Tyr	Asn	Leu	Leu	Glu	Leu	Asp	Pro	Thr	Ser	Asn	160
145					150					155						
gct	ttt	gtc	cat	gac	ctg	gca	gga	ctt	ttg	cct	ttc	ggc	aac	cgc	aac	528
Ala	Phe	Val	His	Asp	Leu	Ala	Gly	Leu	Leu	Pro	Phe	Gly	Asn	Arg	Asn	175
165					170					175						
cca	att	tat	tac	gtg	ctc	cat	gag	tcc	tct	tac	gcc	gac	ggt	gtg	gtg	576
Pro	Ile	Tyr	Tyr	Val	Leu	His	Glu	Ser	Ser	Tyr	Ala	Asp	Gly	Val	Val	
180					185					190						
aca	aat	tgg	gca	gca	gag	cgt	gtg	ctt	cca	gag	gat	ttc	cgc	gag	gat	624
Thr	Asn	Trp	Ala	Ala	Glu	Arg	Val	Leu	Pro	Glu	Asp	Phe	Arg	Glu	Asp	
195					200					205						
cca	aca	ctg	ctc	acc	ggt	gag	cac	gtg	ttc	cag	gag	tgg	aca	gac	acc	672
Pro	Thr	Leu	Leu	Thr	Gly	Glu	His	Val	Phe	Gln	Glu	Trp	Thr	Asp	Thr	
210					215					220						
gtg	ccg	tcg	ctc	aag	ccg	tgg	aag	gac	gtt	gcc	ctg	gca	ttg	gct	cag	720
Val	Pro	Ser	Leu	Lys	Pro	Trp	Lys	Asp	Val	Ala	Leu	Ala	Leu	Ala	Gln	240
225					230					235						
cag	gaa	tgg	ccc	aag	ctt	tat	gat	gcg	aag	gca	ttg	gaa	aac	tca	cag	768
Gln	Glu	Trp	Pro	Lys	Leu	Tyr	Asp	Ala	Lys	Ala	Leu	Glu	Asn	Ser	Gln	255
245					250					255						
gcc	aag	ggc	gct	gca	gca	gtg	tat	gcc	aat	gac	gtt	ttc	gtc	cca	gtg	816
Ala	Lys	Gly	Ala	Ala	Ala	Val	Tyr	Ala	Asn	Asp	Val	Phe	Val	Pro	Val	
260					265					270						
gat	tac	tct	ctg	gaa	acc	gca	caa	cac	ctg	ccc	ggt	gtg	cag	ctg	ttt	864
Asp	Tyr	Ser	Leu	Glu	Thr	Ala	Gln	His	Leu	Pro	Gly	Val	Gln	Leu	Phe	
275					280					285						

atc acc agc cag cat gaa cac aat gga ctt cgt gcc agc tca ggc gca 912
 ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala
 290 295 300

gta ctg aag cac ctt ttc gat ctg gcc cac ggc cga gag gta cgc 957
 Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
 305 310 315

tgattcctcg tgtagtact agc 980

<210> 98

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

Gly Asn Asp Ile Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu
 1 5 10 15

Ser His Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg
 20 25 30

Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly
 35 40 45

Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp
 50 55 60

Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu
 65 70 75 80

Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu
 85 90 95

Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val
 100 105 110

Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val
 115 120 125

Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp
 130 135 140

Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn
 145 150 155 160

Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn
 165 170 175

Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val
 180 185 190

Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp
 195 200 205

Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr
 210 215 220

Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln

225	230	235	240
Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln	245	250	255
Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val	260	265	270
Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe	275	280	285
Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala	290	295	300
Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg	305	310	315

<210> 99

<211> 1788

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1765)

<223> RXN00877

<400> 99.

```

aaataatggg gctcgccggt gatggttccc gccgggcatt caacggtgac ggaagaggtg 60
gcagacatga tgaaaactct agcaactagt atcggtcact atg act gtt gaa cac 115
                                   Met Thr Val Glu His
                                   1      5

ctg ctc aag ccc agc acc ttg ccc tac cag ctg ccc gat ttc gca gcg 163
Leu Leu Lys Pro Ser Thr Leu Pro Tyr Gln Leu Pro Asp Phe Ala Ala
                                   10      15      20

atc aag gtg gct gat ttc ccg ccc gcc ttc gaa ctc gca tta gct gaa 211
Ile Lys Val Ala Asp Phe Pro Pro Ala Phe Glu Leu Ala Leu Ala Glu
                                   25      30      35

cac gat gct gaa att aca gcg atc gct acc aat gag gac gct cct acc 259
His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn Glu Asp Ala Pro Thr
                                   40      45      50

tgg gag aac acc att gag gcc ctg gaa cgc gca ggc ctg tcc ctc aac 307
Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala Gly Leu Ser Leu Asn
                                   55      60      65

cgc gtc gcc gcc gta ttc ttc aac ttg cag ggc acc gat tcc tcc cct 355
Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly Thr Asp Ser Ser Pro
                                   70      75      80      85

gaa atg gat gaa atc gca gcc act atc gcg ccg aaa ctc tcc gcg cat 403
Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro Lys Leu Ser Ala His
                                   90      95      100

tcg gat gcg att ttc cac aat gct gcg ctt ttc gcg cgc att gag gcc 451
Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe Ala Arg Ile Glu Ala

```


105						110						115						
gta	gaa	gca	ccg	gcc	gac	gag	gaa	tcg	caa	cgc	ctg	ttg	tcc	cac	acc	499		
Val	Glu	Ala	Pro	Ala	Asp	Glu	Glu	Ser	Gln	Arg	Leu	Leu	Ser	His	Thr			
		120					125					130						
aag	cgc	gct	ttt	cga	cgt	cgc	ggt	gca	gca	ctc	aac	gcc	gac	ggc	aag	547		
Lys	Arg	Ala	Phe	Arg	Arg	Arg	Gly	Ala	Ala	Leu	Asn	Ala	Asp	Gly	Lys			
		135				140					145							
gcc	cga	ctg	agc	acc	atc	aac	cag	cgc	cta	tcg	gca	ctg	tcc	gaa	cag	595		
Ala	Arg	Leu	Ser	Thr	Ile	Asn	Gln	Arg	Leu	Ser	Ala	Leu	Ser	Glu	Gln			
150					155					160					165			
ttc	ggc	cgc	aac	ctg	ctt	cag	gac	acc	cgc	gat	ctg	gcg	gtc	aac	ttt	643		
Phe	Gly	Arg	Asn	Leu	Leu	Gln	Asp	Thr	Arg	Asp	Leu	Ala	Val	Asn	Phe			
				170					175					180				
gaa	gaa	tct	gaa	ctt	gcc	ggt	ttt	agc	gaa	gcc	cgc	ata	tcc	gcc	gcc	691		
Glu	Glu	Ser	Glu	Leu	Ala	Gly	Phe	Ser	Glu	Ala	Arg	Ile	Ser	Ala	Ala			
			185					190					195					
gct	gac	tac	gca	gca	gca	gtt	ggc	acc	gaa	ggc	tac	gtg	gtt	cca	ctg	739		
Ala	Asp	Tyr	Ala	Ala	Ala	Val	Gly	Thr	Glu	Gly	Tyr	Val	Val	Pro	Leu			
		200					205					210						
gaa	ctg	ccc	acc	gtg	cag	tca	gag	cag	gca	gta	tta	acc	gaa	tcc	gcc	787		
Glu	Leu	Pro	Thr	Val	Gln	Ser	Glu	Gln	Ala	Val	Leu	Thr	Glu	Ser	Ala			
	215					220					225							
tcg	cgt	gca	aag	ctt	tat	gaa	gcc	tcc	cag	aag	cgt	ggc	gcc	agc	ctg	835		
Ser	Arg	Ala	Lys	Leu	Tyr	Glu	Ala	Ser	Gln	Lys	Arg	Gly	Ala	Ser	Leu			
230					235					240					245			
aac	aag	gac	gtg	ctg	ctc	gaa	acc	gtg	cgt	ctg	cgt	gct	gaa	cgc	gcc	883		
Asn	Lys	Asp	Val	Leu	Leu	Glu	Thr	Val	Arg	Leu	Arg	Ala	Glu	Arg	Ala			
			250						255					260				
aca	ctt	tta	ggc	tac	gac	acc	cac	gcc	gat	tac	gtc	atc	gaa	gaa	gaa	931		
Thr	Leu	Leu	Gly	Tyr	Asp	Thr	His	Ala	Asp	Tyr	Val	Ile	Glu	Glu	Glu			
			265					270					275					
acc	gcc	gat	gac	gtc	gca	gcc	gtg	cgc	gcc	ttg	ctt	tat	gat	ctc	gcc	979		
Thr	Ala	Asp	Asp	Val	Ala	Ala	Val	Arg	Ala	Leu	Leu	Tyr	Asp	Leu	Ala			
		280					285					290						
cca	gcc	gcc	tct	gcc	aat	gcg	aaa	gcc	gaa	tac	aaa	ctc	tcc	gca	gaa	1027		
Pro	Ala	Ala	Ser	Ala	Asn	Ala	Lys	Ala	Glu	Tyr	Lys	Leu	Ser	Ala	Glu			
		295				300					305							
gaa	gca	gaa	gaa	cac	ggc	caa	aaa	gtc	ggc	gca	gct	gac	tggt	agc	ttc	1075		
Glu	Ala	Glu	Glu	His	Gly	Gln	Lys	Val	Gly	Ala	Ala	Asp	Trp	Ser	Phe			
310					315					320					325			
tggt	gaa	gcc	aaa	gtc	cgc	gcc	cgc	gac	tac	gcc	ctg	gac	gaa	acc	gaa	1123		
Trp	Glu	Ala	Lys	Val	Arg	Ala	Arg	Asp	Tyr	Ala	Leu	Asp	Glu	Thr	Glu			
				330					335					340				
ctg	cgc	aac	tac	ttc	cca	ttg	aac	caa	gta	ctc	cgt	gac	ggc	gtc	ttc	1171		
Leu	Arg	Asn	Tyr	Phe	Pro	Leu	Asn	Gln	Val	Leu	Arg	Asp	Gly	Val	Phe			
			345					350					355					

ttc gct gct aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac	1219
Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp	
360 365 370	
ctg cgc ggt tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct	1267
Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser	
375 380 385	
gac ggc tcc ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca	1315
Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro	
390 395 400 405	
tcc aag cgg ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag	1363
Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu	
410 415 420	
ctg cta ggc acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa	1411
Leu Leu Gly Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys	
425 430 435	
cca acc acc ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc	1459
Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile	
440 445 450	
ttc cac gaa ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc	1507
Phe His Glu Phe Gly His Gly Leu His Gly Leu Ser Lys Val Arg	
455 460 465	
tac cca agc ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc	1555
Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe	
470 475 480 485	
ccc tcc cag atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc	1603
Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg	
490 495 500	
aac tac gcc cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg	1651
Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu	
505 510 515	
ctt gag gca gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat	1699
Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His	
520 525 530	
gtg agt act tgt ccc cat cta tta tgg acc tgc cct gtc tct ccc tgt	1747
Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys	
535 540 545	
cca cag cgg atg ccg cac tagtcaatga cattgaccaa tta	1788
Pro Gln Arg Met Pro His	
550 555	

<210> 100

<211> 555

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met Thr Val Glu His Leu Leu Lys Pro Ser Thr Leu Pro Tyr Gln Leu

1	5	10	15
Pro Asp Phe	Ala Ala Ile Lys Val	Ala Asp Phe Pro Pro	Ala Phe Glu
	20	25	30
Leu Ala Leu	Ala Glu His Asp	Ala Glu Ile Thr Ala	Ile Ala Thr Asn
	35	40	45
Glu Asp Ala	Pro Thr Trp Glu Asn Thr	Ile Glu Ala Leu Glu Arg Ala	
	50	55	60
Gly Leu Ser	Leu Asn Arg Val Ala Ala	Val Phe Phe Asn Leu Gln Gly	
	65	70	75
Thr Asp Ser	Ser Pro Glu Met Asp	Glu Ile Ala Ala Thr Ile Ala Pro	
	85	90	95
Lys Leu Ser	Ala His Ser Asp Ala	Ile Phe His Asn Ala Ala Leu Phe	
	100	105	110
Ala Arg Ile	Glu Ala Val Glu Ala Pro Ala	Asp Glu Glu Ser Gln Arg	
	115	120	125
Leu Leu Ser	His Thr Lys Arg Ala Phe Arg Arg	Arg Gly Ala Ala Leu	
	130	135	140
Asn Ala Asp	Gly Lys Ala Arg Leu Ser Thr	Ile Asn Gln Arg Leu Ser	
	145	150	155
Ala Leu Ser	Glu Gln Phe Gly Arg Asn Leu Leu	Gln Asp Thr Arg Asp	
	165	170	175
Leu Ala Val	Asn Phe Glu Glu Ser Glu Leu Ala	Gly Phe Ser Glu Ala	
	180	185	190
Arg Ile Ser	Ala Ala Ala Asp Tyr Ala Ala Ala	Val Gly Thr Glu Gly	
	195	200	205
Tyr Val Val	Pro Leu Glu Leu Pro Thr Val Gln Ser	Glu Gln Ala Val	
	210	215	220
Leu Thr Glu	Ser Ala Ser Arg Ala Lys Leu Tyr	Glu Ala Ser Gln Lys	
	225	230	235
Arg Gly Ala	Ser Leu Asn Lys Asp Val Leu Leu	Glu Thr Val Arg Leu	
	245	250	255
Arg Ala Glu	Arg Ala Thr Leu Leu Gly Tyr Asp Thr	His Ala Asp Tyr	
	260	265	270
Val Ile Glu	Glu Glu Thr Ala Asp Asp Val Ala Ala	Val Arg Ala Leu	
	275	280	285
Leu Tyr Asp	Leu Ala Pro Ala Ala Ser Ala Asn Ala	Lys Ala Glu Tyr	
	290	295	300
Lys Leu Ser	Ala Glu Glu Ala Glu Glu His Gly Gln Lys	Val Gly Ala	
	305	310	315
Ala Asp Trp	Ser Phe Trp Glu Ala Lys Val Arg Ala Arg	Asp Tyr Ala	
	325	330	335

Leu Asp Glu Thr Glu Leu Arg Asn Tyr Phe Pro Leu Asn Gln Val Leu
 340 345 350
 Arg Asp Gly Val Phe Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val
 355 360 365
 Glu Pro Arg Pro Asp Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp
 370 375 380
 Glu Val Leu Asp Ser Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp
 385 390 395 400
 Tyr Tyr Gly Arg Pro Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe
 405 410 415
 Val Asp Gln Ser Glu Leu Leu Gly Thr Lys Pro Val Val Val Asn Val
 420 425 430
 Met Gly Ile Thr Lys Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp
 435 440 445
 Glu Val Thr Thr Ile Phe His Glu Phe Gly His Gly Leu His Gly Leu
 450 455 460
 Leu Ser Lys Val Arg Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg
 465 470 475 480
 Asp Tyr Val Glu Phe Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp
 485 490 495
 Pro Ala Val Val Arg Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile
 500 505 510
 Ile Pro Asp Ser Leu Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp
 515 520 525
 Arg Val Val Glu His Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys
 530 535 540
 Pro Val Ser Pro Cys Pro Gln Arg Met Pro His
 545 550 555

<210> 101
 <211> 1088
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1065)
 <223> FRXA00877

<400> 101
 gca gca gca gtt ggc acc gaa ggc tac gtg gtt cca ctg gaa ctg ccc 48
 Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu Glu Leu Pro
 1 5 10 15
 acc gtg cag tca gag cag gca gta tta acc gaa tcc gcc tcg cgt gca 96
 Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala Ser Arg Ala

20						25						30						
aag	ctt	tat	gaa	gcc	tcc	cag	aag	cgt	ggc	gcc	agc	ctg	aac	aag	gac	144		
Lys	Leu	Tyr	Glu	Ala	Ser	Gln	Lys	Arg	Gly	Ala	Ser	Leu	Asn	Lys	Asp			
35						40			45									
gtg	ctg	ctc	gaa	acc	gtg	cgt	ctg	cgt	gct	gaa	cgc	gcc	aca	ctt	tta	192		
Val	Leu	Leu	Glu	Thr	Val	Arg	Leu	Arg	Ala	Glu	Arg	Ala	Thr	Leu	Leu			
50						55			60									
ggc	tac	gac	acc	cac	gcc	gat	tac	gtc	atc	gaa	gaa	gaa	acc	gcc	gat	240		
Gly	Tyr	Asp	Thr	His	Ala	Asp	Tyr	Val	Ile	Glu	Glu	Glu	Thr	Ala	Asp			
65			70			75			80									
gac	gtc	gca	gcc	gtg	cgc	gcc	ttg	ctt	tat	gat	ctc	gcc	cca	gcc	gcc	288		
Asp	Val	Ala	Ala	Val	Arg	Ala	Leu	Leu	Tyr	Asp	Leu	Ala	Pro	Ala	Ala			
			85			90			95									
tct	gcc	aat	gcg	aaa	gcc	gaa	tac	aaa	ctc	tcc	gca	gaa	gaa	gca	gaa	336		
Ser	Ala	Asn	Ala	Lys	Ala	Glu	Tyr	Lys	Leu	Ser	Ala	Glu	Glu	Ala	Glu			
			100			105			110									
gaa	cac	ggc	caa	aaa	gtc	ggc	gca	gct	gac	tgg	agc	ttc	tgg	gaa	gcc	384		
Glu	His	Gly	Gln	Lys	Val	Gly	Ala	Ala	Asp	Trp	Ser	Phe	Trp	Glu	Ala			
115						120			125									
aaa	gtc	cgc	gcc	cgc	gac	tac	gcc	ctg	gac	gaa	acc	gaa	ctg	cgc	aac	432		
Lys	Val	Arg	Ala	Arg	Asp	Tyr	Ala	Leu	Asp	Glu	Thr	Glu	Leu	Arg	Asn			
130						135			140									
tac	ttc	cca	ttg	aac	caa	gta	ctc	cgt	gac	ggc	gtc	ttc	ttc	gct	gct	480		
Tyr	Phe	Pro	Leu	Asn	Gln	Val	Leu	Arg	Asp	Gly	Val	Phe	Phe	Ala	Ala			
145			150			155			160									
aac	cgc	ctc	tac	gga	atc	acc	gtg	gaa	cca	cgc	cct	gac	ctg	cgc	ggc	528		
Asn	Arg	Leu	Tyr	Gly	Ile	Thr	Val	Glu	Pro	Arg	Pro	Asp	Leu	Arg	Gly			
			165			170			175									
tac	gcc	gag	ggc	gtg	gac	gtc	tgg	gaa	gtc	ctc	gat	tct	gac	ggc	tcc	576		
Tyr	Ala	Glu	Gly	Val	Asp	Val	Trp	Glu	Val	Leu	Asp	Ser	Asp	Gly	Ser			
			180			185			190									
ggc	atc	ggc	ctg	atc	ctt	acc	gac	tac	tac	ggc	cga	cca	tcc	aag	cgg	624		
Gly	Ile	Gly	Leu	Ile	Leu	Thr	Asp	Tyr	Tyr	Gly	Arg	Pro	Ser	Lys	Arg			
195						200			205									
ggc	ggc	gct	tgg	atg	tcc	agc	ttt	gtc	gac	caa	tcc	gag	ctg	cta	ggc	672		
Gly	Gly	Ala	Trp	Met	Ser	Ser	Phe	Val	Asp	Gln	Ser	Glu	Leu	Leu	Gly			
210			215			220												
acc	aag	cca	gtc	gtg	gtc	aac	ggt	atg	ggc	att	acc	aaa	cca	acc	acc	720		
Thr	Lys	Pro	Val	Val	Val	Asn	Val	Met	Gly	Ile	Thr	Lys	Pro	Thr	Thr			
225			230			235			240									
ggc	gaa	gca	cta	ctc	agc	ctc	gat	gaa	gta	acc	acc	atc	ttc	cac	gaa	768		
Gly	Glu	Ala	Leu	Leu	Ser	Leu	Asp	Glu	Val	Thr	Thr	Ile	Phe	His	Glu			
			245			250			255									
ttc	ggc	cac	ggc	ctg	cac	ggc	ttg	ctg	tcc	aag	gtg	cgc	tac	cca	agc	816		
Phe	Gly	His	Gly	Leu	His	Gly	Leu	Leu	Ser	Lys	Val	Arg	Tyr	Pro	Ser			
			260			265			270									

ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc ccc tcc cag 864
 Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln
 275 280 285

 atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc aac tac gcc 912
 Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala
 290 295 300

 cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg ctt gag gca 960
 Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala
 305 310 315 320

 gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat gtg agt act 1008
 Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr
 325 330 335

 tgt ccc cat cta tta tgg acc tgc cct gtc tct ccc tgt cca cag cgg 1056
 Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
 340 345 350

 atg ccg cac tagtcaatga cattgaccaa tta 1088
 Met Pro His
 355

<210> 102

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu Glu Leu Pro
 1 5 10 15

 Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala Ser Arg Ala
 20 25 30

 Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu Asn Lys Asp
 35 40 45

 Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala Thr Leu Leu
 50 55 60

 Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu Thr Ala Asp
 65 70 75 80

 Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala Pro Ala Ala
 85 90 95

 Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu Glu Ala Glu
 100 105 110

 Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe Trp Glu Ala
 115 120 125

 Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu Leu Arg Asn
 130 135 140

 Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe Phe Ala Ala
 145 150 155 160

Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly
 165 170 175
 Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser
 180 185 190
 Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg
 195 200 205
 Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly
 210 215 220
 Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr
 225 230 235 240
 Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu
 245 250 255
 Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser
 260 265 270
 Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln
 275 280 285
 Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala
 290 295 300
 Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala
 305 310 315 320
 Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr
 325 330 335
 Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
 340 345 350
 Met Pro His
 355

<210> 103
 <211> 2724
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2701)
 <223> RXN01014

<400> 103
 tcttaaagtt ttctagcaat ccacactagg cgcgaactat cgtggtgtca ttgcgcacct 60
 tctaagggtta ggcggccctc aaatttcaag gagcattaaa ttg acg tcc act aat 115
 Leu Thr Ser Thr Asn
 1 5
 ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt	211
Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser	
25 30 35	
tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt	259
Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe	
40 45 50	
att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg	307
Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val	
55 60 65	
tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag	355
Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu	
70 75 80 85	
acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg	403
Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu	
90 95 100	
cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac	451
Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His	
105 110 115	
cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt	499
Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe	
120 125 130	
gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac	547
Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp	
135 140 145	
ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag	595
Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys	
150 155 160 165	
atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac	643
Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr	
170 175 180	
gat acc cac att tcc cga gtg gac tat ccc ctc tcc acc tac ctg att	691
Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu Ser Thr Tyr Leu Ile	
185 190 195	
gcg gtg tgc gcg ggt cgt tac cac gag gtg tgc gat gtc tgg aag ggt	739
Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys Asp Val Trp Lys Gly	
200 205 210	
acg ctc acc cac cat gca gaa aca cct gcc gat cag cca act gag ctg	787
Thr Leu Thr His His Ala Glu Thr Pro Ala Asp Gln Pro Thr Glu Leu	
215 220 225	
act gtt ccg ctt gct ctc tac tgc cgc agt tct ttg gct aaa gat ctt	835
Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser Leu Ala Lys Asp Leu	
230 235 240 245	
gat gcg gtg cgt ctg ttt acc gaa acg aag cag ggc ttt gat tgg tac	883
Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln Gly Phe Asp Trp Tyr	
250 255 260	

cac cgc aac ttc ggt gtg gcg tac cca ttc ggc aag tac gat cag atc	931
His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly Lys Tyr Asp Gln Ile	
265 270 275	
ttc gtc cct gaa ttt aat gct ggc gcg atg gag aac gcc ggc gct gtc	979
Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu Asn Ala Gly Ala Val	
280 285 290	
acc atc cgc gat gag tac gtt ttt gca tcc aag gca acc cgt tac cgc	1027
Thr Ile Arg Asp Glu Tyr Val Phe Ala Ser Lys Ala Thr Arg Tyr Arg	
295 300 305	
tac gag cgc cgc gct gaa acc atc ctt cac gag ctc gct cac atg tgg	1075
Tyr Glu Arg Arg Ala Glu Thr Ile Leu His Glu Leu Ala His Met Trp	
310 315 320 325	
ttc ggt gtg ctg gtg acc atg cag tgg tgg gat gat ctg tgg ctc aac	1123
Phe Gly Val Leu Val Thr Met Gln Trp Trp Asp Asp Leu Trp Leu Asn	
330 335 340	
gag tcc ttc gcc act tgg tcc gcg gca att tct cag gct gag gaa act	1171
Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile Ser Gln Ala Glu Glu Thr	
345 350 355	
gaa tac aac act gca tgg gtg act ttc gcc aat gtg gag aag tcg tgg	1219
Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn Val Glu Lys Ser Trp	
360 365 370	
gcg tac cag cag gat cag ctg cct tcc acc cac ccg gtg ttc tct gac	1267
Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His Pro Val Phe Ser Asp	
375 380 385	
gga tac gac att gag act gtc gac cag aac ttc gac ggc atc acc tac	1315
Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe Asp Gly Ile Thr Tyr	
390 395 400 405	
gca aag ggc gcc tcg gtg ctc aag cag ctg cag gca tac gtt ggc cgt	1363
Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln Ala Tyr Val Gly Arg	
410 415 420	
gag gaa ttc ctg gca ggc gta cgc agg cac ttt gcc aac cac gca tgg	1411
Glu Glu Phe Leu Ala Gly Val Arg Arg His Phe Ala Asn His Ala Trp	
425 430 435	
ggc aac gcc agc ttt gat gat ctg ctc ggc gcc ctc gag cag tcc tcc	1459
Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly Ala Leu Glu Gln Ser Ser	
440 445 450	
ggc cgc gac ctc tcc gac tgg gca aac cag tgg ctc aag acc acc ggc	1507
Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp Leu Lys Thr Thr Gly	
455 460 465	
atc aac acc ctc ggc gca aag ttc acc acc gac aac ggc aaa tac acc	1555
Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp Asn Gly Lys Tyr Thr	
470 475 480 485	
tcc ttc tcc gtc acc cag acc ggc gcc gcg ccg ggt gcc ggt gag ctg	1603
Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro Gly Ala Gly Glu Leu	
490 495 500	
cgg act cac cgc atc gcg gtg ggt ctt tat aag ctt gtc gac gga tcc	1651

Arg	Thr	His	Arg	Ile	Ala	Val	Gly	Leu	Tyr	Lys	Leu	Val	Asp	Gly	Ser	
			505					510					515			
ctc	aac	cgc	tac	gca	cga	gta	gaa	ctt	gac	tgc	agt	ggc	gcg	tcg	aca	1699
Leu	Asn	Arg	Tyr	Ala	Arg	Val	Glu	Leu	Asp	Cys	Ser	Gly	Ala	Ser	Thr	
		520					525					530				
agc	ggt	gaa	gag	atc	ggt	gga	ctt	gag	cag	gct	gac	ttc	gtg	ctg	gtc	1747
Ser	Val	Glu	Glu	Ile	Val	Gly	Leu	Glu	Gln	Ala	Asp	Phe	Val	Leu	Val	
	535					540					545					
aac	gat	gat	gat	ctg	acg	tat	gcg	ctg	ctg	gat	ctg	gat	gat	gat	tca	1795
Asn	Asp	Asp	Asp	Leu	Thr	Tyr	Ala	Leu	Leu	Asp	Leu	Asp	Asp	Asp	Ser	
550					555					560					565	
cgc	aat	ttt	gtc	atc	gac	aat	att	gat	aag	ttc	agc	gac	cct	atg	cct	1843
Arg	Asn	Phe	Val	Ile	Asp	Asn	Ile	Asp	Lys	Phe	Ser	Asp	Pro	Met	Pro	
			570					575						580		
cgc	acg	ctg	gtg	tgg	tcc	gct	gcg	tgg	gag	atg	act	cgc	gct	ggt	cag	1891
Arg	Thr	Leu	Val	Trp	Ser	Ala	Ala	Trp	Glu	Met	Thr	Arg	Ala	Gly	Gln	
		585						590					595			
atg	aag	gct	cgt	gat	ttc	atc	gcg	ctg	ggt	gct	cgt	ggc	gct	gct	gcg	1939
Met	Lys	Ala	Arg	Asp	Phe	Ile	Ala	Leu	Val	Ala	Arg	Gly	Ala	Ala	Ala	
	600						605					610				
gaa	act	gaa	att	gct	gtg	ctg	gag	cgc	att	ctc	gcg	cag	gct	acc	tct	1987
Glu	Thr	Glu	Ile	Ala	Val	Leu	Glu	Arg	Ile	Leu	Ala	Gln	Ala	Thr	Ser	
	615					620					625					
gcg	ctg	aag	agc	tac	gcc	gac	cca	gcg	tgg	gca	gaa	gca	act	gga	aat	2035
Ala	Leu	Lys	Ser	Tyr	Ala	Asp	Pro	Ala	Trp	Ala	Glu	Ala	Thr	Gly	Asn	
630					635				640						645	
gac	ctg	ctg	gcc	gat	gct	ttc	ctt	gag	ggt	gct	cgc	tcc	gca	gaa	cca	2083
Asp	Leu	Leu	Ala	Asp	Ala	Phe	Leu	Glu	Gly	Ala	Arg	Ser	Ala	Glu	Pro	
			650					655						660		
gac	tcc	gac	act	cag	ttg	gcg	ttc	att	cag	gct	ctg	gca	aaa	gca	acg	2131
Asp	Ser	Asp	Thr	Gln	Leu	Ala	Phe	Ile	Gln	Ala	Leu	Ala	Lys	Ala	Thr	
			665					670					675			
ctc	aat	gat	gct	gct	gcc	gat	tac	ttc	cgc	gac	att	ctt	gcc	ggc	aac	2179
Leu	Asn	Asp	Ala	Ala	Ala	Asp	Tyr	Phe	Arg	Asp	Ile	Leu	Ala	Gly	Asn	
	680						685					690				
gtc	gaa	ggc	ctg	acc	gtg	gat	cct	gac	ctg	cgt	tgg	tgg	gca	ctg	act	2227
Val	Glu	Gly	Leu	Thr	Val	Asp	Pro	Asp	Leu	Arg	Trp	Trp	Ala	Leu	Thr	
	695					700					705					
gcg	ctt	atc	gcc	cgt	ggt	gac	atc	gag	gct	gtc	gaa	gat	gca	atc	gcc	2275
Ala	Leu	Ile	Ala	Arg	Gly	Asp	Ile	Glu	Ala	Val	Glu	Asp	Ala	Ile	Ala	
710					715					720					725	
gct	gaa	ctt	tcc	cgc	gac	aac	tcc	agt	gcc	tcc	ttc	ctc	gca	tca	ctt	2323
Ala	Glu	Leu	Ser	Arg	Asp	Asn	Ser	Ser	Ala	Ser	Phe	Leu	Ala	Ser	Leu	
			730					735					740			
cga	gcc	ggt	gcc	gct	gtg	aac	act	gaa	gaa	gtg	aag	gct	gct	gca	tac	2371
Arg	Ala	Gly	Ala	Ala	Val	Asn	Thr	Glu	Glu	Val	Lys	Ala	Ala	Ala	Tyr	

745										750					755					
aag	cat	gtc	acg	gca	gtt	gat	agt	ggc	cta	tcc	aac	ctg	gag	ctg	cgc	2419				
Lys	His	Val	Thr	Ala	Val	Asp	Ser	Gly	Leu	Ser	Asn	Leu	Glu	Leu	Arg					
760			765					770												
cac	aag	att	gaa	ggc	ctc	aca	ttc	act	ggc	tct	tct	gaa	ctg	ctg	caa	2467				
His	Lys	Ile	Glu	Gly	Leu	Thr	Phe	Thr	Gly	Ser	Ser	Glu	Leu	Leu	Gln					
775			780					785												
gcc	tac	aac	gag	cag	tac	ttc	gaa	atc	ctt	gat	gat	gtg	tgg	gcg	aac	2515				
Ala	Tyr	Asn	Glu	Gln	Tyr	Phe	Glu	Ile	Leu	Asp	Asp	Val	Trp	Ala	Asn					
790		795					800			805										
ttc	tcc	ggc	gaa	atg	gca	cag	cag	atc	gtc	ctc	gga	ctg	ttc	cct	tca	2563				
Phe	Ser	Gly	Glu	Met	Ala	Gln	Gln	Ile	Val	Leu	Gly	Leu	Phe	Pro	Ser					
810				815					820											
tgg	aac	gtt	tcc	gaa	gag	ggc	ctc	aag	cgt	acc	gac	gag	ttt	ctt	gat	2611				
Trp	Asn	Val	Ser	Glu	Glu	Gly	Leu	Lys	Arg	Thr	Asp	Glu	Phe	Leu	Asp					
825			830					835												
ggc	gaa	cat	gtc	gca	ggc	atc	aag	cga	att	gtt	tcc	gaa	tcc	ctc	gac	2659				
Gly	Glu	His	Val	Ala	Gly	Ile	Lys	Arg	Ile	Val	Ser	Glu	Ser	Leu	Asp					
840			845					850												
cgc	act	gcc	cgt	gct	ctg	cgc	aac	cgt	gcg	gca	gat	gct	gcg			2701				
Arg	Thr	Ala	Arg	Ala	Leu	Arg	Asn	Arg	Ala	Ala	Asp	Ala	Ala							
855		860					865													
taagtaaaag attctcaatc cca															2724					

<210> 104

<211> 867

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Leu	Thr	Ser	Thr	Asn	Leu	Thr	Arg	Gln	Glu	Ala	Ser	Asp	Arg	Ser	Arg	
1				5					10					15		
Leu	Leu	Ser	Val	Glu	Asn	Tyr	Asp	Ile	Ala	Leu	Asp	Leu	Asn	Asn	Gly	
			20					25					30			
Asp	Glu	Phe	Phe	Ser	Ser	Ser	Thr	Val	Val	Ser	Phe	Thr	Val	Arg	Lys	
		35					40					45				
Ala	Gly	Asp	Thr	Phe	Ile	Asp	Leu	Arg	Ala	Ala	Ser	Val	Glu	Glu	Val	
	50					55					60					
Arg	Leu	Asp	Asn	Val	Ser	Ile	Lys	Asp	Glu	Ala	Leu	Thr	Leu	Gly	Lys	
65					70					75					80	
Asn	Gly	Tyr	Asp	Glu	Thr	Phe	Gly	Ile	Ala	Leu	Lys	Gly	Leu	Thr	Pro	
				85					90					95		
Gly	Ala	His	Thr	Leu	Arg	Val	Thr	Ala	Ser	Ile	Pro	Tyr	Ser	Arg	Thr	
			100					105					110			
Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr																

115					120					125					
Leu	Tyr	Thr	Gln	Phe	Glu	Thr	Ala	Asp	Ala	Lys	Arg	Met	Phe	Ala	Cys
130						135					140				
Phe	Asp	Gln	Pro	Asp	Leu	Lys	Ala	Thr	Tyr	Asp	Leu	Asn	Ile	Lys	Thr
145					150					155					160
Pro	Lys	Gly	Trp	Lys	Ile	Ile	Ser	Asn	Ser	Glu	Gln	Gln	Val	Ser	Thr
				165					170					175	
Gln	His	Thr	Asp	Tyr	Asp	Thr	His	Ile	Ser	Arg	Val	Asp	Tyr	Pro	Leu
			180					185					190		
Ser	Thr	Tyr	Leu	Ile	Ala	Val	Cys	Ala	Gly	Arg	Tyr	His	Glu	Val	Cys
		195					200					205			
Asp	Val	Trp	Lys	Gly	Thr	Leu	Thr	His	His	Ala	Glu	Thr	Pro	Ala	Asp
	210					215					220				
Gln	Pro	Thr	Glu	Leu	Thr	Val	Pro	Leu	Ala	Leu	Tyr	Cys	Arg	Ser	Ser
225					230					235					240
Leu	Ala	Lys	Asp	Leu	Asp	Ala	Val	Arg	Leu	Phe	Thr	Glu	Thr	Lys	Gln
				245					250					255	
Gly	Phe	Asp	Trp	Tyr	His	Arg	Asn	Phe	Gly	Val	Ala	Tyr	Pro	Phe	Gly
		260						265					270		
Lys	Tyr	Asp	Gln	Ile	Phe	Val	Pro	Glu	Phe	Asn	Ala	Gly	Ala	Met	Glu
		275					280					285			
Asn	Ala	Gly	Ala	Val	Thr	Ile	Arg	Asp	Glu	Tyr	Val	Phe	Ala	Ser	Lys
	290					295					300				
Ala	Thr	Arg	Tyr	Arg	Tyr	Glu	Arg	Arg	Ala	Glu	Thr	Ile	Leu	His	Glu
305					310					315					320
Leu	Ala	His	Met	Trp	Phe	Gly	Val	Leu	Val	Thr	Met	Gln	Trp	Trp	Asp
				325					330					335	
Asp	Leu	Trp	Leu	Asn	Glu	Ser	Phe	Ala	Thr	Trp	Ser	Ala	Ala	Ile	Ser
		340						345					350		
Gln	Ala	Glu	Glu	Thr	Glu	Tyr	Asn	Thr	Ala	Trp	Val	Thr	Phe	Ala	Asn
		355					360					365			
Val	Glu	Lys	Ser	Trp	Ala	Tyr	Gln	Gln	Asp	Gln	Leu	Pro	Ser	Thr	His
	370					375					380				
Pro	Val	Phe	Ser	Asp	Gly	Tyr	Asp	Ile	Glu	Thr	Val	Asp	Gln	Asn	Phe
385					390					395					400
Asp	Gly	Ile	Thr	Tyr	Ala	Lys	Gly	Ala	Ser	Val	Leu	Lys	Gln	Leu	Gln
				405					410					415	
Ala	Tyr	Val	Gly	Arg	Glu	Glu	Phe	Leu	Ala	Gly	Val	Arg	Arg	His	Phe
			420					425					430		
Ala	Asn	His	Ala	Trp	Gly	Asn	Ala	Ser	Phe	Asp	Asp	Leu	Leu	Gly	Ala
		435					440					445			

Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp
 450 455 460
 Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp
 465 470 475 480
 Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro
 485 490 495
 Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys
 500 505 510
 Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys
 515 520 525
 Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala
 530 535 540
 Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp
 545 550 555 560
 Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe
 565 570 575
 Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu Met
 580 585 590
 Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val Ala
 595 600 605
 Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile Leu
 610 615 620
 Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp Ala
 625 630 635 640
 Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly Ala
 645 650 655
 Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln Ala
 660 665 670
 Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg Asp
 675 680 685
 Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu Arg
 690 695 700
 Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala Val
 705 710 715 720
 Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala Ser
 725 730 735
 Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu Val
 740 745 750
 Lys Ala Ala Ala Tyr Lys His Val Thr Ala Val Asp Ser Gly Leu Ser
 755 760 765

Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly Ser
 770 775 780
 Ser Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu Asp
 785 790 795 800
 Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val Leu
 805 810 815
 Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg Thr
 820 825 830
 Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile Val
 835 840 845
 Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn Arg Ala Ala
 850 855 860
 Asp Ala Ala
 865

<210> 105
 <211> 1578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1578)
 <223> FRXA01014

<400> 105
 gat gat ctg tgg ctc aac gag tcc ttc gcc act tgg tcc gcg gca att 48
 Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile
 1 5 10 15
 tct cag gct gag gaa act gaa tac aac act gca tgg gtg act ttc gcc 96
 Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala
 20 25 30
 aat gtg gag aag tcg tgg gcg tac cag cag gat cag ctg cct tcc acc 144
 Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr
 35 40 45
 cac ccg gtg ttc tct gac gga tac gac att gag act gtc gac cag aac 192
 His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn
 50 55 60
 ttc gac ggc atc acc tac gca aag ggc gcc tcg gtg ctc aag cag ctg 240
 Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65 70 75 80
 cag gca tac gtt ggc cgt gag gaa ttc ctg gca ggc gta cgc agg cac 288
 Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
 85 90 95
 ttt gcc aac cac gca tgg ggc aac gcc agc ttt gat gat ctg ctc ggc 336
 Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
 100 105 110

gcc ctc gag cag tcc tcc ggc cgc gac ctc tcc gac tgg gca aac cag	384
Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln	
115 120 125	
tgg ctc aag acc acc ggc atc aac acc ctc ggc gca aag ttc acc acc	432
Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr	
130 135 140	
gac aac ggc aaa tac acc tcc ttc tcc gtc acc cag acc ggc gcc gcg	480
Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala	
145 150 155 160	
ccg ggt gcc ggt gag ctg cgg act cac cgc atc gcg gtg ggt ctt tat	528
Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr	
165 170 175	
aag ctt gtc gac gga tcc ctc aac cgc tac gca cga gta gaa ctt gac	576
Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp	
180 185 190	
tgc agt ggc gcg tcg aca agc gtt gaa gag atc gtt gga ctt gag cag	624
Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln	
195 200 205	
gct gac ttc gtg ctg gtc aac gat gat gat ctg acg tat gcg ctg ctg	672
Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu	
210 215 220	
gat ctg gat gat gat tca cgc aat ttt gtc atc gac aat att gat aag	720
Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys	
225 230 235 240	
ttc agc gac cct atg cct cgc acg ctg gtg tgg tcc gct gcg tgg gag	768
Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu	
245 250 255	
atg act cgc gct ggt cag atg aag gct cgt gat ttc atc gcg ctg gtt	816
Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val	
260 265 270	
gct cgt ggc gct gct gcg gaa act gaa att gct gtg ctg gag cgc att	864
Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile	
275 280 285	
ctc gcg cag gct acc tct gcg ctg aag agc tac gcc gac cca gcg tgg	912
Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp	
290 295 300	
gca gaa gca act gga aat gac ctg ctg gcc gat gct ttc ctt gag ggt	960
Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly	
305 310 315 320	
gct cgc tcc gca gaa cca gac tcc gac act cag ttg gcg ttc att cag	1008
Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln	
325 330 335	
gct ctg gca aaa gca acg ctc aat gat gct gct gcc gat tac ttc cgc	1056
Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg	
340 345 350	
gac att ctt gcc ggc aac gtc gaa ggc ctg acc gtg gat cct gac ctg	1104

Asp	Ile	Leu	Ala	Gly	Asn	Val	Glu	Gly	Leu	Thr	Val	Asp	Pro	Asp	Leu	
		355					360					365				
cgt	tgg	tgg	gca	ctg	act	gcg	ctt	atc	gcc	cgt	ggg	gac	atc	gag	gct	1152
Arg	Trp	Trp	Ala	Leu	Thr	Ala	Leu	Ile	Ala	Arg	Gly	Asp	Ile	Glu	Ala	
	370					375					380					
gtc	gaa	gat	gca	atc	gcc	gct	gaa	ctt	tcc	cgc	gac	aac	tcc	agt	gcc	1200
Val	Glu	Asp	Ala	Ile	Ala	Ala	Glu	Leu	Ser	Arg	Asp	Asn	Ser	Ser	Ala	
	385				390					395					400	
tcc	ttc	ctc	gca	tca	ctt	cga	gcc	ggg	gcc	gct	gtg	aac	act	gaa	gaa	1248
Ser	Phe	Leu	Ala	Ser	Leu	Arg	Ala	Gly	Ala	Ala	Val	Asn	Thr	Glu	Glu	
			405						410					415		
gtg	aag	gct	gct	gca	tac	aag	cat	gtc	ccg	gca	gtt	gat	agt	ggc	cta	1296
Val	Lys	Ala	Ala	Ala	Tyr	Lys	His	Val	Pro	Ala	Val	Asp	Ser	Gly	Leu	
			420					425					430			
tcc	aac	ctg	gag	ctg	cgc	cac	aag	att	gaa	ggc	ctc	aca	ttc	act	ggc	1344
Ser	Asn	Leu	Glu	Leu	Arg	His	Lys	Ile	Glu	Gly	Leu	Thr	Phe	Thr	Gly	
		435					440					445				
tct	ttt	gaa	ctg	ctg	caa	gcc	tac	aac	gag	cag	tac	ttc	gaa	atc	ctt	1392
Ser	Phe	Glu	Leu	Leu	Gln	Ala	Tyr	Asn	Glu	Gln	Tyr	Phe	Glu	Ile	Leu	
	450					455					460					
gat	gat	gtg	tgg	gca	aac	ttc	tcc	ggc	gaa	atg	gca	cag	cag	atc	gtc	1440
Asp	Asp	Val	Trp	Ala	Asn	Phe	Ser	Gly	Glu	Met	Ala	Gln	Gln	Ile	Val	
	465				470				475						480	
ctc	gga	ctg	ttc	cct	tca	tgg	aac	gtt	tcc	gaa	gag	ggg	ctc	aag	cgt	1488
Leu	Gly	Leu	Phe	Pro	Ser	Trp	Asn	Val	Ser	Glu	Glu	Gly	Leu	Lys	Arg	
				485					490					495		
acc	gac	gag	ttt	ctt	gat	ggc	gaa	cat	gtc	gca	ggc	atc	aag	cga	att	1536
Thr	Asp	Glu	Phe	Leu	Asp	Gly	Glu	His	Val	Ala	Gly	Ile	Lys	Arg	Ile	
			500					505					510			
gtt	tcc	gaa	tcc	ctc	gac	cgc	act	gcc	cgt	gct	ctg	cgc	aac			1578
Val	Ser	Glu	Ser	Leu	Asp	Arg	Thr	Ala	Arg	Ala	Leu	Arg	Asn			
		515					520					525				

<210> 106

<211> 526

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Asp	Asp	Leu	Trp	Leu	Asn	Glu	Ser	Phe	Ala	Thr	Trp	Ser	Ala	Ala	Ile	
1				5					10					15		
Ser	Gln	Ala	Glu	Glu	Thr	Glu	Tyr	Asn	Thr	Ala	Trp	Val	Thr	Phe	Ala	
			20					25					30			
Asn	Val	Glu	Lys	Ser	Trp	Ala	Tyr	Gln	Gln	Asp	Gln	Leu	Pro	Ser	Thr	
		35					40					45				
His	Pro	Val	Phe	Ser	Asp	Gly	Tyr	Asp	Ile	Glu	Thr	Val	Asp	Gln	Asn	
	50					55					60					

Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65 70 75 80
 Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
 85 90 95
 Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
 100 105 110
 Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln
 115 120 125
 Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr
 130 135 140
 Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala
 145 150 155 160
 Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr
 165 170 175
 Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp
 180 185 190
 Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln
 195 200 205
 Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu
 210 215 220
 Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys
 225 230 235 240
 Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu
 245 250 255
 Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val
 260 265 270
 Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile
 275 280 285
 Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp
 290 295 300
 Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly
 305 310 315 320
 Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln
 325 330 335
 Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg
 340 345 350
 Asp Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu
 355 360 365
 Arg Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala
 370 375 380

Val Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala
 385 390 395 400

Ser Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu
 405 410 415

Val Lys Ala Ala Ala Tyr Lys His Val Pro Ala Val Asp Ser Gly Leu
 420 425 430

Ser Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly
 435 440 445

Ser Phe Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu
 450 455 460

Asp Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val
 465 470 475 480

Leu Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg
 485 490 495

Thr Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile
 500 505 510

Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
 515 520 525

<210> 107
 <211> 964
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(964)
 <223> FRXA01018

<400> 107
 tcttaaagtt ttctagcaat ccacactagg cgcgaactat cgtggtgtca ttgcgcacct 60

tctaagggtgta gcgccccctc aaattttcaag gagcattaaa ttg acg tcc act aat 115
 Leu Thr Ser Thr Asn
 1 5

ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt 211
 Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
 25 30 35

tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt 259
 Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
 40 45 50

att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg 307
 Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
 55 60 65

tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag	355
Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu	
70 75 80 85	
acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg	403
Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu	
90 95 100	
cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac	451
Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His	
105 110 115	
cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt	499
Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe	
120 125 130	
gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac	547
Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp	
135 140 145	
ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag	595
Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys	
150 155 160 165	
atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac	643
Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr	
170 175 180	
gat acc cac att tcc cga gtg gac tat ccc ctc tcc acc tac ctg att	691
Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu Ser Thr Tyr Leu Ile	
185 190 195	
gcg gtg tgc gcg ggt cgt tac cac gag gtg tgc gat gtc tgg aag ggt	739
Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys Asp Val Trp Lys Gly	
200 205 210	
acg ctc acc cac cat gca gaa aca cct gcc gat cag cca act gag ctg	787
Thr Leu Thr His His Ala Glu Thr Pro Ala Asp Gln Pro Thr Glu Leu	
215 220 225	
act gtt ccg ctt gct ctc tac tgc cgc agt tct ttg gct aaa gat ctt	835
Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser Leu Ala Lys Asp Leu	
230 235 240 245	
gat gcg gtg cgt ctg ttt acc gaa acg aag cag ggc ttt gat tgg tac	883
Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln Gly Phe Asp Trp Tyr	
250 255 260	
cac cgc aac ttc ggt gtg gcg tac cca ttc ggc aag tac gat cag atc	931
His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly Lys Tyr Asp Gln Ile	
265 270 275	
ttc gtc cct gaa ttt aat gct ggc gcg atg gag	964
Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu	
280 285	

<210> 108

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

```

Leu Thr Ser Thr Asn Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg
 1             5             10             15

Leu Leu Ser Val Glu Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly
 20             25             30

Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys
 35             40             45

Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val
 50             55             60

Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys
 65             70             75             80

Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro
 85             90             95

Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr
100             105             110

Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr
115             120             125

Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys
130             135             140

Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr
145             150             155             160

Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr
165             170             175

Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu
180             185             190

Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys
195             200             205

Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp
210             215             220

Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser
225             230             235             240

Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln
245             250             255

Gly Phe Asp Trp Tyr His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly
260             265             270

Lys Tyr Asp Gln Ile Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
275             280             285

```

<210> 109

<211> 1383
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1360)
 <223> RXA01147

<400> 109

```

ataatgatca cctactttaa cggcttcagg tgacattgtg gattcgcatt gtggattcgg 60
gggcccgcgc tgtttccaag aatttggcta cccttggttct atg cat gta act gac 115
                                         Met His Val Thr Asp
                                         1           5

gat ttc tta agt ttt att gcc cta agc cca agt tcc tat cac gcg gcc 163
Asp Phe Leu Ser Phe Ile Ala Leu Ser Pro Ser Ser Tyr His Ala Ala
                        10                15                20

gcg gcg gtg gag cgc agg ttg ctc cat gag ggg ttc att cgt cag gaa 211
Ala Ala Val Glu Arg Arg Leu Leu His Glu Gly Phe Ile Arg Gln Glu
                        25                30                35

gat acc gat gaa tgg gat gcc cgc cct ggt ggg cat gtg acg gtg cgt 259
Asp Thr Asp Glu Trp Asp Ala Arg Pro Gly Gly His Val Thr Val Arg
                        40                45                50

ggg gga gca gta gtg gcg tgg tgg gtg cct gag gat gct tcg cca gat 307
Gly Gly Ala Val Val Ala Trp Trp Val Pro Glu Asp Ala Ser Pro Asp
                        55                60                65

tcc ggg ttc cgc atc att ggg tca cat act gat tca ccg ggt ttc aag 355
Ser Gly Phe Arg Ile Ile Gly Ser His Thr Asp Ser Pro Gly Phe Lys
                        70                75                80                85

tta aag ccc cgt ggg gat ctt tcc tca cac ggt tgg cag cag gcc ggc 403
Leu Lys Pro Arg Gly Asp Leu Ser Ser His Gly Trp Gln Gln Ala Gly
                        90                95                100

gtc gag gtt tac ggc gga ccg atc ctg cca agc tgg ctg gat cgc gag 451
Val Glu Val Tyr Gly Gly Pro Ile Leu Pro Ser Trp Leu Asp Arg Glu
                        105                110                115

ctg gcc tta gca ggc cgc att gtg ctt gcc gac ggg tcc gtc aag ctt 499
Leu Ala Leu Ala Gly Arg Ile Val Leu Ala Asp Gly Ser Val Lys Leu
                        120                125                130

gtc aac acc ggc ccg att ctg cgc atc ccg cac gtg gct att cat ttg 547
Val Asn Thr Gly Pro Ile Leu Arg Ile Pro His Val Ala Ile His Leu
                        135                140                145

gac cgt act gtt aat tcc caa ctc acc ctt aat cca cag cgt cac ctg 595
Asp Arg Thr Val Asn Ser Gln Leu Thr Leu Asn Pro Gln Arg His Leu
                        150                155                160                165

cag cct gtg ttt gct gtt ggt gag ccc gac gta tca att ctg gat gtc 643
Gln Pro Val Phe Ala Val Gly Glu Pro Asp Val Ser Ile Leu Asp Val
                        170                175                180

att gct ggt gct gcg gta gtg gat cct gca gat att gtc agc cat gat 691

```

Ile Ala Gly Ala Ala Val Val Asp Pro Ala Asp Ile Val Ser His Asp	
185 190 195	
ctg atc acg gtg gct acc caa gat gct gaa gta ttt ggc gca cat ggg	739
Leu Ile Thr Val Ala Thr Gln Asp Ala Glu Val Phe Gly Ala His Gly	
200 205 210	
gat ttc ttg gcg tct ggt cgc ctg gat aac ctg agc agc gtg cat cca	787
Asp Phe Leu Ala Ser Gly Arg Leu Asp Asn Leu Ser Ser Val His Pro	
215 220 225	
tcc atg act gca ttg att gcg gct tcg caa tct gac gat act ggt tcg	835
Ser Met Thr Ala Leu Ile Ala Ala Ser Gln Ser Asp Asp Thr Gly Ser	
230 235 240 245	
gat att ttg gtt ctt gct gca ttc gat cat gaa gaa gtg gga agt aat	883
Asp Ile Leu Val Leu Ala Ala Phe Asp His Glu Glu Val Gly Ser Asn	
250 255 260	
tcc acc tcg ggt gcc ggg gcc ccc ctg ttg gag gat gtg ctc aac cgt	931
Ser Thr Ser Gly Ala Gly Gly Pro Leu Leu Glu Asp Val Leu Asn Arg	
265 270 275	
act gct cgt gcg ttg ggt gca gat gaa gat gag cga cgc cgg atg ttt	979
Thr Ala Arg Ala Leu Gly Ala Asp Glu Asp Glu Arg Arg Arg Met Phe	
280 285 290	
aac cgt tcc acc atg gtc tca gct gac gcg gca cac tcc att cac ccc	1027
Asn Arg Ser Thr Met Val Ser Ala Asp Ala Ala His Ser Ile His Pro	
295 300 305	
aac ttc ccc gag aag cat gat caa gct aat tac ccc atc att ggt aaa	1075
Asn Phe Pro Glu Lys His Asp Gln Ala Asn Tyr Pro Ile Ile Gly Lys	
310 315 320 325	
ggg cct gta ttg aag gtc aac gcc aac cag cgc tac acc tcc gat gca	1123
Gly Pro Val Leu Lys Val Asn Ala Asn Gln Arg Tyr Thr Ser Asp Ala	
330 335 340	
gtc act tca ggc atg tgg atc agg gca tgt cag att gcc ggt gtg cca	1171
Val Thr Ser Gly Met Trp Ile Arg Ala Cys Gln Ile Ala Gly Val Pro	
345 350 355	
cac cag gtg ttt gcc ggc aac aac gat gtg ccg tgt ggt tcc acc atc	1219
His Gln Val Phe Ala Gly Asn Asn Asp Val Pro Cys Gly Ser Thr Ile	
360 365 370	
ggc ccg atc agt gcg act cgc ctg ggt atc gat tct gtc gat gtc ggt	1267
Gly Pro Ile Ser Ala Thr Arg Leu Gly Ile Asp Ser Val Asp Val Gly	
375 380 385	
att cca ttg ctg tcc atg cac tcc gca cgc gaa atg gcc gga gtg aag	1315
Ile Pro Leu Leu Ser Met His Ser Ala Arg Glu Met Ala Gly Val Lys	
390 395 400 405	
gat ctg atg tgg ttt gaa caa gcc ctg gaa gcc tat ctg gta aat	1360
Asp Leu Met Trp Phe Glu Gln Ala Leu Glu Ala Tyr Leu Val Asn	
410 415 420	
taacgccgag ttcaatcaag aca	1383

<210> 110
 <211> 420
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 110

```

Met His Val Thr Asp Asp Phe Leu Ser Phe Ile Ala Leu Ser Pro Ser
 1          5          10          15

Ser Tyr His Ala Ala Ala Val Glu Arg Arg Leu Leu His Glu Gly
          20          25          30

Phe Ile Arg Gln Glu Asp Thr Asp Glu Trp Asp Ala Arg Pro Gly Gly
          35          40          45

His Val Thr Val Arg Gly Gly Ala Val Val Ala Trp Trp Val Pro Glu
 50          55          60

Asp Ala Ser Pro Asp Ser Gly Phe Arg Ile Ile Gly Ser His Thr Asp
 65          70          75          80

Ser Pro Gly Phe Lys Leu Lys Pro Arg Gly Asp Leu Ser Ser His Gly
          85          90          95

Trp Gln Gln Ala Gly Val Glu Val Tyr Gly Gly Pro Ile Leu Pro Ser
          100          105          110

Trp Leu Asp Arg Glu Leu Ala Leu Ala Gly Arg Ile Val Leu Ala Asp
 115          120          125

Gly Ser Val Lys Leu Val Asn Thr Gly Pro Ile Leu Arg Ile Pro His
 130          135          140

Val Ala Ile His Leu Asp Arg Thr Val Asn Ser Gln Leu Thr Leu Asn
 145          150          155          160

Pro Gln Arg His Leu Gln Pro Val Phe Ala Val Gly Glu Pro Asp Val
          165          170          175

Ser Ile Leu Asp Val Ile Ala Gly Ala Ala Val Val Asp Pro Ala Asp
          180          185          190

Ile Val Ser His Asp Leu Ile Thr Val Ala Thr Gln Asp Ala Glu Val
 195          200          205

Phe Gly Ala His Gly Asp Phe Leu Ala Ser Gly Arg Leu Asp Asn Leu
 210          215          220

Ser Ser Val His Pro Ser Met Thr Ala Leu Ile Ala Ala Ser Gln Ser
 225          230          235          240

Asp Asp Thr Gly Ser Asp Ile Leu Val Leu Ala Ala Phe Asp His Glu
          245          250          255

Glu Val Gly Ser Asn Ser Thr Ser Gly Ala Gly Gly Pro Leu Leu Glu
          260          265          270

Asp Val Leu Asn Arg Thr Ala Arg Ala Leu Gly Ala Asp Glu Asp Glu
 275          280          285

```

Arg Arg Arg Met Phe Asn Arg Ser Thr Met Val Ser Ala Asp Ala Ala
 290 295 300
 His Ser Ile His Pro Asn Phe Pro Glu Lys His Asp Gln Ala Asn Tyr
 305 310 315 320
 Pro Ile Ile Gly Lys Gly Pro Val Leu Lys Val Asn Ala Asn Gln Arg
 325 330 335
 Tyr Thr Ser Asp Ala Val Thr Ser Gly Met Trp Ile Arg Ala Cys Gln
 340 345 350
 Ile Ala Gly Val Pro His Gln Val Phe Ala Gly Asn Asn Asp Val Pro
 355 360 365
 Cys Gly Ser Thr Ile Gly Pro Ile Ser Ala Thr Arg Leu Gly Ile Asp
 370 375 380
 Ser Val Asp Val Gly Ile Pro Leu Leu Ser Met His Ser Ala Arg Glu
 385 390 395 400
 Met Ala Gly Val Lys Asp Leu Met Trp Phe Glu Gln Ala Leu Glu Ala
 405 410 415
 Tyr Leu Val Asn
 420

<210> 111
 <211> 1260
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1237)
 <223> RXA01161

<400> 111
 tttttcgtga tcaacaatcc gctggcatag cgtccagcag atttgattct gacagtgtgg 60
 tttgatcgca cacctgccta ggctactagg gttggagact atg agt gat cct tca 115
 Met Ser Asp Pro Ser
 1 5
 aca aac aat ttc ccc aca tcg gta tat gca cag cgt ctt gcg gat gca 163
 Thr Asn Asn Phe Pro Thr Ser Val Tyr Ala Gln Arg Leu Ala Asp Ala
 10 15 20
 caa gaa ggc gca cgc aag gct ggc ttg aac ggt ttg atc atc ggt aca 211
 Gln Glu Gly Ala Arg Lys Ala Gly Leu Asn Gly Leu Ile Ile Gly Thr
 25 30 35
 ggc gca gaa ctt gcg tat cta acc ggc agc tgg atc tcc acc cat gag 259
 Gly Ala Glu Leu Ala Tyr Leu Thr Gly Ser Trp Ile Ser Thr His Glu
 40 45 50
 cgt cta acc gct ttg gtg atc ccc agc gaa gga acc gca acc att gtt 307
 Arg Leu Thr Ala Leu Val Ile Pro Ser Glu Gly Thr Ala Thr Ile Val
 55 60 65

ctt	ccc	gct	gta	gac	cgc	gga	gac	tta	gca	ctg	tct	gct	att	cca	gga	355
Leu	Pro	Ala	Val	Asp	Arg	Gly	Asp	Leu	Ala	Leu	Ser	Ala	Ile	Pro	Gly	
70					75					80					85	
cta	gac	atc	aat	gtg	gcc	gga	tgg	gtt	gat	ggc	gat	aat	gcc	cat	gag	403
Leu	Asp	Ile	Asn	Val	Ala	Gly	Trp	Val	Asp	Gly	Asp	Asn	Ala	His	Glu	
				90					95					100		
ttg	gcc	gta	gat	gct	ctc	ggg	gtt	tca	gag	ttc	gaa	gca	ttg	ggg	att	451
Leu	Ala	Val	Asp	Ala	Leu	Gly	Val	Ser	Glu	Phe	Glu	Ala	Leu	Gly	Ile	
			105					110					115			
ggg	tcc	tcc	atc	acg	gca	gat	cac	ctg	att	cct	atc	cag	aac	ctg	gtg	499
Gly	Ser	Ser	Ile	Thr	Ala	Asp	His	Leu	Ile	Pro	Ile	Gln	Asn	Leu	Val	
		120					125					130				
ggc	tcc	acc	tgc	cgc	atg	gag	ttg	gca	gtt	caa	gtg	ctg	aaa	gaa	ttg	547
Gly	Ser	Thr	Cys	Arg	Met	Glu	Leu	Ala	Val	Gln	Val	Leu	Lys	Glu	Leu	
	135					140					145					
ttt	gtc	tct	aaa	gac	gaa	gca	gag	atc	gag	cag	ctt	cgc	ggc	gca	ggg	595
Phe	Val	Ser	Lys	Asp	Glu	Ala	Glu	Ile	Glu	Gln	Leu	Arg	Gly	Ala	Gly	
150					155					160					165	
gca	gcc	att	gac	cgt	gtc	cac	gcc	aaa	gtc	ccg	gag	ctt	ctt	caa	gac	643
Ala	Ala	Ile	Asp	Arg	Val	His	Ala	Lys	Val	Pro	Glu	Leu	Leu	Gln	Asp	
				170					175					180		
gga	cgc	acc	gaa	gca	gag	gtt	gca	gca	cag	ctc	aac	gat	ctc	atc	ttg	691
Gly	Arg	Thr	Glu	Ala	Glu	Val	Ala	Ala	Gln	Leu	Asn	Asp	Leu	Ile	Leu	
			185					190					195			
gaa	gag	cac	tct	gag	gtg	gac	ttc	gtg	att	gtg	gga	tcc	gct	gaa	aac	739
Glu	Glu	His	Ser	Glu	Val	Asp	Phe	Val	Ile	Val	Gly	Ser	Ala	Glu	Asn	
		200					205					210				
ggc	gcg	aac	cct	cac	cac	ggg	ttc	tct	gac	cga	gtc	ctc	cgc	aat	ggc	787
Gly	Ala	Asn	Pro	His	His	Gly	Phe	Ser	Asp	Arg	Val	Leu	Arg	Asn	Gly	
	215					220					225					
gac	atc	gtg	gtg	gtt	gat	ata	gga	ggc	acc	ttc	ggc	cct	ggg	tac	cac	835
Asp	Ile	Val	Val	Val	Asp	Ile	Gly	Gly	Thr	Phe	Gly	Pro	Gly	Tyr	His	
230					235					240					245	
tct	gac	tgc	aca	cgc	acc	tac	att	gtg	ggc	gga	aac	cct	gac	gat	gcg	883
Ser	Asp	Cys	Thr	Arg	Thr	Tyr	Ile	Val	Gly	Gly	Asn	Pro	Asp	Asp	Ala	
				250					255					260		
gat	cca	gag	ttc	gct	aag	ttc	tac	caa	gtg	ctc	tac	gaa	gca	cag	ctc	931
Asp	Pro	Glu	Phe	Ala	Lys	Phe	Tyr	Gln	Val	Leu	Tyr	Glu	Ala	Gln	Leu	
			265					270					275			
gca	gcc	gtt	gcg	cat	gtt	cgc	cct	ggc	gtt	act	gca	gaa	tca	gtg	gac	979
Ala	Ala	Val	Ala	His	Val	Arg	Pro	Gly	Val	Thr	Ala	Glu	Ser	Val	Asp	
		280					285					290				
gct	gtt	gct	cgc	gat	cac	att	gct	gcg	gct	gga	tac	ggc	gaa	tac	ttc	1027
Ala	Val	Ala	Arg	Asp	His	Ile	Ala	Ala	Ala	Gly	Tyr	Gly	Glu	Tyr	Phe	
	295					300					305					
att	cac	cgc	aca	gga	cac	ggc	att	ggg	cta	tcc	acc	cat	gag	gag	cca	1075

Ile His Arg Thr Gly His Gly Ile Gly Leu Ser Thr His Glu Glu Pro
 310 315 320 325
 ttc atc atg gcg ggt aac tca ctc gtg ttg gaa gcc gga atg gcc ttt 1123
 Phe Ile Met Ala Gly Asn Ser Leu Val Leu Glu Ala Gly Met Ala Phe
 330 335 340
 tcc att gag cct ggc atc tac att gaa gga atc cac gga gcg cgc atc 1171
 Ser Ile Glu Pro Gly Ile Tyr Ile Glu Gly Ile His Gly Ala Arg Ile
 345 350 355
 gaa gac atc gtt gtg gtg aat gaa gac ggt tgt gaa acc ctc aac aac 1219
 Glu Asp Ile Val Val Asn Glu Asp Gly Cys Glu Thr Leu Asn Asn
 360 365 370
 cag ccc aag gaa ctg cgt tgagcattct tctcctaggc gga 1260
 Gln Pro Lys Glu Leu Arg
 375

<210> 112
 <211> 379
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 112
 Met Ser Asp Pro Ser Thr Asn Asn Phe Pro Thr Ser Val Tyr Ala Gln
 1 5 10 15
 Arg Leu Ala Asp Ala Gln Glu Gly Ala Arg Lys Ala Gly Leu Asn Gly
 20 25 30
 Leu Ile Ile Gly Thr Gly Ala Glu Leu Ala Tyr Leu Thr Gly Ser Trp
 35 40 45
 Ile Ser Thr His Glu Arg Leu Thr Ala Leu Val Ile Pro Ser Glu Gly
 50 55 60
 Thr Ala Thr Ile Val Leu Pro Ala Val Asp Arg Gly Asp Leu Ala Leu
 65 70 75 80
 Ser Ala Ile Pro Gly Leu Asp Ile Asn Val Ala Gly Trp Val Asp Gly
 85 90 95
 Asp Asn Ala His Glu Leu Ala Val Asp Ala Leu Gly Val Ser Glu Phe
 100 105 110
 Glu Ala Leu Gly Ile Gly Ser Ser Ile Thr Ala Asp His Leu Ile Pro
 115 120 125
 Ile Gln Asn Leu Val Gly Ser Thr Cys Arg Met Glu Leu Ala Val Gln
 130 135 140
 Val Leu Lys Glu Leu Phe Val Ser Lys Asp Glu Ala Glu Ile Glu Gln
 145 150 155 160
 Leu Arg Gly Ala Gly Ala Ala Ile Asp Arg Val His Ala Lys Val Pro
 165 170 175
 Glu Leu Leu Gln Asp Gly Arg Thr Glu Ala Glu Val Ala Ala Gln Leu
 180 185 190

Asn Asp Leu Ile Leu Glu Glu His Ser Glu Val Asp Phe Val Ile Val
 195 200 205
 Gly Ser Ala Glu Asn Gly Ala Asn Pro His His Gly Phe Ser Asp Arg
 210 215 220
 Val Leu Arg Asn Gly Asp Ile Val Val Val Asp Ile Gly Gly Thr Phe
 225 230 235 240
 Gly Pro Gly Tyr His Ser Asp Cys Thr Arg Thr Tyr Ile Val Gly Gly
 245 250 255
 Asn Pro Asp Asp Ala Asp Pro Glu Phe Ala Lys Phe Tyr Gln Val Leu
 260 265 270
 Tyr Glu Ala Gln Leu Ala Ala Val Ala His Val Arg Pro Gly Val Thr
 275 280 285
 Ala Glu Ser Val Asp Ala Val Ala Arg Asp His Ile Ala Ala Ala Gly
 290 295 300
 Tyr Gly Glu Tyr Phe Ile His Arg Thr Gly His Gly Ile Gly Leu Ser
 305 310 315 320
 Thr His Glu Glu Pro Phe Ile Met Ala Gly Asn Ser Leu Val Leu Glu
 325 330 335
 Ala Gly Met Ala Phe Ser Ile Glu Pro Gly Ile Tyr Ile Glu Gly Ile
 340 345 350
 His Gly Ala Arg Ile Glu Asp Ile Val Val Val Asn Glu Asp Gly Cys
 355 360 365
 Glu Thr Leu Asn Asn Gln Pro Lys Glu Leu Arg
 370 375

<210> 113
 <211> 980
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(957)
 <223> RXN01181

<400> 113
 tct gta ctg ctc gct cgc gac ttg gtg aac acc cct tca tca cac ctg 48
 Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
 1 5 10 15
 tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac 96
 Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30
 ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt 144
 Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45

ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt	192
Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg	
50 55 60	
ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct	240
Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala	
65 70 75 80	
ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag	288
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys	
85 90 95	
cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca	336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala	
100 105 110	
tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc	384
Ser Val Leu Ala Thr Ile Ile Ala Ala Arg Leu Asn Leu Ser Ile	
115 120 125	
aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac	432
Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp	
130 135 140	
gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc	480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser	
145 150 155 160	
gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc	528
Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala	
165 170 175	
att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca	576
Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala	
180 185 190	
acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt	624
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly	
195 200 205	
gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc	672
Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg	
210 215 220	
gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat	720
Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp	
225 230 235 240	
gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc	768
Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser	
245 250 255	
cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt	816
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val	
260 265 270	
ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac	864
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr	
275 280 285	
aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa	912

Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300

cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc 957
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

taaacgctag ttaaagatca gga 980

<210> 114

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
 1 5 10 15

Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45

Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
 50 55 60

Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65 70 75 80

Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
 85 90 95

Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
 100 105 110

Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
 115 120 125

Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140

Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160

Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175

Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190

Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205

Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220

Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240

Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
 245 250 255

Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
 260 265 270

Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
 275 280 285

Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300

Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

<210> 115

<211> 980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA01181

<400> 115

tct gta ctg ctc gct cgc gac ttg gtg aac acc cct tca tca cac ctg	48
Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu	
1 5 10 15	
tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac	96
Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His	
20 25 30	
ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt	144
Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly	
35 40 45	
ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt	192
Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg	
50 55 60	
ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct	240
Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala	
65 70 75 80	
ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag	288
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys	
85 90 95	
cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca	336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala	
100 105 110	
tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc	384
Ser Val Leu Ala Thr Ile Ile Ala Ala Arg Leu Asn Leu Ser Ile	
115 120 125	
aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac	432
Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp	

130	135	140	
gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc			480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser			
145	150	155	160
gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc			528
Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala			
	165	170	175
att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca			576
Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala			
	180	185	190
acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt			624
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly			
	195	200	205
gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc			672
Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg			
	210	215	220
gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat			720
Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp			
	225	230	235
gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc			768
Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser			
	245	250	255
cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt			816
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val			
	260	265	270
ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac			864
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr			
	275	280	285
aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa			912
Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln			
	290	295	300
cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc			957
Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser			
	305	310	315
taaacgctag ttaaagatca gga			980

<210> 116

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Ser	Val	Leu	Leu	Ala	Arg	Asp	Leu	Val	Asn	Thr	Pro	Ser	Ser	His	Leu
1				5					10					15	

Tyr	Pro	Glu	Ser	Tyr	Ser	Val	Ile	Ala	Ser	Asn	Glu	Ala	Ser	Lys	His
		20						25					30		

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45
 Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
 50 55 60
 Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65 70 75 80
 Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
 85 90 95
 Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
 100 105 110
 Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
 115 120 125
 Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140
 Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160
 Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175
 Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190
 Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205
 Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220
 Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240
 Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
 245 250 255
 Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
 260 265 270
 Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
 275 280 285
 Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

<210> 117

<211> 2127

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2104)

<223> RXN01277

<400> 117

```

tactactcgg ttcacgttta cgtcggctga tccaattgga ggcgccctcg gaagccgcoct 60

taaaaaacct gccggtcaaa agatcactaa cctgaacttc atg act gat tac acg 115
                                   Met Thr Asp Tyr Thr
                                   1 5

ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa 163
Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
      10      15      20

tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
      25      30      35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
      40      45      50

tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
      55      60      65

cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa 355
Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
      70      75      80      85

agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg 403
Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
      90      95      100

gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg 451
Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
      105      110      115

ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat 499
Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
      120      125      130

gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat 547
Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
      135      140      145

gat tcg ccg ttt gaa ttg aag gag gcg aag tcc gat gtc acg tgg gtt 595
Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser Asp Val Thr Trp Val
      150      155      160      165

gat ctg gat acg ttg ctg gtg ggc acg gat acc ggc gag ggg tca ctg 643
Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr Gly Glu Gly Ser Leu
      170      175      180

acg gat tct ggg tac ccg gcg cgg gtg ctc acg tgg aag cgt ggg act 691
Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr Trp Lys Arg Gly Thr
      185      190      195

ccg ctt gag cag gcg gag ttg ttc ttt gag ggg tcg cgt cag gat gtg 739
Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly Ser Arg Gln Asp Val

```

200						205						210						
gcg	act	cat	gcg	tgg	cgg	gat	tca	aca	cct	ggt	ttt	gag	cgg	acg	ttt	787		
Ala	Thr	His	Ala	Trp	Arg	Asp	Ser	Thr	Pro	Gly	Phe	Glu	Arg	Thr	Phe			
215						220						225						
gtg	tca	agg	tcg	ttg	gat	ttc	tat	aat	tcg	gag	acg	tcg	ctg	gaa	acc	835		
Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu	Thr	Ser	Leu	Glu	Thr			
230						235						240				245		
gag	ggt	ggc	ctg	gtc	aag	ctt	gat	gtg	ccg	acc	gat	tgc	gat	gtc	att	883		
Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr	Asp	Cys	Asp	Val	Ile			
250						255						260						
gtg	aag	aag	cag	tgg	att	ttt	gtg	agt	cct	cgg	acg	gat	ttc	gct	ggg	931		
Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg	Thr	Asp	Phe	Ala	Gly			
265						270						275						
att	cca	gca	ggt	ggc	ttg	gga	gtg	ctg	ctg	tta	aag	gag	ttc	ctt	gag	979		
Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu	Lys	Glu	Phe	Leu	Glu			
280						285						290						
ggc	ggg	cgc	gat	ttt	cag	cct	gtg	ttt	acg	cct	act	gag	tcg	acg	tcg	1027		
Gly	Gly	Arg	Asp	Phe	Gln	Pro	Val	Phe	Thr	Pro	Thr	Glu	Ser	Thr	Ser			
295						300						305						
ctg	cag	gga	ttg	gcc	acg	aca	aag	aat	ttc	ctg	gtt	tta	acg	ctc	ctt	1075		
Leu	Gln	Gly	Leu	Ala	Thr	Thr	Lys	Asn	Phe	Leu	Val	Leu	Thr	Leu	Leu			
310						315						320				325		
aat	aat	gtc	tcc	aca	gaa	atc	gtc	aca	gtg	ccg	ctc	aat	gat	ccg	aca	1123		
Asn	Asn	Val	Ser	Thr	Glu	Ile	Val	Thr	Val	Pro	Leu	Asn	Asp	Pro	Thr			
330						335						340						
acg	gag	cat	gaa	cac	att	gac	ctc	cca	gag	cat	gtc	acc	gcg	cat	gtg	1171		
Thr	Glu	His	Glu	His	Ile	Asp	Leu	Pro	Glu	His	Val	Thr	Ala	His	Val			
345						350						355						
gtt	gct	acc	tcc	ccg	ttg	gat	ggc	gat	gaa	att	tgg	gtg	cag	gca	gcg	1219		
Val	Ala	Thr	Ser	Pro	Leu	Asp	Gly	Asp	Glu	Ile	Trp	Val	Gln	Ala	Ala			
360						365						370						
agt	ttc	acc	gaa	gcg	cca	acg	ttg	ctg	cgt	gcg	gag	ctg	cct	ggt	gcg	1267		
Ser	Phe	Thr	Glu	Ala	Pro	Thr	Leu	Leu	Arg	Ala	Glu	Leu	Pro	Gly	Ala			
375						380						385						
ctt	gag	gct	gtg	aag	aag	gcg	ccg	ttg	cag	ttt	gaa	aat	gct	ggt	cag	1315		
Leu	Glu	Ala	Val	Lys	Lys	Ala	Pro	Leu	Gln	Phe	Glu	Asn	Ala	Gly	Gln			
390						395						400				405		
gag	act	cgt	cag	cat	tgg	gca	acc	tcg	gcg	gat	gga	acg	aag	att	ccg	1363		
Glu	Thr	Arg	Gln	His	Trp	Ala	Thr	Ser	Ala	Asp	Gly	Thr	Lys	Ile	Pro			
410						415						420						
tac	ttt	att	aca	gga	gcc	ttc	gag	gag	gaa	cca	caa	aac	acc	ctg	gtc	1411		
Tyr	Phe	Ile	Thr	Gly	Ala	Phe	Glu	Glu	Glu	Pro	Gln	Asn	Thr	Leu	Val			
425						430						435						
cac	gcc	tac	ggc	ggc	ttc	gag	gtt	tcc	ctt	acc	cca	agc	cac	tcc	ccg	1459		
His	Ala	Tyr	Gly	Gly	Phe	Glu	Val	Ser	Leu	Thr	Pro	Ser	His	Ser	Pro			
440						445						450						

acc cgc ggc atc gca tgg ttg gaa aag ggc tac tac ttt gtg gaa gcc	1507
Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala	
455 460 465	
aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca	1555
Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala	
470 475 480 485	
acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc	1603
Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu	
490 495 500	
gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att	1651
Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile	
505 510 515	
cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag	1699
Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln	
520 525 530	
tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat	1747
Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp	
535 540 545	
atg ttg cgc tat cac acc tgg tca gcg ggt gct tcg tgg atg gcg gag	1795
Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala Ser Trp Met Ala Glu	
550 555 560 565	
tac ggc aac cct gac gat ccg gag gaa cgg gcg gtg att gag cag tac	1843
Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala Val Ile Glu Gln Tyr	
570 575 580	
tcg ccg gtg cag gcg gtg gtg ggc gtc gag aag cga att tat cca ccc	1891
Ser Pro Val Gln Ala Val Val Gly Val Glu Lys Arg Ile Tyr Pro Pro	
585 590 595	
gca ttg gtg acg acc tca acc cgg gac gac cgc gtc cac ccc gcg cac	1939
Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg Val His Pro Ala His	
600 605 610	
gcg cgc ctt ttt gct caa gct ttg ctt gat gcg ggc cag gcc gtg gat	1987
Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala Gly Gln Ala Val Asp	
615 620 625	
tac tac gaa aac acc gag ggc ggc cat gcc ggc gcg gcg gat aac aag	2035
Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly Ala Ala Asp Asn Lys	
630 635 640 645	
cag acc gcg ttt gtg gaa tcg ctg atc tac acc tgg atc gag aag act	2083
Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr Trp Ile Glu Lys Thr	
650 655 660	
ttg gat cag cag ggt agc att taatacctat gattatgcga agg	2127
Leu Asp Gln Gln Gly Ser Ile	
665	

<210> 118
 <211> 668
 <212> PRT

<213> Corynebacterium glutamicum

<400> 118

Met Thr Asp Tyr Thr Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu
 1 5 10 15
 Ala Trp Ala Glu Lys Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser
 20 25 30
 Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
 35 40 45
 Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
 50 55 60
 Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
 65 70 75 80
 Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
 85 90 95
 Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
 100 105 110
 Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
 115 120 125
 Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
 130 135 140
 Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
 145 150 155 160
 Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
 165 170 175
 Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
 180 185 190
 Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
 195 200 205
 Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
 210 215 220
 Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
 225 230 235 240
 Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
 245 250 255
 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
 260 265 270
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
 275 280 285
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
 290 295 300
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu

305	310	315	320
Val Leu Thr Leu	Leu Asn Asn Val	Ser Thr Glu Ile Val Thr	Val Pro
	325	330	335
Leu Asn Asp Pro	Thr Thr Glu His	Glu His Ile Asp Leu Pro	Glu His
	340	345	350
Val Thr Ala His	Val Val Ala Thr	Ser Pro Leu Asp Gly Asp	Glu Ile
	355	360	365
Trp Val Gln Ala	Ala Ser Phe Thr	Glu Ala Pro Thr Leu Leu Arg	Ala
	370	375	380
Glu Leu Pro Gly	Ala Leu Glu Ala	Val Lys Lys Ala Pro Leu Gln	Phe
	385	390	400
Glu Asn Ala Gly	Gln Glu Thr Arg	Gln His Trp Ala Thr Ser	Ala Asp
	405	410	415
Gly Thr Lys Ile	Pro Tyr Phe Ile	Thr Gly Ala Phe Glu Glu Glu	Pro
	420	425	430
Gln Asn Thr Leu	Val His Ala Tyr	Gly Gly Phe Glu Val Ser Leu Thr	
	435	440	445
Pro Ser His Ser	Pro Thr Arg Gly	Ile Ala Trp Leu Glu Lys Gly Tyr	
	450	455	460
Tyr Phe Val Glu	Ala Asn Leu Arg	Gly Gly Gly Glu Phe Gly Pro Glu	
	465	470	475
Trp His Ser Gln	Ala Thr Lys Leu Asn	Arg Met Lys Val Trp Glu Asp	
	485	490	495
His Arg Ala Val	Leu Ala Asp Leu Val	Glu Arg Gly Tyr Ala Thr Pro	
	500	505	510
Glu Gln Ile Ala	Ile Arg Gly Gly	Ser Asn Gly Gly Leu Leu Thr Ser	
	515	520	525
Gly Ala Leu Thr	Gln Tyr Pro Glu	Ala Phe Gly Ala Ala Val Val Gln	
	530	535	540
Val Pro Leu Ala	Asp Met Leu Arg Tyr	His Thr Trp Ser Ala Gly Ala	
	545	550	555
Ser Trp Met Ala	Glu Tyr Gly Asn Pro	Asp Asp Pro Glu Glu Arg Ala	
	565	570	575
Val Ile Glu Gln	Tyr Ser Pro Val	Gln Ala Val Val Gly Val Glu Lys	
	580	585	590
Arg Ile Tyr Pro	Pro Ala Leu Val	Thr Thr Ser Thr Arg Asp Asp Arg	
	595	600	605
Val His Pro Ala	His Ala Arg Leu Phe	Ala Gln Ala Leu Leu Asp Ala	
	610	615	620
Gly Gln Ala Val	Asp Tyr Tyr Glu	Asn Thr Glu Gly Gly His Ala Gly	
	625	630	635
			640

Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr
 645 650 655

Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile
 660 665

<210> 119
 <211> 1812
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1789)
 <223> FRXA01277

<400> 119
 tactactcgg ttcacgttta cgtcggctga tccaattgga ggcgccctcg gaagccgcct 60
 taaaaaacct gccgggtcaaa agatcactaa cctgaacttc atg act gat tac acg 115
 Met Thr Asp Tyr Thr
 1 5
 ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa 163
 Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
 10 15 20
 tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
 Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
 25 30 35
 ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
 Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
 40 45 50
 tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
 Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
 55 60 65
 cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa 355
 Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
 70 75 80 85
 agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg 403
 Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
 90 95 100
 gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg 451
 Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
 105 110 115
 ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat 499
 Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
 120 125 130
 gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat 547
 Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
 135 140 145

gat	tcg	ccg	ttt	gaa	ttg	aag	gag	gcg	aag	tcc	gat	gtc	acg	tgg	gtt	595
Asp	Ser	Pro	Phe	Glu	Leu	Lys	Glu	Ala	Lys	Ser	Asp	Val	Thr	Trp	Val	
150					155					160					165	
gat	ctg	gat	acg	ttg	ctg	gtg	ggc	acg	gat	acc	ggc	gag	ggg	tca	ctg	643
Asp	Leu	Asp	Thr	Leu	Leu	Val	Gly	Thr	Asp	Thr	Gly	Glu	Gly	Ser	Leu	
				170					175					180		
acg	gat	tct	ggg	tac	ccg	gcg	cgg	gtg	ctc	acg	tgg	aag	cgt	ggg	act	691
Thr	Asp	Ser	Gly	Tyr	Pro	Ala	Arg	Val	Leu	Thr	Trp	Lys	Arg	Gly	Thr	
			185					190					195			
ccg	ctt	gag	cag	gcg	gag	ttg	ttc	ttt	gag	ggg	tcg	cgt	cag	gat	gtg	739
Pro	Leu	Glu	Gln	Ala	Glu	Leu	Phe	Phe	Glu	Gly	Ser	Arg	Gln	Asp	Val	
		200					205					210				
gcg	act	cat	gcg	tgg	cgg	gat	tca	aca	cct	ggt	ttt	gag	cgg	acg	ttt	787
Ala	Thr	His	Ala	Trp	Arg	Asp	Ser	Thr	Pro	Gly	Phe	Glu	Arg	Thr	Phe	
	215					220					225					
gtg	tca	agg	tcg	ttg	gat	ttc	tat	aat	tcg	gag	acg	tcg	ctg	gaa	acc	835
Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu	Thr	Ser	Leu	Glu	Thr	
230					235					240					245	
gag	ggt	ggc	ctg	gtc	aag	ctt	gat	gtg	ccg	acc	gat	tgc	gat	gtc	att	883
Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr	Asp	Cys	Asp	Val	Ile	
				250					255					260		
gtg	aag	aag	cag	tgg	att	ttt	gtg	agt	cct	cgg	acg	gat	ttc	gct	ggg	931
Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg	Thr	Asp	Phe	Ala	Gly	
			265					270					275			
att	cca	gca	ggt	ggc	ttg	gga	gtg	ctg	ctg	tta	aag	gag	ttc	ctt	gag	979
Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu	Lys	Glu	Phe	Leu	Glu	
		280					285					290				
ggc	ggg	cgc	gat	ttt	cag	cct	gtg	ttt	acg	cct	act	gag	tcg	acg	tcg	1027
Gly	Gly	Arg	Asp	Phe	Gln	Pro	Val	Phe	Thr	Pro	Thr	Glu	Ser	Thr	Ser	
	295					300					305					
ctg	cag	gga	ttg	gcc	acg	aca	aag	aat	ttc	ctg	gtt	tta	acg	ctc	ctt	1075
Leu	Gln	Gly	Leu	Ala	Thr	Thr	Lys	Asn	Phe	Leu	Val	Leu	Thr	Leu	Leu	
310					315					320					325	
aat	aat	gtc	tcc	aca	gaa	atc	gtc	aca	gtg	ccg	ctc	aat	gat	ccg	aca	1123
Asn	Asn	Val	Ser	Thr	Glu	Ile	Val	Thr	Val	Pro	Leu	Asn	Asp	Pro	Thr	
				330					335					340		
acg	gag	cat	gaa	cac	att	gac	ctc	cca	gag	cat	gtc	acc	gcg	cat	gtg	1171
Thr	Glu	His	Glu	His	Ile	Asp	Leu	Pro	Glu	His	Val	Thr	Ala	His	Val	
			345					350					355			
gtt	gct	acc	tcc	ccg	ttg	gat	ggc	gat	gaa	att	tgg	gtg	cag	gca	gcg	1219
Val	Ala	Thr	Ser	Pro	Leu	Asp	Gly	Asp	Glu	Ile	Trp	Val	Gln	Ala	Ala	
		360					365					370				
agt	ttc	acc	gaa	gcg	cca	acg	ttg	ctg	cgt	gcg	gag	ctg	cct	ggt	gcg	1267
Ser	Phe	Thr	Glu	Ala	Pro	Thr	Leu	Leu	Arg	Ala	Glu	Leu	Pro	Gly	Ala	
	375					380					385					
ctt	gag	gct	gtg	aag	aag	gcg	ccg	ttg	cag	ttt	gaa	aat	gct	ggt	cag	1315

Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln
 390 395 400 405
 gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg 1363
 Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro
 410 415 420
 tac ttt att aca gga gcc ttc gag gag gaa cca caa aac acc ctg gtc 1411
 Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val
 425 430 435
 cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg 1459
 His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro
 440 445 450
 acc cgc ggc atc gca tgg ttg gaa aag ggc tac tac ttt gtg gaa gcc 1507
 Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala
 455 460 465
 aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca 1555
 Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala
 470 475 480 485
 acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc 1603
 Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu
 490 495 500
 gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att 1651
 Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile
 505 510 515
 cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag 1699
 Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln
 520 525 530
 tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat 1747
 Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp
 535 540 545
 atg ttg cgc tat cac acc tgg tca gcg ggt acc tcg tgg atg 1789
 Met Leu Arg Tyr His Thr Trp Ser Ala Gly Thr Ser Trp Met
 550 555 560
 taggtgtcgg caaccatggg aac 1812

<210> 120

<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Met Thr Asp Tyr Thr Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu
 1 5 10 15

Ala Trp Ala Glu Lys Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser
 20 25 30

Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
 35 40 45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
 50 55 60
 Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
 65 70 75 80
 Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
 85 90 95
 Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
 100 105 110
 Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
 115 120 125
 Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
 130 135 140
 Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
 145 150 155 160
 Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
 165 170 175
 Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
 180 185 190
 Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
 195 200 205
 Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
 210 215 220
 Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
 225 230 235 240
 Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
 245 250 255
 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
 260 265 270
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
 275 280 285
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
 290 295 300
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
 305 310 315 320
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
 325 330 335
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
 340 345 350
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala

```
<210> 121
<211> 526
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(526)
<223> RXA01914
```

```

<400> 121
ggttttgagg aatggctagg cttgttaaaa gttagtttca atttgatgcc tcccccaacc 60

aaagcggaga cacaacttca acgagaggac tcagctttca  atg gcg aaa aat gcc 115
                                         Met Ala Lys Asn Ala
                                         1           5

tac agc aca aca gca cca acc aag gtg tcc aag gat gcc act ctt cca 163
Tyr Ser Thr Thr Ala Pro Thr Lys Val Ser Lys Asp Ala Thr Leu Pro
                        10                        15                        20

gtt cgt gga acg gtc gct gaa ctc aag ctc gaa aag aag ttg cca aag 211

```

Val	Arg	Gly	Thr	Val	Ala	Glu	Leu	Lys	Leu	Glu	Lys	Lys	Leu	Pro	Lys		
			25					30					35				
aag	att	gat	gcc	atc	atc	gtc	gcg	att	ttt	gaa	ggc	gaa	gat	tcc	atc	259	
Lys	Ile	Asp	Ala	Ile	Ile	Val	Ala	Ile	Phe	Glu	Gly	Glu	Asp	Ser	Ile		
		40					45					50					
gaa	ctc	gcc	ggc	ggc	gaa	atc	ctc	gat	ttc	atc	ttc	agt	acc	gag	cag	307	
Glu	Leu	Ala	Gly	Gly	Glu	Ile	Leu	Asp	Phe	Ile	Phe	Ser	Thr	Glu	Gln		
	55					60					65						
cag	gcc	gac	atc	ctc	act	cag	ctc	gaa	gct	gtc	ggc	gca	aag	gcc	acc	355	
Gln	Ala	Asp	Ile	Leu	Thr	Gln	Leu	Glu	Ala	Val	Gly	Ala	Lys	Ala	Thr		
	70				75				80						85		
gca	aac	agc	atc	acc	cgc	gtc	cca	ggc	acc	gac	gtt	gcg	cct	gtc	att	403	
Ala	Asn	Ser	Ile	Thr	Arg	Val	Pro	Gly	Thr	Asp	Val	Ala	Pro	Val	Ile		
				90					95					100			
gcg	gtt	ggt	ttg	ggc	aag	gct	gat	ttg	ctt	gac	gac	gag	acc	ctc	cgc	451	
Ala	Val	Gly	Leu	Gly	Lys	Ala	Asp	Leu	Leu	Asp	Asp	Glu	Thr	Leu	Arg		
			105					110					115				
cgc	gct	tcc	ggc	acg	gcg	gcc	cgc	tcc	ctc	ggt	ggt	ttt	gaa	aat	gtc	499	
Arg	Ala	Ser	Gly	Thr	Ala	Ala	Arg	Ser	Leu	Gly	Gly	Phe	Glu	Asn	Val		
		120					125					130					
gcc	acc	acc	att	ggc	gat	ttg	gga	ctt								526	
Ala	Thr	Thr	Ile	Gly	Asp	Leu	Gly	Leu									
	135					140											

<210> 122

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Met	Ala	Lys	Asn	Ala	Tyr	Ser	Thr	Thr	Ala	Pro	Thr	Lys	Val	Ser	Lys		
1				5					10					15			
Asp	Ala	Thr	Leu	Pro	Val	Arg	Gly	Thr	Val	Ala	Glu	Leu	Lys	Leu	Glu		
			20					25					30				
Lys	Lys	Leu	Pro	Lys	Lys	Ile	Asp	Ala	Ile	Ile	Val	Ala	Ile	Phe	Glu		
		35					40					45					
Gly	Glu	Asp	Ser	Ile	Glu	Leu	Ala	Gly	Gly	Glu	Ile	Leu	Asp	Phe	Ile		
	50					55					60						
Phe	Ser	Thr	Glu	Gln	Gln	Ala	Asp	Ile	Leu	Thr	Gln	Leu	Glu	Ala	Val		
	65				70					75					80		
Gly	Ala	Lys	Ala	Thr	Ala	Asn	Ser	Ile	Thr	Arg	Val	Pro	Gly	Thr	Asp		
				85					90					95			
Val	Ala	Pro	Val	Ile	Ala	Val	Gly	Leu	Gly	Lys	Ala	Asp	Leu	Leu	Asp		
		100					105						110				
Asp	Glu	Thr	Leu	Arg	Arg	Ala	Ser	Gly	Thr	Ala	Ala	Arg	Ser	Leu	Gly		
	115						120					125					

Gly Phe Glu Asn Val Ala Thr Thr Ile Gly Asp Leu Gly Leu
 130 135 140

<210> 123
 <211> 1497
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1474)
 <223> RXA02048

<400> 123
 gcgcggcgga taacaagcag accgcgtttg tggaatcgct gatctacacc tggatcgaaa 60
 agactttgga tcagcagggt agcatttaac acctatgatt atg cga agg ctg cgc 115
 Met Arg Arg Leu Arg
 1 5
 tcc acc ccg gtc cct ggt aca cgc gat tcc tac aca gga att gat ttc 163
 Ser Thr Pro Val Pro Gly Thr Arg Asp Ser Tyr Thr Gly Ile Asp Phe
 10 15 20
 aac tta ggc ttc cac atc cga cgc tac gag ctt gat ctc acc tac cgc 211
 Asn Leu Gly Phe His Ile Arg Arg Tyr Glu Leu Asp Leu Thr Tyr Arg
 25 30 35
 gta gca ccc aac ctg ctc atg ggc acc gca acg ctg cac atg gat aat 259
 Val Ala Pro Asn Leu Leu Met Gly Thr Ala Thr Leu His Met Asp Asn
 40 45 50
 tac cgt gcg ctc gac gcg ctg acc ctg gac ctc ggc ggc agc ctg cgc 307
 Tyr Arg Ala Leu Asp Ala Leu Thr Leu Asp Leu Gly Gly Ser Leu Arg
 55 60 65
 gtg gaa aaa gtc acc gcc aaa ggc acc gcc ggc acc cac atc caa gtc 355
 Val Glu Lys Val Thr Ala Lys Gly Thr Ala Gly Thr His Ile Gln Val
 70 75 80 85
 gcg cgc ttc cgc cac gcc ggc cgc aaa ctg cgc atc acc ttc cgc aac 403
 Ala Arg Phe Arg His Ala Gly Arg Lys Leu Arg Ile Thr Phe Arg Asn
 90 95 100
 caa atc ccg gtt gac cag gaa ttt tca ctc acc atc cgc tac cgc ggc 451
 Gln Ile Pro Val Asp Gln Glu Phe Ser Leu Thr Ile Arg Tyr Arg Gly
 105 110 115
 aac ccg cgc ccc ctg cgc agc gaa tgg ggc atg atc ggc tgg gaa gag 499
 Asn Pro Arg Pro Leu Arg Ser Glu Trp Gly Met Ile Gly Trp Glu Glu
 120 125 130
 ctc gac aac ggc gcc ctc gtc gcc gcc cag cca aac ggc gcg ccg agc 547
 Leu Asp Asn Gly Ala Leu Val Ala Ala Gln Pro Asn Gly Ala Pro Ser
 135 140 145
 tgg ttc ccc tgc gac gac acg ccc gac gag aag gcg ctt ttc gac gtc 595
 Trp Phe Pro Cys Asp Asp Thr Pro Asp Glu Lys Ala Leu Phe Asp Val
 150 155 160 165

cac ttc cac acc gac aac gga tac gcc gcc att atc acc ggt gat tta	643
His Phe His Thr Asp Asn Gly Tyr Ala Ala Ile Ile Thr Gly Asp Leu	
170 175 180	
atc tca aaa cac gtc agt ggc agc atg acc acc tgg cac tac caa tcc	691
Ile Ser Lys His Val Ser Gly Ser Met Thr Thr Trp His Tyr Gln Ser	
185 190 195	
cgc gaa ccc atg gcc acc tac ctc gca gcc gtc cac gtc gga gaa tac	739
Arg Glu Pro Met Ala Thr Tyr Leu Ala Ala Val His Val Gly Glu Tyr	
200 205 210	
gac act gta tcc ctg ggc gtt tgc gaa tgc ggc gtt gtg gtg gag gcg	787
Asp Thr Val Ser Leu Gly Val Ser Glu Ser Gly Val Val Val Glu Ala	
215 220 225	
tat gtg cct gtg ggg gat gcg gcc ttg cgg gct cgg att ttg gag gac	835
Tyr Val Pro Val Gly Asp Ala Ala Leu Arg Ala Arg Ile Leu Glu Asp	
230 235 240 245	
ttt gcc aaa caa gtc gac atg tta gac gcc tac gaa aaa ctc ttc ggc	883
Phe Ala Lys Gln Val Asp Met Leu Asp Ala Tyr Glu Lys Leu Phe Gly	
250 255 260	
ccc tac cca ttc cgc agc tac cgc gta gtc atc acc gaa gac gaa ctc	931
Pro Tyr Pro Phe Arg Ser Tyr Arg Val Val Ile Thr Glu Asp Glu Leu	
265 270 275	
gaa atc cca ctc gaa gcc caa ggc ctc tcc agc ttc gga gcc aac cac	979
Glu Ile Pro Leu Glu Ala Gln Gly Leu Ser Ser Phe Gly Ala Asn His	
280 285 290	
gcc acc ggc gaa gga acc tgg gaa cga ctc atc gcc cac gaa ctc tcc	1027
Ala Thr Gly Glu Gly Thr Trp Glu Arg Leu Ile Ala His Glu Leu Ser	
295 300 305	
cac cag tgg ttt ggc aac tca ctc ggc ctc gcc caa tgg aac gac atc	1075
His Gln Trp Phe Gly Asn Ser Leu Gly Leu Ala Gln Trp Asn Asp Ile	
310 315 320 325	
tgg ctc aac gaa ggc ttc gcc tgt tac gcg gaa tgg ctc tgg ttt gag	1123
Trp Leu Asn Glu Gly Phe Ala Cys Tyr Ala Glu Trp Leu Trp Phe Glu	
330 335 340	
gca gct gga gtt aag tgc gct gcg gaa agt gcg ttg gaa ttc tat cga	1171
Ala Ala Gly Val Lys Ser Ala Ala Glu Ser Ala Leu Glu Phe Tyr Arg	
345 350 355	
ggc ctg gag gcg ctg ccg aag gat att ttg ctg gcc aac ccc ggc gcg	1219
Gly Leu Glu Ala Leu Pro Lys Asp Ile Leu Leu Ala Asn Pro Gly Ala	
360 365 370	
aag gat atg ttc gac gac cgc gtc tac aag cgc ggc gct ctg act gtc	1267
Lys Asp Met Phe Asp Asp Arg Val Tyr Lys Arg Gly Ala Leu Thr Val	
375 380 385	
cat gca ttg cgg gaa ttg ctt ggc gat gat gca ttc ttc aaa gct gtg	1315
His Ala Leu Arg Glu Leu Leu Gly Asp Asp Ala Phe Phe Lys Ala Val	
390 395 400 405	

cgc tcc tac gtt gcc gaa ggc cga cac gga ctc gtt gaa ccc cgc gac 1363
 Arg Ser Tyr Val Ala Glu Gly Arg His Gly Leu Val Glu Pro Arg Asp
 410 415 420
 ctg aaa cga cac ctc tac gca gtc tcc aca gac cac gca gct tta gat 1411
 Leu Lys Arg His Leu Tyr Ala Val Ser Thr Asp His Ala Ala Leu Asp
 425 430 435
 gca gtg tgg cag tcc tgg ctt cgc gat ctg gag ttg ccg gag ttt cct 1459
 Ala Val Trp Gln Ser Trp Leu Arg Asp Leu Glu Leu Pro Glu Phe Pro
 440 445 450
 tct ggt ggt ttg gac tagtgcgcta tctgacgctg gcc 1497
 Ser Gly Gly Leu Asp
 455

<210> 124

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Arg Arg Leu Arg Ser Thr Pro Val Pro Gly Thr Arg Asp Ser Tyr
 1 5 10 15
 Thr Gly Ile Asp Phe Asn Leu Gly Phe His Ile Arg Arg Tyr Glu Leu
 20 25 30
 Asp Leu Thr Tyr Arg Val Ala Pro Asn Leu Leu Met Gly Thr Ala Thr
 35 40 45
 Leu His Met Asp Asn Tyr Arg Ala Leu Asp Ala Leu Thr Leu Asp Leu
 50 55 60
 Gly Gly Ser Leu Arg Val Glu Lys Val Thr Ala Lys Gly Thr Ala Gly
 65 70 75 80
 Thr His Ile Gln Val Ala Arg Phe Arg His Ala Gly Arg Lys Leu Arg
 85 90 95
 Ile Thr Phe Arg Asn Gln Ile Pro Val Asp Gln Glu Phe Ser Leu Thr
 100 105 110
 Ile Arg Tyr Arg Gly Asn Pro Arg Pro Leu Arg Ser Glu Trp Gly Met
 115 120 125
 Ile Gly Trp Glu Glu Leu Asp Asn Gly Ala Leu Val Ala Ala Gln Pro
 130 135 140
 Asn Gly Ala Pro Ser Trp Phe Pro Cys Asp Asp Thr Pro Asp Glu Lys
 145 150 155 160
 Ala Leu Phe Asp Val His Phe His Thr Asp Asn Gly Tyr Ala Ala Ile
 165 170 175
 Ile Thr Gly Asp Leu Ile Ser Lys His Val Ser Gly Ser Met Thr Thr
 180 185 190
 Trp His Tyr Gln Ser Arg Glu Pro Met Ala Thr Tyr Leu Ala Ala Val
 195 200 205

His Val Gly Glu Tyr Asp Thr Val Ser Leu Gly Val Ser Glu Ser Gly
 210 215 220
 Val Val Val Glu Ala Tyr Val Pro Val Gly Asp Ala Ala Leu Arg Ala
 225 230 235 240
 Arg Ile Leu Glu Asp Phe Ala Lys Gln Val Asp Met Leu Asp Ala Tyr
 245 250 255
 Glu Lys Leu Phe Gly Pro Tyr Pro Phe Arg Ser Tyr Arg Val Val Ile
 260 265 270
 Thr Glu Asp Glu Leu Glu Ile Pro Leu Glu Ala Gln Gly Leu Ser Ser
 275 280 285
 Phe Gly Ala Asn His Ala Thr Gly Glu Gly Thr Trp Glu Arg Leu Ile
 290 295 300
 Ala His Glu Leu Ser His Gln Trp Phe Gly Asn Ser Leu Gly Leu Ala
 305 310 315 320
 Gln Trp Asn Asp Ile Trp Leu Asn Glu Gly Phe Ala Cys Tyr Ala Glu
 325 330 335
 Trp Leu Trp Phe Glu Ala Ala Gly Val Lys Ser Ala Ala Glu Ser Ala
 340 345 350
 Leu Glu Phe Tyr Arg Gly Leu Glu Ala Leu Pro Lys Asp Ile Leu Leu
 355 360 365
 Ala Asn Pro Gly Ala Lys Asp Met Phe Asp Asp Arg Val Tyr Lys Arg
 370 375 380
 Gly Ala Leu Thr Val His Ala Leu Arg Glu Leu Leu Gly Asp Asp Ala
 385 390 395 400
 Phe Phe Lys Ala Val Arg Ser Tyr Val Ala Glu Gly Arg His Gly Leu
 405 410 415
 Val Glu Pro Arg Asp Leu Lys Arg His Leu Tyr Ala Val Ser Thr Asp
 420 425 430
 His Ala Ala Leu Asp Ala Val Trp Gln Ser Trp Leu Arg Asp Leu Glu
 435 440 445
 Leu Pro Glu Phe Pro Ser Gly Gly Leu Asp
 450 455

<210> 125

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXN00621

<400> 125

188

gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245

cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
 250 255 260

tgaagtacgc gtgcttcctt tcg 906

<210> 126

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
 1 5 10 15

Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
 20 25 30

Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
 35 40 45

Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
 50 55 60

Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65 70 75 80

Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
 85 90 95

Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
 100 105 110

Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
 115 120 125

Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
 130 135 140

Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
 145 150 155 160

Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
 165 170 175

Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
 180 185 190

Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
 195 200 205

Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
 210 215 220

Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr

<400> 127																
aaatgaatcc gggttttttca gtttcgggggt gcaaatacaga atgtcgccaa tggcgaacac																60
acgagcgtgc agaagatgtg cgtgactaag atcgggggct atg tct gaa cgc cta																115
Met Ser Glu Arg Leu																5
1																
aac gct ccg caa gca cca atc cat ccc atc acc cga acc cac cac ggt																163
Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr Arg Thr His His Gly																20
10 15																
att gat ttc gta gac aac tat gaa tgg ctg agg gat aaa gaa tcc caa																211
Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg Asp Lys Glu Ser Gln																35
25 30																
gaa acc ttg gac tac ctg gag gcg gag aat gcg ttc acc aag cag gag																259
Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala Phe Thr Lys Gln Glu																50
40 45																
act gaa cag cta gcc aca ctg cgg gac aac atc tat gaa gag att aag																307
Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile Tyr Glu Glu Ile Lys																65
55 60																
tca cgc gtt aaa gaa acc gac atg tcc atc cca gtg cgt gcc gga aag																355
Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro Val Arg Ala Gly Lys																85
70 75 80																
cac tgg tat tac tct cgc act gaa gaa ggc aag agc tac ggc tat tcc																403
His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys Ser Tyr Gly Tyr Ser																100
90 95																
tgc cgc att cca gtg act gaa ggg tcg gat gca tgg acc cct cct gtt																451
Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala Trp Thr Pro Pro Val																115
105 110																
atc cct gag ggt gag cca gcg cag ggt gaa acc atc atc atg gat gcc																499
Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr Ile Ile Met Asp Ala																130
120 125																
aac gag ttg gca gaa ggc cac gaa ttc ttc tcc atg ggt gca tca tct																547
Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser Met Gly Ala Ser Ser																145
135 140																

gtc acc acc tct ggc cgc tac ctt gcg tat tcc acc gat gtc acg ggc 595
 Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser Thr Asp Val Thr Gly
 150 155 160 165
 gaa gag cgc ttt acg ttg cgc atc aag gat cta gaa act ggc gag ctg 643
 Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu Glu Thr Gly Glu Leu
 170 175 180
 ctt cct gat acc ctg act ggc att ttc tac ggt gct act tgg gtg ggg 691
 Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly Ala Thr Trp Val Gly
 185 190 195
 gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat 739
 Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
 200 205 210
 act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg 787
 Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
 215 220 225
 gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245
 cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
 250 255 260
 tgaagtacgc gtgcttcctt tcg 906

<210> 128

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
 1 5 10 15
 Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
 20 25 30
 Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
 35 40 45
 Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
 50 55 60
 Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65 70 75 80
 Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
 85 90 95
 Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
 100 105 110
 Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
 115 120 125

Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
 130 135 140

Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
 145 150 155 160

Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
 165 170 175

Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
 180 185 190

Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
 195 200 205

Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
 210 215 220

Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr
 225 230 235 240

Trp Val Gly Thr Thr Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg
 245 250 255

Leu Gln Asp His Leu
 260

<210> 129
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1516)
 <223> RXN00622

<400> 129
 ttttaccagc gcgttgatga tgcgtggcgt ccagatactg tgtggcgcca caaggtgggt 60

accccggttg aagaagacgt gttggtgtac cacgagcctg atg aac gtt att cca 115
 Met Asn Val Ile Pro 5

cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
 Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys 20

gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca 211
 Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro 25 30 35

gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac 259
 Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr 40 45 50

gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca 307
 Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr 55 60 65

cac His 70	aac Asn	gcc Ala	gag Glu	ggc Gly	ccg Pro 75	aac Asn	ttt Phe	tcg Ser	gtg Val	ggg Gly 80	tgg Trp	gct Ala	ggc Gly	gtc Val	gac Asp 85	355
aag Lys	ctc Leu	aat Asn	tct Ser	ttg Leu 90	gac Asp	gcg Ala	ctg Leu	gcg Ala	cca Pro 95	ctc Leu	gtc Val	gcg Ala	cac His	aag Lys 100	gat Asp	403
gac Asp	gtg Val	cgc Arg	att Ile 105	gag Glu	ggt Gly	gtc Val	gat Asp 110	acc Thr	tac Tyr	cgc Arg	gat Asp	ttc Phe	atc Ile 115	atc Ile	ctg Leu	451
ggc Gly	tac Tyr	agg Arg	tcc Ser 120	ggc Gly	gcg Ala	atc Ile	ggc Gly 125	cag Gln	gtc Val	gcg Ala	atc Ile	atg Met 130	aag Lys	ctt Leu	atc Ile	499
gac Asp 135	gga Gly	acc Thr	ttc Phe	ggc Gly	gat Asp	ttc Phe 140	caa Gln	cag Gln	ctg Leu	gaa Glu 145	ttt Phe	gac Asp	gag Glu	gaa Glu	atc Ile	547
tac Tyr 150	acc Thr	gtc Val	gca Ala	tcg Ser	ggc Gly	gga Gly 155	aac Asn	cca Pro	gaa Glu	tgg Trp 160	gac Asp	gcc Ala	ccc Pro	gtc Val	att Ile 165	595
cgc Arg	ctt Leu	tct Ser	tac Tyr	gga Gly 170	tca Ser	ttc Phe	acc Thr	acc Thr	ccg Pro 175	gcg Ala	cag Gln	ctg Leu	ttt Phe	aac Asn 180	tac Tyr	643
tgg Trp	att Ile	gaa Glu	tcc Ser 185	ggc Gly	gaa Glu	cgc Arg	acg Thr	ctg Leu	ctg Leu	aag Lys	cag Gln	cag Gln	gaa Glu	gtg Val	ctc Leu	691
ggc Gly	gga Gly	tac Tyr 200	aag Lys	ccg Pro	tca Ser	gac Asp	tat Tyr 205	gtg Val	gcc Ala	tcc Ser	cga Arg	ttg Leu	tgg Trp	gtc Val	act Thr	739
gcg Ala 215	aaa Lys	gat Asp	ggc Gly	gcg Ala	cag Gln	att Ile 220	cca Pro	gtg Val	tcc Ser	ttg Leu	gtg Val	cac His	cgc Arg	acc Thr	gac Asp	787
ctg Leu 230	gat Asp	gta Val	tcc Ser	aag Lys	ccc Pro	aac Asn	ccc Pro	acg Thr	ttg Leu	ctc Leu	tac Tyr	ggc Gly	tat Tyr	ggt Gly	tcc Ser 245	835
tac Tyr	gaa Glu	tca Ser	tcc Ser	att Ile 250	gat Asp	cca Pro	ggc Gly	ttc Phe	tct Ser	atc Ile 255	gcg Ala	cgt Arg	ttg Leu	tca Ser	ctg Leu 260	883
atg Met	gat Asp	cgt Arg	ggc Gly	atg Met	att Ile	ttt Phe	gcg Ala	att Ile	gcc Ala	cac His	gtt Val	cgt Arg	ggc Gly	ggt Gly	ggc Gly	931
gaa Glu	atg Met	ggt Gly	cgt Arg	ggc Gly	tgg Trp	tac Tyr	gac Asp	aac Asn	ggc Gly	aaa Lys	acc Thr	acc Thr	acg Thr	aag Lys	aaa Lys	979
aac Asn 295	acc Thr	ttc Phe	acc Thr	gac Asp	ttc Phe	att Ile 300	gat Asp	gtt Val	gcc Ala	gac Asp	gcc Ala	ctc Leu	atc Ile	gag Glu	cag Gln	1027

aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt 1075
Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly
310 315 320 325

ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag 1123
Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys
330 335 340

gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc 1171
Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
345 350 355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat 1219
Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
360 365 370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca 1267
Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
375 380 385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca 1315
Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
390 395 400 405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta 1363
Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
410 415 420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act 1411
Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
425 430 435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg 1459
Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
440 445 450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt 1507
Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
455 460 465

gtg acc gaa taaaacttgt tcgactagcg aac 1539
Val Thr Glu
470

<210> 130

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
1 5 10 15

Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
20 25 30

Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
35 40 45

Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp

50	55	60
Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly 65 70 75 80		
Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu 85 90 95		
Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg 100 105 110		
Asp Phe Ile Ile Leu Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala 115 120 125		
Ile Met Lys Leu Ile Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu 130 135 140		
Phe Asp Glu Glu Ile Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp 145 150 155 160		
Asp Ala Pro Val Ile Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala 165 170 175		
Gln Leu Phe Asn Tyr Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys 180 185 190		
Gln Gln Glu Val Leu Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser 195 200 205		
Arg Leu Trp Val Thr Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu 210 215 220		
Val His Arg Thr Asp Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu 225 230 235 240		
Tyr Gly Tyr Gly Ser Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile 245 250 255		
Ala Arg Leu Ser Leu Met Asp Arg Gly Met Ile Phe Ala Ile Ala His 260 265 270		
Val Arg Gly Gly Gly Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys 275 280 285		
Thr Thr Thr Lys Lys Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp 290 295 300		
Ala Leu Ile Glu Gln Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu 305 310 315 320		
Gly Gly Ser Ala Gly Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala 325 330 335		
Gly Asp Arg Phe Lys Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro 340 345 350		
Leu Thr Ser Met Leu Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp 355 360 365		
Asp Glu Trp Gly Asp Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met 370 375 380		

Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn
 385 390 395 400

Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu
 405 410 415

Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu
 420 425 430

Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
 435 440 445

Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
 450 455 460

Asn Gln Ala Thr Gly Val Thr Glu
 465 470

<210> 131
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1516)
 <223> FRXA00622

<400> 131
 ttttaccagc gcgttgatga tgcgtggcgt ccagatactg tgtggcgcca caaggtgggt 60

accccggttg aagaagacgt gttggtgtac cacgagcctg atg aac gtt att cca 115
 Met Asn Val Ile Pro
 1 5

cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
 Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
 10 15 20

gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca 211
 Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro
 25 30 35

gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac 259
 Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr
 40 45 50

gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca 307
 Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr
 55 60 65

cac aac gcc gag ggc ccg aac ttt tcg gtg ggg tgg gct ggc gtc gac 355
 His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp
 70 75 80 85

aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat 403
 Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp
 90 95 100

gac	gtg	cgc	att	gag	ggt	gtc	gat	acc	tac	cgc	gat	ttc	atc	atc	ctg	451
Asp	Val	Arg	Ile	Glu	Gly	Val	Asp	Thr	Tyr	Arg	Asp	Phe	Ile	Ile	Leu	
			105					110					115			
ggc	tac	agg	tcc	ggc	gcg	atc	ggc	cag	gtc	gcg	atc	atg	aag	ctt	atc	499
Gly	Tyr	Arg	Ser	Gly	Ala	Ile	Gly	Gln	Val	Ala	Ile	Met	Lys	Leu	Ile	
		120					125					130				
gac	gga	acc	ttc	ggc	gat	ttc	caa	cag	ctg	gaa	ttt	gac	gag	gaa	atc	547
Asp	Gly	Thr	Phe	Gly	Asp	Phe	Gln	Gln	Leu	Glu	Phe	Asp	Glu	Glu	Ile	
	135					140					145					
tac	acc	gtc	gca	tcg	ggc	gga	aac	cca	gaa	tgg	gac	gcc	ccc	gtc	att	595
Tyr	Thr	Val	Ala	Ser	Gly	Gly	Asn	Pro	Glu	Trp	Asp	Ala	Pro	Val	Ile	
150					155					160					165	
cgc	ctt	tct	tac	gga	tca	ttc	acc	acc	ccg	gcg	cag	ctg	ttt	aac	tac	643
Arg	Leu	Ser	Tyr	Gly	Ser	Phe	Thr	Thr	Pro	Ala	Gln	Leu	Phe	Asn	Tyr	
				170					175					180		
tgg	att	gaa	tcc	ggc	gaa	cgc	acg	ctg	ctg	aag	cag	cag	gaa	gtg	ctc	691
Trp	Ile	Glu	Ser	Gly	Glu	Arg	Thr	Leu	Leu	Lys	Gln	Gln	Glu	Val	Leu	
		185						190					195			
ggc	gga	tac	aag	ccg	tca	gac	tat	gtg	gcc	tcc	cga	ttg	tgg	gtc	act	739
Gly	Gly	Tyr	Lys	Pro	Ser	Asp	Tyr	Val	Ala	Ser	Arg	Leu	Trp	Val	Thr	
		200					205					210				
gcg	aaa	gat	ggc	gcg	cag	att	cca	gtg	tcc	ttg	gtg	cac	cgc	acc	gac	787
Ala	Lys	Asp	Gly	Ala	Gln	Ile	Pro	Val	Ser	Leu	Val	His	Arg	Thr	Asp	
	215					220					225					
ctg	gat	gta	tcc	aag	ccc	aac	ccc	acg	ttg	ctc	tac	ggc	tat	ggg	tcc	835
Leu	Asp	Val	Ser	Lys	Pro	Asn	Pro	Thr	Leu	Leu	Tyr	Gly	Tyr	Gly	Ser	
230					235					240					245	
tac	gaa	tca	tcc	att	gat	cca	ggc	ttc	tct	atc	gcg	cgt	ttg	tca	ctg	883
Tyr	Glu	Ser	Ser	Ile	Asp	Pro	Gly	Phe	Ser	Ile	Ala	Arg	Leu	Ser	Leu	
				250					255					260		
atg	gat	cgt	ggc	atg	att	ttt	gcg	att	gcc	cac	gtt	cgt	ggc	ggg	ggc	931
Met	Asp	Arg	Gly	Met	Ile	Phe	Ala	Ile	Ala	His	Val	Arg	Gly	Gly	Gly	
			265				270						275			
gaa	atg	ggg	cgt	ggc	tgg	tac	gac	aac	ggc	aaa	acc	acc	acg	aag	aaa	979
Glu	Met	Gly	Arg	Gly	Trp	Tyr	Asp	Asn	Gly	Lys	Thr	Thr	Thr	Lys	Lys	
		280					285					290				
aac	acc	ttc	acc	gac	ttc	att	gat	gtt	gcc	gac	gcc	ctc	atc	gag	cag	1027
Asn	Thr	Phe	Thr	Asp	Phe	Ile	Asp	Val	Ala	Asp	Ala	Leu	Ile	Glu	Gln	
	295					300					305					
aag	att	tct	gcc	cct	gaa	atg	ctg	gtt	gca	gaa	ggc	ggc	tca	gct	ggg	1075
Lys	Ile	Ser	Ala	Pro	Glu	Met	Leu	Val	Ala	Glu	Gly	Gly	Ser	Ala	Gly	
310					315					320					325	
ggc	atg	ctc	atg	ggc	gcc	att	gcc	aac	atg	gcc	ggg	gac	cgc	ttc	aag	1123
Gly	Met	Leu	Met	Gly	Ala	Ile	Ala	Asn	Met	Ala	Gly	Asp	Arg	Phe	Lys	
				330				335						340		
gcg	atc	gaa	gcc	aac	gtg	cca	ttc	gtc	gat	ccg	ctg	acc	tct	atg	ctc	1171

Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
 345 350 355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat 1219
 Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
 360 365 370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca 1267
 Pro Leu His Asp Lys Asp Thr Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
 375 380 385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca 1315
 Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
 390 395 400 405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta 1363
 Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
 410 415 420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act 1411
 Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
 425 430 435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg 1459
 Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
 440 445 450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt 1507
 Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
 455 460 465

gtg acc gaa taaaacttgt tcgactagcg aac 1539
 Val Thr Glu
 470

<210> 132

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
 1 5 10 15

Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
 20 25 30

Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
 35 40 45

Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
 50 55 60

Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly
 65 70 75 80

Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu
 85 90 95

Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg

100					105					110					
Asp	Phe	Ile	Ile	Leu	Gly	Tyr	Arg	Ser	Gly	Ala	Ile	Gly	Gln	Val	Ala
	115						120					125			
Ile	Met	Lys	Leu	Ile	Asp	Gly	Thr	Phe	Gly	Asp	Phe	Gln	Gln	Leu	Glu
	130					135					140				
Phe	Asp	Glu	Glu	Ile	Tyr	Thr	Val	Ala	Ser	Gly	Gly	Asn	Pro	Glu	Trp
145					150					155					160
Asp	Ala	Pro	Val	Ile	Arg	Leu	Ser	Tyr	Gly	Ser	Phe	Thr	Thr	Pro	Ala
				165					170					175	
Gln	Leu	Phe	Asn	Tyr	Trp	Ile	Glu	Ser	Gly	Glu	Arg	Thr	Leu	Leu	Lys
			180					185					190		
Gln	Gln	Glu	Val	Leu	Gly	Gly	Tyr	Lys	Pro	Ser	Asp	Tyr	Val	Ala	Ser
		195					200					205			
Arg	Leu	Trp	Val	Thr	Ala	Lys	Asp	Gly	Ala	Gln	Ile	Pro	Val	Ser	Leu
	210					215					220				
Val	His	Arg	Thr	Asp	Leu	Asp	Val	Ser	Lys	Pro	Asn	Pro	Thr	Leu	Leu
225					230					235					240
Tyr	Gly	Tyr	Gly	Ser	Tyr	Glu	Ser	Ser	Ile	Asp	Pro	Gly	Phe	Ser	Ile
				245					250					255	
Ala	Arg	Leu	Ser	Leu	Met	Asp	Arg	Gly	Met	Ile	Phe	Ala	Ile	Ala	His
			260					265					270		
Val	Arg	Gly	Gly	Gly	Glu	Met	Gly	Arg	Gly	Trp	Tyr	Asp	Asn	Gly	Lys
		275					280					285			
Thr	Thr	Thr	Lys	Lys	Asn	Thr	Phe	Thr	Asp	Phe	Ile	Asp	Val	Ala	Asp
	290					295					300				
Ala	Leu	Ile	Glu	Gln	Lys	Ile	Ser	Ala	Pro	Glu	Met	Leu	Val	Ala	Glu
305					310					315					320
Gly	Gly	Ser	Ala	Gly	Gly	Met	Leu	Met	Gly	Ala	Ile	Ala	Asn	Met	Ala
				325					330					335	
Gly	Asp	Arg	Phe	Lys	Ala	Ile	Glu	Ala	Asn	Val	Pro	Phe	Val	Asp	Pro
			340					345					350		
Leu	Thr	Ser	Met	Leu	Met	Pro	Glu	Leu	Pro	Leu	Thr	Val	Ile	Glu	Trp
		355					360					365			
Asp	Glu	Trp	Gly	Asp	Pro	Leu	His	Asp	Lys	Asp	Val	Tyr	Glu	Tyr	Met
	370					375					380				
Ala	Ser	Tyr	Ala	Pro	Tyr	Glu	Asn	Ile	Glu	Ala	Lys	Asn	Tyr	Pro	Asn
385					390					395					400
Ile	Leu	Ala	Val	Thr	Ser	Leu	Asn	Asp	Thr	Arg	Val	Leu	Tyr	Val	Glu
				405					410					415	
Pro	Ala	Lys	Trp	Val	Ala	Gln	Leu	Arg	Ala	Thr	Ala	Thr	Gly	Gly	Glu
			420					425					430		

Ile	Gly	Thr	Pro	Gly	Tyr	Thr	Ser	Ser	Leu	Thr	Thr	Asp	Asn	Thr	Ala		
	135					140					145						
aac	gac	tgg	gag	cgc	gtc	cgc	caa	gca	ctt	ggc	gat	gac	aag	atc	tcc	595	
Asn	Asp	Trp	Glu	Arg	Val	Arg	Gln	Ala	Leu	Gly	Asp	Asp	Lys	Ile	Ser		
	150				155					160					165		
atc	ttc	gga	ctg	tcc	tac	gga	acc	tac	ctc	gga	tcg	gtc	tac	gcc	acc	643	
Ile	Phe	Gly	Leu	Ser	Tyr	Gly	Thr	Tyr	Leu	Gly	Ser	Val	Tyr	Ala	Thr		
				170					175					180			
cgc	tac	cca	cag	cac	acc	gac	aag	gtt	gtc	ctc	gat	tcc	gca	atg	gcg	691	
Arg	Tyr	Pro	Gln	His	Thr	Asp	Lys	Val	Val	Leu	Asp	Ser	Ala	Met	Ala		
			185					190					195				
ccc	agc	ctg	gca	tgg	aac	ggc	atc	atg	gcc	tcc	caa	gaa	cag	ggc	tac	739	
Pro	Ser	Leu	Ala	Trp	Asn	Gly	Ile	Met	Ala	Ser	Gln	Glu	Gln	Gly	Tyr		
		200					205					210					
aaa	aac	tcc	ctc	aac	gac	ttc	ttc	acc	tgg	gtt	gca	gaa	aac	aac	gac	787	
Lys	Asn	Ser	Leu	Asn	Asp	Phe	Phe	Thr	Trp	Val	Ala	Glu	Asn	Asn	Asp		
	215					220					225						
acg	tat	ggc	ctc	ggc	act	acc	cca	cta	gcc	gtg	tac	caa	aac	tgg	tca	835	
Thr	Tyr	Gly	Leu	Gly	Thr	Thr	Pro	Leu	Ala	Val	Tyr	Gln	Asn	Trp	Ser		
	230				235					240					245		
aac	aag	atc	gtc	gcc	gaa	acc	gga	acc	aac	cca	acc	gtt	gct	cca	cca	883	
Asn	Lys	Ile	Val	Ala	Glu	Thr	Gly	Thr	Asn	Pro	Thr	Val	Ala	Pro	Pro		
				250					255					260			
cca	gca	caa	gtt	ggc	gat	gtc	cca	cca	gca	ttc	gca	tgg	gcc	ggc	caa	931	
Pro	Ala	Gln	Val	Gly	Asp	Val	Pro	Pro	Ala	Phe	Ala	Trp	Ala	Gly	Gln		
			265				270						275				
gca	ggc	gca	gac	atg	atg	acc	gcc	acc	aac	cca	acc	tcc	gtg	caa	ctc	979	
Ala	Gly	Ala	Asp	Met	Met	Thr	Ala	Thr	Asn	Pro	Thr	Ser	Val	Gln	Leu		
		280					285						290				
cag	ggc	ctt	gcc	acc	cag	ctc	cta	aac	cct	gga	tcc	aac	cag	tca	ctg	1027	
Gln	Gly	Leu	Ala	Thr	Gln	Leu	Leu	Asn	Pro	Gly	Ser	Asn	Gln	Ser	Leu		
	295					300					305						
agc	cct	ctg	ctc	aac	gtc	acc	cgc	gcc	tac	att	cca	cag	cca	tca	acc	1075	
Ser	Pro	Leu	Leu	Asn	Val	Thr	Arg	Ala	Tyr	Ile	Pro	Gln	Pro	Ser	Thr		
	310				315					320					325		
tgg	ccc	atg	ctc	gca	ggc	gcc	atc	tca	ggg	caa	aca	ccc	atc	cct	gac	1123	
Trp	Pro	Met	Leu	Ala	Gly	Ala	Ile	Ser	Gly	Gln	Thr	Pro	Ile	Pro	Asp		
				330					335					340			
gta	act	gac	acc	ggc	gac	gac	cca	tac	gtc	atc	gaa	agc	atc	aac	gcc	1171	
Val	Thr	Asp	Thr	Gly	Asp	Asp	Pro	Tyr	Val	Ile	Glu	Ser	Ile	Asn	Ala		
			345					350					355				
agc	gtc	aac	atg	cag	cgc	atg	gtc	atg	tgc	aac	gaa	aac	acc	gtc	gca	1219	
Ser	Val	Asn	Met	Gln	Arg	Met	Val	Met	Cys	Asn	Glu	Asn	Thr	Val	Ala		
		360					365					370					
cca	gac	cca	gta	gca	atg	gca	cgc	atg	gcc	tgg	aca	agc	atg	gtc	acc	1267	
Pro	Asp	Pro	Val	Ala	Met	Ala	Arg	Met	Ala	Trp	Thr	Ser	Met	Val	Thr		

375	380	385	
ggc gac gtc ttt gac att tac tcc gtt aaa ttc agc tcc gga caa gcc Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe Ser Ser Gly Gln Ala 390 395 400 405			1315
tgc tcc ggc atc acc cca aca agc ggc cgc cag cca acc gac gga tct Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln Pro Thr Asp Gly Ser 410 415 420			1363
caa cta gca gtc caa cca cta ctc ctc cag gga acc agc gac cca caa Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly Thr Ser Asp Pro Gln 425 430 435			1411
acc cca tac tgg acc cac aac gag ctt gcc gac gcc atg aac gcc cac Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp Ala Met Asn Ala His 440 445 450			1459
gtg gtc acc gtc aac gga cca gga cac ggc caa tcc atc ggc ggc acc Val Val Thr Val Asn Gly Pro Gly His Gly Gln Ser Ile Gly Gly Thr 455 460 465			1507
aac caa gca atc aac gac att gtt gtg gac tac ctc cgc acc gga cac Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly His 470 475 480 485			1555
acc gac gcc acc tgg gtc gaa ggc aac aca ccc acc cca att acg gct Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr Ala 490 495 500			1603
ggc taattgcttt ccacttagta gat Gly			1629

<210> 134

<211> 502

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro 1 5 10 15
Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro 20 25 30
Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val 35 40 45
Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser 50 55 60
Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met 65 70 75 80
Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln 85 90 95
Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala 100 105 110

Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
 115 120 125
 Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
 130 135 140
 Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
 145 150 155 160
 Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
 165 170 175
 Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
 180 185 190
 Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
 195 200 205
 Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
 210 215 220
 Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
 225 230 235 240
 Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
 245 250 255
 Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
 260 265 270
 Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
 275 280 285
 Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
 290 295 300
 Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
 305 310 315 320
 Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
 325 330 335
 Thr Pro Ile Pro Asp Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile
 340 345 350
 Glu Ser Ile Asn Ala Ser Val Asn Met Gln Arg Met Val Met Cys Asn
 355 360 365
 Glu Asn Thr Val Ala Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp
 370 375 380
 Thr Ser Met Val Thr Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe
 385 390 395 400
 Ser Ser Gly Gln Ala Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln
 405 410 415
 Pro Thr Asp Gly Ser Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly
 420 425 430

Thr Ser Asp Pro Gln Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp
 435 440 445

Ala Met Asn Ala His Val Val Thr Val Asn Gly Pro Gly His Gly Gln
 450 455 460

Ser Ile Gly Gly Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr
 465 470 475 480

Leu Arg Thr Gly His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro
 485 490 495

Thr Pro Ile Thr Ala Gly
 500

<210> 135

<211> 1114

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> FRXA00977

<400> 135

gaaaacaaac gtccttgaag ccgtaatgcc ccgttcgaca ataaaaaggg tagtagcagt 60

tcttgccgcc tcgactgcgc ttagccctt tttggtatca atg ccc act gca gca 115
 Met Pro Thr Ala Ala
 1 5

gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att 163
 Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile
 10 15 20

gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat 211
 Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp
 25 30 35

ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa 259
 Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln
 40 45 50

ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc 307
 Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly
 55 60 65

gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc 355
 Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala
 70 75 80 85

atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc 403
 Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val
 90 95 100

ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc 451
 Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe
 105 110 115

ctc tgc ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag	499
Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu	
120 125 130	
atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc	547
Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala	
135 140 145	
aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc	595
Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser	
150 155 160 165	
atc ttc gga ctg tcc tac gga acc tac ctc gga tgc gtc tac gcc acc	643
Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr	
170 175 180	
cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg	691
Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala	
185 190 195	
ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag ggc tac	739
Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr	
200 205 210	
aaa aac tcc ctc aac gac ttc ttc acc tgg gtt gca gaa aac aac gac	787
Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp	
215 220 225	
acg tat ggc ctc ggc act acc cca cta gcc gtg tac caa aac tgg tca	835
Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser	
230 235 240 245	
aac aag atc gtc gcc gaa acc gga acc aac cca acc gtt gct cca cca	883
Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro	
250 255 260	
cca gca caa gtt ggc gat gtc cca cca gca ttc gca tgg gcc ggc caa	931
Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln	
265 270 275	
gca ggc gca gac atg atg acc gcc acc aac cca acc tcc gtg caa ctc	979
Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu	
280 285 290	
cag ggc ctt gcc acc cag ctc cta aac cct gga tcc aac cag tca ctg	1027
Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu	
295 300 305	
agc cct ctg ctc aac gtc acc cgc gcc tac att cca cag cca tca acc	1075
Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr	
310 315 320 325	
tgg ccc atg ctc gca ggc gcc atc tca ggg caa aca ccc	1114
Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln Thr Pro	
330 335	

<210> 136

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro
 1 5 10 15
 Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro
 20 25 30
 Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val
 35 40 45
 Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser
 50 55 60
 Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met
 65 70 75 80
 Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln
 85 90 95
 Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala
 100 105 110
 Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
 115 120 125
 Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
 130 135 140
 Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
 145 150 155 160
 Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
 165 170 175
 Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
 180 185 190
 Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
 195 200 205
 Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
 210 215 220
 Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
 225 230 235 240
 Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
 245 250 255
 Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
 260 265 270
 Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
 275 280 285
 Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
 290 295 300
 Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
 305 310 315 320

Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
 325 330 335

Thr Pro

<210> 137

<211> 269

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(246)

<223> FRXA00982

<400> 137

tct	caa	cta	gca	gtc	caa	cca	cta	ctc	ctc	cag	gga	acc	agc	gac	cca	48
Ser	Gln	Leu	Ala	Val	Gln	Pro	Leu	Leu	Leu	Gln	Gly	Thr	Ser	Asp	Pro	
1				5					10					15		
caa	acc	cca	tac	tg	acc	cac	aac	gag	ctt	gcc	gac	gcc	atg	aac	gcc	96
Gln	Thr	Pro	Tyr	Trp	Thr	His	Asn	Glu	Leu	Ala	Asp	Ala	Met	Asn	Ala	
			20					25					30			
cac	gtg	gtc	acc	gtc	aac	gga	cca	gga	cac	ggc	caa	tcc	atc	ggc	ggc	144
His	Val	Val	Thr	Val	Asn	Gly	Pro	Gly	His	Gly	Gln	Ser	Ile	Gly	Gly	
			35				40					45				
acc	aac	caa	gca	atc	aac	gac	att	gtt	gtg	gac	tac	ctc	cgc	acc	gga	192
Thr	Asn	Gln	Ala	Ile	Asn	Asp	Ile	Val	Val	Asp	Tyr	Leu	Arg	Thr	Gly	
	50					55				60						
cac	acc	gac	gcc	acc	tg	gtc	gaa	ggc	aac	aca	ccc	acc	cca	att	acg	240
His	Thr	Asp	Ala	Thr	Trp	Val	Glu	Gly	Asn	Thr	Pro	Thr	Pro	Ile	Thr	
65					70					75					80	
gct ggc taattgcttt ccacttagta gat															269	
Ala Gly																

<210> 138

<211> 82

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Ser	Gln	Leu	Ala	Val	Gln	Pro	Leu	Leu	Leu	Gln	Gly	Thr	Ser	Asp	Pro
1				5					10					15	
Gln	Thr	Pro	Tyr	Trp	Thr	His	Asn	Glu	Leu	Ala	Asp	Ala	Met	Asn	Ala
			20					25					30		
His	Val	Val	Thr	Val	Asn	Gly	Pro	Gly	His	Gly	Gln	Ser	Ile	Gly	Gly
			35				40					45			
Thr	Asn	Gln	Ala	Ile	Asn	Asp	Ile	Val	Val	Asp	Tyr	Leu	Arg	Thr	Gly
	50					55				60					

His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr
 65 70 75 80

Ala Gly

<210> 139
 <211> 1419
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1396)
 <223> RXA00152

<400> 139
 gtcattgata tccaaggcac gaccgcgatt gtatggaaag aagcctaaat ttttaacaat 60
 caaatagtagtac tggccattcc caactaaaac tggagtaacg atg aca gga cta atc 115
 Met Thr Gly Leu Ile 5
 ctc gcc ata gtt ttc ctg gtc ttt gtc gcc gtc gtg gtg atc aag tcc 163
 Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser 20
 ata gcc ctg att ccc cag ggt gaa gcc gcc gtc att gaa cgc ctt ggt 211
 Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly 35
 agc tac acc cgc acc gtt tca ggt ggc ctg acc ctg ctg gtt cca ttc 259
 Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe 50
 gtg gac cga gta cgc gca agg atc gac acc cgt gag cgc gtg gtc tca 307
 Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser 65
 ttc cca ccg cag gct gtt att acc caa gac aac ctg acc gtg gcc atc 355
 Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile 85
 gat atc gtg gtg acc ttc caa atc aac gaa cca gag cgc gcc atc tac 403
 Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro Glu Arg Ala Ile Tyr 100
 ggc gtg gac aac tac atc gtc ggt gtg gag cag att tct gta gca aca 451
 Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln Ile Ser Val Ala Thr 115
 ctt cga gac gtt gtc ggt ggc atg acc ctg gaa gaa acc ctc act tca 499
 Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu Glu Thr Leu Thr Ser 130
 cgt gac gtg atc aac cgc cgc ctc cgt ggc gag ctc gat gca gca acc 547
 Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr 145

acc	aaa	tgg	ggc	ctg	cgc	atc	agc	cgt	gtg	gaa	cta	aag	gca	att	gat	595
Thr	Lys	Trp	Gly	Leu	Arg	Ile	Ser	Arg	Val	Glu	Leu	Lys	Ala	Ile	Asp	
150					155					160					165	
ccg	cca	cca	tcc	atc	cag	caa	tcg	atg	gaa	aag	cag	atg	aag	gca	gac	643
Pro	Pro	Pro	Ser	Ile	Gln	Gln	Ser	Met	Glu	Lys	Gln	Met	Lys	Ala	Asp	
				170					175						180	
cgt	gaa	aag	cgc	gcc	acc	att	ttg	acc	gca	gaa	ggt	cag	cgc	gaa	gcc	691
Arg	Glu	Lys	Arg	Ala	Thr	Ile	Leu	Thr	Ala	Glu	Gly	Gln	Arg	Glu	Ala	
			185					190					195			
gac	atc	aaa	act	gcc	gaa	ggt	gaa	aag	caa	gcc	aag	atc	ctc	caa	gct	739
Asp	Ile	Lys	Thr	Ala	Glu	Gly	Glu	Lys	Gln	Ala	Lys	Ile	Leu	Gln	Ala	
		200					205					210				
gag	ggt	gaa	aag	cac	gca	tcc	atc	ctg	aac	gca	gaa	gca	gaa	cgc	caa	787
Glu	Gly	Glu	Lys	His	Ala	Ser	Ile	Leu	Asn	Ala	Glu	Ala	Glu	Arg	Gln	
	215					220					225					
gcg	atg	atc	ctg	cgc	gcc	gaa	ggt	gaa	cgc	gca	gca	cgc	tac	ctc	cag	835
Ala	Met	Ile	Leu	Arg	Ala	Glu	Gly	Glu	Arg	Ala	Ala	Arg	Tyr	Leu	Gln	
230					235					240					245	
gcg	cag	ggt	gaa	gcc	cga	gca	atc	caa	aag	gtc	aac	gca	gca	atc	aag	883
Ala	Gln	Gly	Glu	Ala	Arg	Ala	Ile	Gln	Lys	Val	Asn	Ala	Ala	Ile	Lys	
				250					255					260		
tct	gcc	aag	ttg	acc	cca	gag	gtt	ctt	gct	tat	caa	tac	ctc	gaa	aag	931
Ser	Ala	Lys	Leu	Thr	Pro	Glu	Val	Leu	Ala	Tyr	Gln	Tyr	Leu	Glu	Lys	
			265					270					275			
ctt	cct	aag	atc	gca	gag	ggc	aac	gcc	tcc	aag	atg	tgg	gtc	atc	cca	979
Leu	Pro	Lys	Ile	Ala	Glu	Gly	Asn	Ala	Ser	Lys	Met	Trp	Val	Ile	Pro	
		280					285					290				
agc	cag	ttc	tcc	gat	tct	ctg	gaa	ggt	ttt	gcg	aag	cag	ttc	ggc	gca	1027
Ser	Gln	Phe	Ser	Asp	Ser	Leu	Glu	Gly	Phe	Ala	Lys	Gln	Phe	Gly	Ala	
		295				300					305					
aag	gat	gca	gaa	ggt	gtc	ttc	cgc	tac	gaa	cca	aac	acc	gtg	gat	gaa	1075
Lys	Asp	Ala	Glu	Gly	Val	Phe	Arg	Tyr	Glu	Pro	Asn	Thr	Val	Asp	Glu	
310					315					320					325	
gaa	acc	cgc	gac	atc	gca	aac	gcc	gac	aac	gtg	gaa	gac	tgg	ttc	tcc	1123
Glu	Thr	Arg	Asp	Ile	Ala	Asn	Ala	Asp	Asn	Val	Glu	Asp	Trp	Phe	Ser	
				330					335					340		
acc	gaa	tca	gac	cct	gaa	atc	gca	gca	gca	gtc	gcc	gca	gca	aac	gcc	1171
Thr	Glu	Ser	Asp	Pro	Glu	Ile	Ala	Ala	Ala	Val	Ala	Ala	Ala	Asn	Ala	
			345					350					355			
gtg	gcc	aac	aag	cca	gtc	gat	cca	gaa	ccc	ggt	gag	atc	ctt	tcc	aag	1219
Val	Ala	Asn	Lys	Pro	Val	Asp	Pro	Glu	Pro	Gly	Glu	Ile	Leu	Ser	Lys	
		360					365					370				
aag	acc	gca	cga	cgc	gtt	gaa	cct	gaa	gca	gta	ttg	gag	gct	ttg	caa	1267
Lys	Thr	Ala	Arg	Arg	Val	Glu	Pro	Glu	Ala	Val	Leu	Glu	Ala	Leu	Gln	
		375				380					385					
aac	gga	acc	act	aca	caa	cct	gag	gtt	gag	gca	gca	cct	cct	acc	gca	1315

Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala Ala Pro Pro Thr Ala
 390 395 400 405
 aac ttc gcc caa gaa ttc cct gca cca cag gca aac cct gaa gat tac 1363
 Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala Asn Pro Glu Asp Tyr
 410 415 420
 tcc gac caa cac cga gag aat cct tac gga aac taatcaggca taagaaaagg 1416
 Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 425 430
 cgg 1419

<210> 140
 <211> 432
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 140
 Met Thr Gly Leu Ile Leu Ala Ile Val Phe Leu Val Phe Val Ala Val
 1 5 10 15
 Val Val Ile Lys Ser Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val
 20 25 30
 Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr
 35 40 45
 Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg
 50 55 60
 Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn
 65 70 75 80
 Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro
 85 90 95
 Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln
 100 105 110
 Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu
 115 120 125
 Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu
 130 135 140
 Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu
 145 150 155 160
 Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys
 165 170 175
 Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu
 180 185 190
 Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala
 195 200 205
 Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala
 210 215 220

Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala
 225 230 235 240
 Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val
 245 250 255
 Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr
 260 265 270
 Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys
 275 280 285
 Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala
 290 295 300
 Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro
 305 310 315 320
 Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val
 325 330 335
 Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val
 340 345 350
 Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly
 355 360 365
 Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val
 370 375 380
 Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala
 385 390 395 400
 Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala
 405 410 415
 Asn Pro Glu Asp Tyr Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 420 425 430

<210> 141
 <211> 1098
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1075)
 <223> RXA02558

<400> 141
 ccctcccga attagaaatc cccttttaat gtgatatac tttctgttaa actgatata 60
 cattcttttt cagcacccca gacttaaaag gagcaccacc atg agc acc ata gaa 115
 Met Ser Thr Ile Glu
 1 5

gag cgc act cct gga gct gtc gcc aca gaa cca gtg gga cac gaa ggc	163
Glu Arg Thr Pro Gly Ala Val Ala Thr Glu Pro Val Gly His Glu Gly	
10 15 20	
gca cgc gtc agc att aat gag aag aac gtg tgg tct ttg ggc gca ggt	211
Ala Arg Val Ser Ile Asn Glu Lys Asn Val Trp Ser Leu Gly Ala Gly	
25 30 35	
cca gca gct ttc gca ctg ctc gca atg att gtg ctc atg att gcc agt	259
Pro Ala Ala Phe Ala Leu Leu Ala Met Ile Val Leu Met Ile Ala Ser	
40 45 50	
gga gtt ttc ttc gct caa tcc atc aac act tta gaa aac gat ggc ggt	307
Gly Val Phe Phe Ala Gln Ser Ile Asn Thr Leu Glu Asn Asp Gly Gly	
55 60 65	
gga aca ctt gcg gtt acg gga ctg att gcc agc atc gtc gtt ttc act	355
Gly Thr Leu Ala Val Thr Gly Leu Ile Ala Ser Ile Val Val Phe Thr	
70 75 80 85	
gtt gca ttg gtg gtc acc ata act tcg gtg aag gtg gtc agc cct gga	403
Val Ala Leu Val Val Thr Ile Thr Ser Val Lys Val Val Ser Pro Gly	
90 95 100	
cat act ctg act gtg cag ttc ttt gga cga tac atc gga acc ctg cgt	451
His Thr Leu Thr Val Gln Phe Phe Gly Arg Tyr Ile Gly Thr Leu Arg	
105 110 115	
cga act ggg ttg tct ttc gtt ccc cca ctg tct gtg acg aag aaa gtg	499
Arg Thr Gly Leu Ser Phe Val Pro Pro Leu Ser Val Thr Lys Lys Val	
120 125 130	
tcc gtg agg gtc cga aac ttt gaa acc aac gaa gcc aaa gtt aat gac	547
Ser Val Arg Val Arg Asn Phe Glu Thr Asn Glu Ala Lys Val Asn Asp	
135 140 145	
tac aac ggc aac ccc atc aac att gca gcg atc atc gtg tgg cag gta	595
Tyr Asn Gly Asn Pro Ile Asn Ile Ala Ala Ile Ile Val Trp Gln Val	
150 155 160 165	
gcc gat act gca cag gct agc ttc tct gtg gag gat ttc gaa gag ttc	643
Ala Asp Thr Ala Gln Ala Ser Phe Ser Val Glu Asp Phe Glu Glu Phe	
170 175 180	
ctg cac cag cag gcc gag tcc gca ctg cgt cac gtg gca acc cag cac	691
Leu His Gln Gln Ala Glu Ser Ala Leu Arg His Val Ala Thr Gln His	
185 190 195	
ccc tat gat tcc cca gtt gat ggt cgt gtt tcc ttg cgt ggc gct acc	739
Pro Tyr Asp Ser Pro Val Asp Gly Arg Val Ser Leu Arg Gly Ala Thr	
200 205 210	
gat gag gtc agt gaa gaa ctc gca gat gag gtg gca caa cga gca gct	787
Asp Glu Val Ser Glu Glu Leu Ala Asp Glu Val Ala Gln Arg Ala Ala	
215 220 225	
gtt gca ggt ctt gaa atc gtc gaa gcc cgc atc tct tcc ttg agc tac	835
Val Ala Gly Leu Glu Ile Val Glu Ala Arg Ile Ser Ser Leu Ser Tyr	
230 235 240 245	
gca ccg gaa att gcc cag gcg atg ctg cag cgc cag cag gct tcc gcg	883

Ala Pro Glu Ile Ala Gln Ala Met Leu Gln Arg Gln Gln Ala Ser Ala
 250 255 260

att gtt gat gcc cgc gaa aag atc gtc gag ggc gct gtc acc atg gtg 931
 Ile Val Asp Ala Arg Glu Lys Ile Val Glu Gly Ala Val Thr Met Val
 265 270 275

gaa acc gca ctt gac cag ctt gag caa cgt gaa att gtg gat ttg gat 979
 Glu Thr Ala Leu Asp Gln Leu Glu Gln Arg Glu Ile Val Asp Leu Asp
 280 285 290

cca gag cga cgc gcc gcg atg gtt tcc aac ctg ttg gtt gtg ttg tgt 1027
 Pro Glu Arg Arg Ala Ala Met Val Ser Asn Leu Leu Val Val Leu Cys
 295 300 305

tcc gac acc aat gct cag cca atc gtc aac gcc ggt agc ctc tac caa 1075
 Ser Asp Thr Asn Ala Gln Pro Ile Val Asn Ala Gly Ser Leu Tyr Gln
 310 315 320 325

taagacaatg gcccgcaaac agg 1098

<210> 142
 <211> 325
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 142
 Met Ser Thr Ile Glu Glu Arg Thr Pro Gly Ala Val Ala Thr Glu Pro
 1 5 10 15

Val Gly His Glu Gly Ala Arg Val Ser Ile Asn Glu Lys Asn Val Trp
 20 25 30

Ser Leu Gly Ala Gly Pro Ala Ala Phe Ala Leu Leu Ala Met Ile Val
 35 40 45

Leu Met Ile Ala Ser Gly Val Phe Phe Ala Gln Ser Ile Asn Thr Leu
 50 55 60

Glu Asn Asp Gly Gly Gly Thr Leu Ala Val Thr Gly Leu Ile Ala Ser
 65 70 75 80

Ile Val Val Phe Thr Val Ala Leu Val Val Thr Ile Thr Ser Val Lys
 85 90 95

Val Val Ser Pro Gly His Thr Leu Thr Val Gln Phe Phe Gly Arg Tyr
 100 105 110

Ile Gly Thr Leu Arg Arg Thr Gly Leu Ser Phe Val Pro Pro Leu Ser
 115 120 125

Val Thr Lys Lys Val Ser Val Arg Val Arg Asn Phe Glu Thr Asn Glu
 130 135 140

Ala Lys Val Asn Asp Tyr Asn Gly Asn Pro Ile Asn Ile Ala Ala Ile
 145 150 155 160

Ile Val Trp Gln Val Ala Asp Thr Ala Gln Ala Ser Phe Ser Val Glu
 165 170 175

Asp Phe Glu Glu Phe Leu His Gln Gln Ala Glu Ser Ala Leu Arg His
 180 185 190
 Val Ala Thr Gln His Pro Tyr Asp Ser Pro Val Asp Gly Arg Val Ser
 195 200 205
 Leu Arg Gly Ala Thr Asp Glu Val Ser Glu Glu Leu Ala Asp Glu Val
 210 215 220
 Ala Gln Arg Ala Ala Val Ala Gly Leu Glu Ile Val Glu Ala Arg Ile
 225 230 235 240
 Ser Ser Leu Ser Tyr Ala Pro Glu Ile Ala Gln Ala Met Leu Gln Arg
 245 250 255
 Gln Gln Ala Ser Ala Ile Val Asp Ala Arg Glu Lys Ile Val Glu Gly
 260 265 270
 Ala Val Thr Met Val Glu Thr Ala Leu Asp Gln Leu Glu Gln Arg Glu
 275 280 285
 Ile Val Asp Leu Asp Pro Glu Arg Arg Ala Ala Met Val Ser Asn Leu
 290 295 300
 Leu Val Val Leu Cys Ser Asp Thr Asn Ala Gln Pro Ile Val Asn Ala
 305 310 315 320
 Gly Ser Leu Tyr Gln
 325

<210> 143
 <211> 798
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(775)
 <223> RXA00500

<400> 143
 caccagccag catgaacaca atggacttcg tgccagctca ggcgcagtac tgaagcacct 60
 ttctgatctg gccacggcc gagaggtacg ctgattcctc gtg tta gta cta gcc 115
 Val Leu Val Leu Ala
 1 5
 cta gac acc tca acc cct gac ctg atc gtc ggc gtc gtc gac tcc gac 163
 Leu Asp Thr Ser Thr Pro Asp Leu Ile Val Gly Val Val Asp Ser Asp
 10 15 20
 acc gga aac acc cgc gcc gaa acc atc atc gag gac acc cgc gca cac 211
 Thr Gly Asn Thr Arg Ala Glu Thr Ile Ile Glu Asp Thr Arg Ala His
 25 30 35
 aac gag cag ctg acg ccc acc gtc cag aag acg ctt ctg gac gcc aac 259
 Asn Glu Gln Leu Thr Pro Thr Val Gln Lys Thr Leu Leu Asp Ala Asn
 40 45 50
 ttg agc ttt tca gat atc gac gcg atc gtc gtg ggt tgc ggc ccg gga 307

Leu Ser Phe Ser Asp Ile Asp Ala Ile Val Val Gly Cys Gly Pro Gly
 55 60 65
 ccg ttc act gga ctt cga gta ggc atg gtg tcc ggc gca gcg ttc ggt 355
 Pro Phe Thr Gly Leu Arg Val Gly Met Val Ser Gly Ala Ala Phe Gly
 70 75 80 85
 gat gcc ctg gga atc cct gtc tat gga gtc tgc tca ctc gac gcg atc 403
 Asp Ala Leu Gly Ile Pro Val Tyr Gly Val Cys Ser Leu Asp Ala Ile
 90 95 100
 gct cac aat att ggt gca cgc aac atc ccg cac gca tta gtt gcc act 451
 Ala His Asn Ile Gly Ala Arg Asn Ile Pro His Ala Leu Val Ala Thr
 105 110 115
 gat gcg cgc cgc cgt gaa atc tac tgg gca acc tac cgc tcc ggc gaa 499
 Asp Ala Arg Arg Arg Glu Ile Tyr Trp Ala Thr Tyr Arg Ser Gly Glu
 120 125 130
 cgt gat cag gga cca gat gtc atc gca cca gca aac atc cag atc agc 547
 Arg Asp Gln Gly Pro Asp Val Ile Ala Pro Ala Asn Ile Gln Ile Ser
 135 140 145
 ggc gct gta gac acc att tcg att cct gag cac ctg gtg gaa aaa ctc 595
 Gly Ala Val Asp Thr Ile Ser Ile Pro Glu His Leu Val Glu Lys Leu
 150 155 160 165
 cca gaa gaa ctc cag aat gtc acc atg cat agc ggc aaa cct gcc ccc 643
 Pro Glu Glu Leu Gln Asn Val Thr Met His Ser Gly Lys Pro Ala Pro
 170 175 180
 gca agc ttg gtg gca gtg gct gat ttc agt gtg gaa cca caa cca ttg 691
 Ala Ser Leu Val Ala Val Ala Asp Phe Ser Val Glu Pro Gln Pro Leu
 185 190 195
 gtt cct ctt tac ctg cgc cgc cca gat gcc aaa gaa cca aaa cca aaa 739
 Val Pro Leu Tyr Leu Arg Arg Pro Asp Ala Lys Glu Pro Lys Pro Lys
 200 205 210
 cct aaa tct gca gcc atc ccc gag gtg gat ctt tca tgagtgaaca 785
 Pro Lys Ser Ala Ala Ile Pro Glu Val Asp Leu Ser
 215 220 225
 attcgagcta cgg 798

<210> 144

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Val Leu Val Leu Ala Leu Asp Thr Ser Thr Pro Asp Leu Ile Val Gly
 1 5 10 15

Val Val Asp Ser Asp Thr Gly Asn Thr Arg Ala Glu Thr Ile Ile Glu
 20 25 30

Asp Thr Arg Ala His Asn Glu Gln Leu Thr Pro Thr Val Gln Lys Thr
 35 40 45

Leu Leu Asp Ala Asn Leu Ser Phe Ser Asp Ile Asp Ala Ile Val Val
 50 55 60
 Gly Cys Gly Pro Gly Pro Phe Thr Gly Leu Arg Val Gly Met Val Ser
 65 70 75 80
 Gly Ala Ala Phe Gly Asp Ala Leu Gly Ile Pro Val Tyr Gly Val Cys
 85 90 95
 Ser Leu Asp Ala Ile Ala His Asn Ile Gly Ala Arg Asn Ile Pro His
 100 105 110
 Ala Leu Val Ala Thr Asp Ala Arg Arg Arg Glu Ile Tyr Trp Ala Thr
 115 120 125
 Tyr Arg Ser Gly Glu Arg Asp Gln Gly Pro Asp Val Ile Ala Pro Ala
 130 135 140
 Asn Ile Gln Ile Ser Gly Ala Val Asp Thr Ile Ser Ile Pro Glu His
 145 150 155 160
 Leu Val Glu Lys Leu Pro Glu Glu Leu Gln Asn Val Thr Met His Ser
 165 170 175
 Gly Lys Pro Ala Pro Ala Ser Leu Val Ala Val Ala Asp Phe Ser Val
 180 185 190
 Glu Pro Gln Pro Leu Val Pro Leu Tyr Leu Arg Arg Pro Asp Ala Lys
 195 200 205
 Glu Pro Lys Pro Lys Pro Lys Ser Ala Ala Ile Pro Glu Val Asp Leu
 210 215 220
 Ser
 225

<210> 145
 <211> 630
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(607)
 <223> RXA00501

<400> 145
 tggaaccaca accattggtt cctctttacc tgcgcgccc agatgccaaa gaacccaaaac 60

caaaacctaa atctgcagcc atccccgagg tggatctttc atg agt gaa caa ttc 115
 Met Ser Glu Gln Phe
 1 5

gag cta cgg gaa ctc cgc agg gaa gac gcg ggg cgc tgc gcc gac ctg 163
 Glu Leu Arg Glu Leu Arg Arg Glu Asp Ala Gly Arg Cys Ala Asp Leu
 10 15 20

gag caa atc ctg ttc cca ggt gat aac ccc tgg cca cgt gat gtc ttt 211
 Glu Gln Ile Leu Phe Pro Gly Asp Asn Pro Trp Pro Arg Asp Val Phe
 25 30 35

gcc gtg gag ttt tcc cac ccc acc aat ttc tac atc ggc gct ttc gac 259
 Ala Val Glu Phe Ser His Pro Thr Asn Phe Tyr Ile Gly Ala Phe Asp
 40 45 50
 gaa gga tac ttg gtg gcg tac gca ggt ctt gcc atg atg gga cct gcg 307
 Glu Gly Tyr Leu Val Ala Tyr Ala Gly Leu Ala Met Met Gly Pro Ala
 55 60 65
 gat gat cca gag ttt gaa atc cac acc att ggt gtc gat ccg gaa ttc 355
 Asp Asp Pro Glu Phe Glu Ile His Thr Ile Gly Val Asp Pro Glu Phe
 70 75 80 85
 caa aga aaa ggc ttg gga cgc gta ctc atg gat caa atg atg cat gca 403
 Gln Arg Lys Gly Leu Gly Arg Val Leu Met Asp Gln Met Met His Ala
 90 95 100
 gcg gac agc cac gac ggt cca gtt ttc ttg gaa gtc cgc acc gac aac 451
 Ala Asp Ser His Asp Gly Pro Val Phe Leu Glu Val Arg Thr Asp Asn
 105 110 115
 gta ccc gcg att tcc atg tac gag gct ttc ggc ttt aaa acc ttg gcc 499
 Val Pro Ala Ile Ser Met Tyr Glu Ala Phe Gly Phe Lys Thr Leu Ala
 120 125 130
 gtg cgc aaa aac tac tac cgg cca tcc gga gct gac gcc tac acc atg 547
 Val Arg Lys Asn Tyr Tyr Arg Pro Ser Gly Ala Asp Ala Tyr Thr Met
 135 140 145
 caa cgc cca cgc ttg agc gat cgc aaa gat caa cag aca gac aca gag 595
 Gln Arg Pro Arg Leu Ser Asp Arg Lys Asp Gln Gln Thr Asp Thr Glu
 150 155 160 165
 ggg aca ccc agc taaaccatga tcgttttggg aat 630
 Gly Thr Pro Ser

<210> 146

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

Met Ser Glu Gln Phe Glu Leu Arg Glu Leu Arg Arg Glu Asp Ala Gly
 1 5 10 15
 Arg Cys Ala Asp Leu Glu Gln Ile Leu Phe Pro Gly Asp Asn Pro Trp
 20 25 30
 Pro Arg Asp Val Phe Ala Val Glu Phe Ser His Pro Thr Asn Phe Tyr
 35 40 45
 Ile Gly Ala Phe Asp Glu Gly Tyr Leu Val Ala Tyr Ala Gly Leu Ala
 50 55 60
 Met Met Gly Pro Ala Asp Asp Pro Glu Phe Glu Ile His Thr Ile Gly
 65 70 75 80
 Val Asp Pro Glu Phe Gln Arg Lys Gly Leu Gly Arg Val Leu Met Asp
 85 90 95

Gln Met Met His Ala Ala Asp Ser His Asp Gly Pro Val Phe Leu Glu
 100 105 110

Val Arg Thr Asp Asn Val Pro Ala Ile Ser Met Tyr Glu Ala Phe Gly
 115 120 125

Phe Lys Thr Leu Ala Val Arg Lys Asn Tyr Tyr Arg Pro Ser Gly Ala
 130 135 140

Asp Ala Tyr Thr Met Gln Arg Pro Arg Leu Ser Asp Arg Lys Asp Gln
 145 150 155 160

Gln Thr Asp Thr Glu Gly Thr Pro Ser
 165

<210> 147

<211> 1155

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA00502

<400> 147

ctaccggcca tccggagctg acgcctacac catgcaacgc ccacgcttga gcgatcgcaa 60

agatcaacag acagacacag aggggacacc cagctaaacc atg atc gtt ttg gga 115
 Met Ile Val Leu Gly
 1 5

att gaa agc tcc tgc gat gaa aca ggc gta ggc gta gtc aaa ctt gac 163
 Ile Glu Ser Ser Cys Asp Glu Thr Gly Val Gly Val Val Lys Leu Asp
 10 15 20

ggc gaa gga aac cta gag atc ctc gcc gac tca gtg gcc tcc tcc atg 211
 Gly Glu Gly Asn Leu Glu Ile Leu Ala Asp Ser Val Ala Ser Ser Met
 25 30 35

caa gaa cat gcc cgc ttt ggt ggc gtc gtg cca gaa atc gcc tcc cgg 259
 Gln Glu His Ala Arg Phe Gly Gly Val Val Pro Glu Ile Ala Ser Arg
 40 45 50

gcg cac ctg gaa tct atg gtc ccc gtg atg cgt gaa gcg ttg agg cag 307
 Ala His Leu Glu Ser Met Val Pro Val Met Arg Glu Ala Leu Arg Gln
 55 60 65

gcg ggc gtc gac agg cca gat gct gtg gct gca acc gtg ggc cct ggt 355
 Ala Gly Val Asp Arg Pro Asp Ala Val Ala Ala Thr Val Gly Pro Gly
 70 75 80 85

ttg gcg ggc gcg ctg ctc gtt gga gcc agc gct gcg aag gcg tat gcc 403
 Leu Ala Gly Ala Leu Leu Val Gly Ala Ser Ala Ala Lys Ala Tyr Ala
 90 95 100

gct gcg tgg gga gtt ccg ttt tac gcg gtc aac cac ctg ggc gga cac 451
 Ala Ala Trp Gly Val Pro Phe Tyr Ala Val Asn His Leu Gly Gly His
 105 110 115

gtc	gcc	gtg	gcc	aat	ctg	gaa	ggt	gaa	act	ctt	cca	cac	gcg	gtg	gct	499
Val	Ala	Val	Ala	Asn	Leu	Glu	Gly	Glu	Thr	Leu	Pro	His	Ala	Val	Ala	
		120					125					130				
ttg	ctg	gtt	tcc	ggc	gga	cac	act	caa	ttg	ttg	gaa	gtc	gac	gcg	gtg	547
Leu	Leu	Val	Ser	Gly	Gly	His	Thr	Gln	Leu	Leu	Glu	Val	Asp	Ala	Val	
	135					140					145					
gga	tta	ccc	atg	aag	gaa	ttg	gga	tcc	acc	ctc	gac	gat	gcc	gct	ggc	595
Gly	Leu	Pro	Met	Lys	Glu	Leu	Gly	Ser	Thr	Leu	Asp	Asp	Ala	Ala	Gly	
150					155					160					165	
gaa	gcc	tat	gac	aaa	gtc	tca	agg	ctg	ttg	gga	ttg	ggc	tac	cca	ggc	643
Glu	Ala	Tyr	Asp	Lys	Val	Ser	Arg	Leu	Leu	Gly	Leu	Gly	Tyr	Pro	Gly	
				170				175						180		
ggc	ccc	atc	att	gat	aaa	ttg	gcg	cgc	cgg	ggt	aat	cca	gag	gcc	att	691
Gly	Pro	Ile	Ile	Asp	Lys	Leu	Ala	Arg	Arg	Gly	Asn	Pro	Glu	Ala	Ile	
		185						190					195			
gct	ttc	ccc	cgc	gga	ttg	atg	aaa	aag	tcg	gat	tct	cgg	cat	gat	ttc	739
Ala	Phe	Pro	Arg	Gly	Leu	Met	Lys	Lys	Ser	Asp	Ser	Arg	His	Asp	Phe	
		200					205					210				
agc	ttt	tcc	ggt	ttg	aaa	acc	tcc	gtt	gcc	cgc	tac	gtg	gaa	gct	gcg	787
Ser	Phe	Ser	Gly	Leu	Lys	Thr	Ser	Val	Ala	Arg	Tyr	Val	Glu	Ala	Ala	
	215					220					225					
gaa	aga	aac	ggt	gaa	gtt	att	tcc	gtg	gag	gac	gtc	tgc	gca	tca	ttc	835
Glu	Arg	Asn	Gly	Glu	Val	Ile	Ser	Val	Glu	Asp	Val	Cys	Ala	Ser	Phe	
230					235					240					245	
caa	gaa	gcg	gtg	tgt	gat	gtg	ttg	acg	ttt	aag	gcc	gtg	cgt	gcg	tgc	883
Gln	Glu	Ala	Val	Cys	Asp	Val	Leu	Thr	Phe	Lys	Ala	Val	Arg	Ala	Cys	
				250					255					260		
cgc	gat	gtc	ggt	gcg	aag	gtg	ctg	ctg	ttg	ggt	gga	gga	gtg	gct	gcc	931
Arg	Asp	Val	Gly	Ala	Lys	Val	Leu	Leu	Leu	Gly	Gly	Gly	Val	Ala	Ala	
			265				270						275			
aac	tct	cgt	ctg	cgg	gag	ctt	gct	caa	gaa	cgt	tgc	gat	aaa	gcc	gac	979
Asn	Ser	Arg	Leu	Arg	Glu	Leu	Ala	Gln	Glu	Arg	Cys	Asp	Lys	Ala	Asp	
		280					285					290				
atc	gaa	ctc	cgg	gtt	cct	cgt	ttc	aat	ttg	tgc	acc	gat	aat	ggt	gtc	1027
Ile	Glu	Leu	Arg	Val	Pro	Arg	Phe	Asn	Leu	Cys	Thr	Asp	Asn	Gly	Val	
	295				300						305					
atg	att	gca	gcg	ttg	gcg	gct	caa	aga	atc	cac	gaa	ggt	gcc	caa	gaa	1075
Met	Ile	Ala	Ala	Leu	Ala	Ala	Gln	Arg	Ile	His	Glu	Gly	Ala	Gln	Glu	
310					315					320					325	
tca	cca	att	tcg	gtc	gga	act	gat	cct	tct	ttg	tcc	gtt	gag	acc	cca	1123
Ser	Pro	Ile	Ser	Val	Gly	Thr	Asp	Pro	Ser	Leu	Ser	Val	Glu	Thr	Pro	
				330				335					340			
cag	gtg	ttt	taa	acatt	ta	gtatt	agttc	cat								1155
Gln	Val	Phe														

<210> 148

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

```

Met Ile Val Leu Gly Ile Glu Ser Ser Cys Asp Glu Thr Gly Val Gly
 1           5           10           15

Val Val Lys Leu Asp Gly Glu Gly Asn Leu Glu Ile Leu Ala Asp Ser
      20           25           30

Val Ala Ser Ser Met Gln Glu His Ala Arg Phe Gly Gly Val Val Pro
      35           40           45

Glu Ile Ala Ser Arg Ala His Leu Glu Ser Met Val Pro Val Met Arg
      50           55           60

Glu Ala Leu Arg Gln Ala Gly Val Asp Arg Pro Asp Ala Val Ala Ala
      65           70           75           80

Thr Val Gly Pro Gly Leu Ala Gly Ala Leu Leu Val Gly Ala Ser Ala
      85           90           95

Ala Lys Ala Tyr Ala Ala Ala Trp Gly Val Pro Phe Tyr Ala Val Asn
      100          105          110

His Leu Gly Gly His Val Ala Val Ala Asn Leu Glu Gly Glu Thr Leu
      115          120          125

Pro His Ala Val Ala Leu Leu Val Ser Gly Gly His Thr Gln Leu Leu
      130          135          140

Glu Val Asp Ala Val Gly Leu Pro Met Lys Glu Leu Gly Ser Thr Leu
      145          150          155          160

Asp Asp Ala Ala Gly Glu Ala Tyr Asp Lys Val Ser Arg Leu Leu Gly
      165          170          175

Leu Gly Tyr Pro Gly Gly Pro Ile Ile Asp Lys Leu Ala Arg Arg Gly
      180          185          190

Asn Pro Glu Ala Ile Ala Phe Pro Arg Gly Leu Met Lys Lys Ser Asp
      195          200          205

Ser Arg His Asp Phe Ser Phe Ser Gly Leu Lys Thr Ser Val Ala Arg
      210          215          220

Tyr Val Glu Ala Ala Glu Arg Asn Gly Glu Val Ile Ser Val Glu Asp
      225          230          235          240

Val Cys Ala Ser Phe Gln Glu Ala Val Cys Asp Val Leu Thr Phe Lys
      245          250          255

Ala Val Arg Ala Cys Arg Asp Val Gly Ala Lys Val Leu Leu Leu Gly
      260          265          270

Gly Gly Val Ala Ala Asn Ser Arg Leu Arg Glu Leu Ala Gln Glu Arg
      275          280          285

```


Cys Asp Lys Ala Asp Ile Glu Leu Arg Val Pro Arg Phe Asn Leu Cys
 290 295 300

Thr Asp Asn Gly Val Met Ile Ala Ala Leu Ala Ala Gln Arg Ile His
 305 310 315 320

Glu Gly Ala Gln Glu Ser Pro Ile Ser Val Gly Thr Asp Pro Ser Leu
 325 330 335

Ser Val Glu Thr Pro Gln Val Phe
 340

<210> 149
 <211> 888
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(865)
 <223> RXN02589

<400> 149
 gcctaaattg cagcgagagg tctaaaaggt agtgctctag ggattcatcc aaactcacga 60

atattgaagt tttaaagttg aacaggaaaa ataacaaata atg tct att tct gat 115
 Met Ser Ile Ser Asp
 1 5

aat tcc cgc gat caa tta gga gaa ctg cca gct ggt cgg cct ctc caa 163
 Asn Ser Arg Asp Gln Leu Gly Glu Leu Pro Ala Gly Arg Pro Leu Gln
 10 15 20

tcc gat ttt gat aat gac ctc gac tac cca cgt cta ggc agt gtc acg 211
 Ser Asp Phe Asp Asn Asp Leu Asp Tyr Pro Arg Leu Gly Ser Val Thr
 25 30 35

ttt agg cgt ggc acc ctc act gaa aac cag caa acc atg tgg gat gaa 259
 Phe Arg Arg Gly Thr Leu Thr Glu Asn Gln Gln Thr Met Trp Asp Glu
 40 45 50

aag tgg cct gaa ctg ggt cgc gtc ctc gaa gat gag ctg att gat gtt 307
 Lys Trp Pro Glu Leu Gly Arg Val Leu Glu Asp Glu Leu Ile Asp Val
 55 60 65

gat gcg tgg ttc ggg cgc gaa ggc gca aaa acc atc gta gag atc ggc 355
 Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr Ile Val Glu Ile Gly
 70 75 80 85

tct ggc act gga act tcg act gct gcc atg gct cca ctt gag gct gat 403
 Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala Pro Leu Glu Ala Asp
 90 95 100

acc aac att gtc gcc gtc gaa cta tac aag ccg ggc ttg gcc aag ttg 451
 Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro Gly Leu Ala Lys Leu
 105 110 115

atg ggc tct gtt gtc cgt gga gag atc gac aac gtg cgc atg gtc cgc 499
 Met Gly Ser Val Val Arg Gly Glu Ile Asp Asn Val Arg Met Val Arg
 120 125 130

gga gac ggc atc gag gtg ctc aac cgc atg ttt gcc gat ggg tcc ctg 547
 Gly Asp Gly Ile Glu Val Leu Asn Arg Met Phe Ala Asp Gly Ser Leu
 135 140 145

 gac ggc atc cgc gta tac ttc ccg gac cct tgg cca aag gcg cgc cac 595
 Asp Gly Ile Arg Val Tyr Phe Pro Asp Pro Trp Pro Lys Ala Arg His
 150 155 160 165

 aac aag cgc cgc atc atc cag tct ggt ccg ctg aac ctg ttt gca aag 643
 Asn Lys Arg Arg Ile Ile Gln Ser Gly Pro Leu Asn Leu Phe Ala Lys
 170 175 180

 aag ctc aag cca ggt gga gtt ctg cac gtt gct acc gac cac gct gat 691
 Lys Leu Lys Pro Gly Gly Val Leu His Val Ala Thr Asp His Ala Asp
 185 190 195

 tac gca gag tgg atc aat gag cta gtt gag gtc gaa cca ctg ctt gag 739
 Tyr Ala Glu Trp Ile Asn Glu Leu Val Glu Val Glu Pro Leu Leu Glu
 200 205 210

 tac aaa ggc tgg cca tgg gag gaa tgc cct cag ctg act gac cgt cag 787
 Tyr Lys Gly Trp Pro Trp Glu Glu Cys Pro Gln Leu Thr Asp Arg Gln
 215 220 225

 gtc atc acc aag ttt gaa ggc aaa ggc ttg gaa aaa gat cac gtg atc 835
 Val Ile Thr Lys Phe Glu Gly Lys Gly Leu Glu Lys Asp His Val Ile
 230 235 240 245

 aat gag tac ttg tgg cag aag gtg caa aac taatgtctga tgtgcatgag 885
 Asn Glu Tyr Leu Trp Gln Lys Val Gln Asn
 250 255

 gtc 888

<210> 150
 <211> 255
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 150
 Met Ser Ile Ser Asp Asn Ser Arg Asp Gln Leu Gly Glu Leu Pro Ala
 1 5 10 15

 Gly Arg Pro Leu Gln Ser Asp Phe Asp Asn Asp Leu Asp Tyr Pro Arg
 20 25 30

 Leu Gly Ser Val Thr Phe Arg Arg Gly Thr Leu Thr Glu Asn Gln Gln
 35 40 45

 Thr Met Trp Asp Glu Lys Trp Pro Glu Leu Gly Arg Val Leu Glu Asp
 50 55 60

 Glu Leu Ile Asp Val Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr
 65 70 75 80

 Ile Val Glu Ile Gly Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala
 85 90 95

 Pro Leu Glu Ala Asp Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro

100					105					110						
Gly	Leu	Ala	Lys	Leu	Met	Gly	Ser	Val	Val	Arg	Gly	Glu	Ile	Asp	Asn	
115					120					125						
Val	Arg	Met	Val	Arg	Gly	Asp	Gly	Ile	Glu	Val	Leu	Asn	Arg	Met	Phe	
130					135					140						
Ala	Asp	Gly	Ser	Leu	Asp	Gly	Ile	Arg	Val	Tyr	Phe	Pro	Asp	Pro	Trp	
145					150					155					160	
Pro	Lys	Ala	Arg	His	Asn	Lys	Arg	Arg	Ile	Ile	Gln	Ser	Gly	Pro	Leu	
165					170					175						
Asn	Leu	Phe	Ala	Lys	Lys	Leu	Lys	Pro	Gly	Gly	Val	Leu	His	Val	Ala	
180					185					190						
Thr	Asp	His	Ala	Asp	Tyr	Ala	Glu	Trp	Ile	Asn	Glu	Leu	Val	Glu	Val	
195					200					205						
Glu	Pro	Leu	Leu	Glu	Tyr	Lys	Gly	Trp	Pro	Trp	Glu	Glu	Cys	Pro	Gln	
210					215					220						
Leu	Thr	Asp	Arg	Gln	Val	Ile	Thr	Lys	Phe	Glu	Gly	Lys	Gly	Leu	Glu	
225					230					235					240	
Lys	Asp	His	Val	Ile	Asn	Glu	Tyr	Leu	Trp	Gln	Lys	Val	Gln	Asn		
245					250					255						

<210> 151

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> FRXA02589

<400> 151

gcctaaattg cagcgagagg tctaaaaggt agtgctctag ggattcatcc aaactcacga 60

atattgaagt	tttaaagttg	aacaggaaaa	ataacaaata	atg	tct	att	tct	gat	115
				Met	Ser	Ile	Ser	Asp	
				1				5	

aat	tcc	cgc	gat	caa	tta	gga	gaa	ctg	cca	gct	ggg	cgg	cct	ctc	caa	163
Asn	Ser	Arg	Asp	Gln	Leu	Gly	Glu	Leu	Pro	Ala	Gly	Arg	Pro	Leu	Gln	
				10					15					20		

tcc	gat	ttt	gat	aat	gac	ctc	gac	taç	cca	cgt	cta	ggc	agt	gtc	acg	211
Ser	Asp	Phe	Asp	Asn	Asp	Leu	Asp	Tyr	Pro	Arg	Leu	Gly	Ser	Val	Thr	
				25				30					35			

ttt	agg	cgt	ggc	acc	ctc	act	gaa	aac	cag	caa	acc	atg	tgg	gat	gaa	259
Phe	Arg	Arg	Gly	Thr	Leu	Thr	Glu	Asn	Gln	Gln	Thr	Met	Trp	Asp	Glu	
				40				45				50				

aag	tgg	cct	gaa	ctg	ggg	cgc	gtc	ctc	gaa	gat	gag	ctg	att	gat	gtt	307
Lys	Trp	Pro	Glu	Leu	Gly	Arg	Val	Leu	Glu	Asp	Glu	Leu	Ile	Asp	Val	

55	60	65	
gat gcg tgg ttc ggg cgc gaa ggc gca aaa acc atc gta gag atc ggc Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr Ile Val Glu Ile Gly 70 75 80 85			355
tct ggc act gga act tcg act gct gcc atg gct cca ctt gag gct gat Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala Pro Leu Glu Ala Asp 90 95 100			403
acc aac att gtc gcc gtc gaa cta tac aag ccg ggc ttg gcc aag ttg Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro Gly Leu Ala Lys Leu 105 110 115			451
atg ggc tct gtt gtc cgt gga gag atc gac aac gtg cgc atg gtc cgc Met Gly Ser Val Val Arg Gly Glu Ile Asp Asn Val Arg Met Val Arg 120 125 130			499
gga gac ggc atc gag gtg ctc aac cgc atg ttt gcc gat ggg tcc ctg Gly Asp Gly Ile Glu Val Leu Asn Arg Met Phe Ala Asp Gly Ser Leu 135 140 145			547
gac ggc atc cgc gta tac ttc ccg gac cct tgg cca aag gcg cgc cac Asp Gly Ile Arg Val Tyr Phe Pro Asp Pro Trp Pro Lys Ala Arg His 150 155 160 165			595
aac aag cgc cgc atc atc cag tct ggt ccg ctg aac ctg ttt gca aag Asn Lys Arg Arg Ile Ile Gln Ser Gly Pro Leu Asn Leu Phe Ala Lys 170 175 180			643
aag ctc aag cca ggt gga gtt ctg cac gtt gct acc gac cac gct gat Lys Leu Lys Pro Gly Gly Val Leu His Val Ala Thr Asp His Ala Asp 185 190 195			691
tac gca gag tgg atc aat gag cta gtt gag gtc gaa cca ctg ctt gag Tyr Ala Glu Trp Ile Asn Glu Leu Val Glu Val Glu Pro Leu Leu Glu 200 205 210			739
tac aaa ggc tgg cca tgg gag gaa tgc cct cag ctg act gac cgt cag Tyr Lys Gly Trp Pro Trp Glu Glu Cys Pro Gln Leu Thr Asp Arg Gln 215 220 225			787
gtc atc acc aag ttt gaa ggc aaa ggc ttg gaa aaa gat cac gtg atc Val Ile Thr Lys Phe Glu Gly Lys Gly Leu Glu Lys Asp His Val Ile 230 235 240 245			835
aat gag tac ttg tgg cag aag gtg caa aac taatgtctga tgtgcatgag Asn Glu Tyr Leu Trp Gln Lys Val Gln Asn 250 255			885
gtc			888

<210> 152

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Met	Ser	Ile	Ser	Asp	Asn	Ser	Arg	Asp	Gln	Leu	Gly	Glu	Leu	Pro	Ala
1				5					10					15	

Gly Arg Pro Leu Gln Ser Asp Phe Asp Asn Asp Leu Asp Tyr Pro Arg
 20 25 30
 Leu Gly Ser Val Thr Phe Arg Arg Gly Thr Leu Thr Glu Asn Gln Gln
 35 40 45
 Thr Met Trp Asp Glu Lys Trp Pro Glu Leu Gly Arg Val Leu Glu Asp
 50 55 60
 Glu Leu Ile Asp Val Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr
 65 70 75 80
 Ile Val Glu Ile Gly Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala
 85 90 95
 Pro Leu Glu Ala Asp Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro
 100 105 110
 Gly Leu Ala Lys Leu Met Gly Ser Val Val Arg Gly Glu Ile Asp Asn
 115 120 125
 Val Arg Met Val Arg Gly Asp Gly Ile Glu Val Leu Asn Arg Met Phe
 130 135 140
 Ala Asp Gly Ser Leu Asp Gly Ile Arg Val Tyr Phe Pro Asp Pro Trp
 145 150 155 160
 Pro Lys Ala Arg His Asn Lys Arg Arg Ile Ile Gln Ser Gly Pro Leu
 165 170 175
 Asn Leu Phe Ala Lys Lys Leu Lys Pro Gly Gly Val Leu His Val Ala
 180 185 190
 Thr Asp His Ala Asp Tyr Ala Glu Trp Ile Asn Glu Leu Val Glu Val
 195 200 205
 Glu Pro Leu Leu Glu Tyr Lys Gly Trp Pro Trp Glu Glu Cys Pro Gln
 210 215 220
 Leu Thr Asp Arg Gln Val Ile Thr Lys Phe Glu Gly Lys Gly Leu Glu
 225 230 235 240
 Lys Asp His Val Ile Asn Glu Tyr Leu Trp Gln Lys Val Gln Asn
 245 250 255

<210> 153

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> RXA00226

<400> 153

ccgcctgcgg tgtcagcgga gcgcgcccgg cgtctgaaaa ctgcacttgg tgagaacgtg 60

attgttcattg atgtcacctg ttccatcggt acggaggggc atg aac tta tctg atg 115

											Met	Asn	Leu	Ser	Met	
											1				5	
ccg	gcc	ttc	gct	acc	tgg	gtt	ctg	atc	cta	gat	ttc	tca	cgc	acc	ctc	163
Pro	Ala	Phe	Ala	Thr	Trp	Val	Leu	Ile	Leu	Asp	Phe	Ser	Arg	Thr	Leu	
				10					15					20		
atg	gca	gcc	cac	aat	ctc	cag	ggc	aaa	aac	gcc	ctg	att	ttc	cgc	gcc	211
Met	Ala	Ala	His	Asn	Leu	Gln	Gly	Lys	Asn	Ala	Leu	Ile	Phe	Arg	Ala	
				25					30					35		
gac	gcg	ctc	cag	ccc	gca	agc	agg	gga	gcc	gac	gtc	atc	atc	gcg	gac	259
Asp	Ala	Leu	Gln	Pro	Ala	Ser	Arg	Gly	Ala	Asp	Val	Ile	Ile	Ala	Asp	
				40					45					50		
cct	gcc	aga	cgc	gcc	ggg	ggc	aag	cgc	att	aca	aat	ccg	gca	cag	ctc	307
Pro	Ala	Arg	Arg	Ala	Gly	Gly	Lys	Arg	Ile	Thr	Asn	Pro	Ala	Gln	Leu	
				55					60					65		
ctg	cca	cct	ctg	cct	tcg	ctt	ctc	gac	gcc	tgg	atc	aac	caa	cca	ctc	355
Leu	Pro	Pro	Leu	Pro	Ser	Leu	Leu	Asp	Ala	Trp	Ile	Asn	Gln	Pro	Leu	
				70					75					80		
gcc	gtt	aaa	tgt	gcc	ccc	ggc	ctt	gat	ttt	tcg	gaa	tgg	cca	ggt	ctc	403
Ala	Val	Lys	Cys	Ala	Pro	Gly	Leu	Asp	Phe	Ser	Glu	Trp	Pro	Gly	Leu	
				90					95					100		
gtc	agt	att	gcc	agc	gtt	gat	gga	ggc	gtg	aaa	gaa	gca	tgc	ctc	tac	451
Val	Ser	Ile	Ala	Ser	Val	Asp	Gly	Gly	Val	Lys	Glu	Ala	Cys	Leu	Tyr	
				105					110					115		
act	acg	gat	ctg	gca	gat	ggg	gaa	act	cgc	gaa	gct	atc	gtg	atc	aaa	499
Thr	Thr	Asp	Leu	Ala	Asp	Gly	Glu	Thr	Arg	Glu	Ala	Ile	Val	Ile	Lys	
				120					125					130		
gat	ggg	ctc	att	gac	cgc	atc	acc	aac	ttt	gaa	gac	gat	gcc	acg	gga	547
Asp	Gly	Leu	Ile	Asp	Arg	Ile	Thr	Asn	Phe	Glu	Asp	Asp	Ala	Thr	Gly	
				135					140					145		
caa	gac	ctt	gcg	gct	gca	cct	ggt	gag	ttc	atc	atc	gac	cca	gac	ggt	595
Gln	Asp	Leu	Ala	Ala	Ala	Pro	Gly	Glu	Phe	Ile	Ile	Asp	Pro	Asp	Gly	
				150					155					160		
gcc	atc	gtg	cgc	gcc	ggg	ttg	gtt	cgc	cac	tat	gca	gtg	cgt	gag	cag	643
Ala	Ile	Val	Arg	Ala	Gly	Leu	Val	Arg	His	Tyr	Ala	Val	Arg	Glu	Gln	
				170					175					180		
ctg	tgg	atg	ttg	gat	gag	cgg	atc	gca	tac	ctt	acg	ggc	aat	cgg	att	691
Leu	Trp	Met	Leu	Asp	Glu	Arg	Ile	Ala	Tyr	Leu	Thr	Gly	Asn	Arg	Ile	
				185					190					195		
cca	gag	ggt	acc	agc	ggt	ttt	agg	ttt	att	gaa	gag	gtt	ccg	ctg	aag	739
Pro	Glu	Gly	Thr	Ser	Gly	Phe	Arg	Phe	Ile	Glu	Glu	Val	Pro	Leu	Lys	
				200					205					210		
aag	ctg	aaa	tcg	gcg	atg	gca	gca	cat	gat	gcg	ggg	gcg	gtt	gaa	att	787
Lys	Leu	Lys	Ser	Ala	Met	Ala	Ala	His	Asp	Ala	Gly	Ala	Val	Glu	Ile	
				215					220					225		
tta	gtg	cgt	ggt	gtt	gat	gtt	gat	cct	gat	cag	ttg	cgg	aaa	aga	ttg	835
Leu	Val	Arg	Gly	Val	Asp	Val	Asp	Pro	Asp	Gln	Leu	Arg	Lys	Arg	Leu	

230	235	240	245	
cag ctg aag ggt acc aag gcg atg tct gtg gtg atc act cga att ggc				883
Gln Leu Lys Gly Thr Lys Ala Met Ser Val Val Ile Thr Arg Ile Gly				
250		255	260	
agc cga ggg gtt gca ttg att tgt ggt cct cgc gag cgc gcc				925
Ser Arg Gly Val Ala Leu Ile Cys Gly Pro Arg Glu Arg Ala				
265	270		275	
taaagccgat gcaaataaaaa ttg				948

<210> 154
 <211> 275
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 154
 Met Asn Leu Ser Met Pro Ala Phe Ala Thr Trp Val Leu Ile Leu Asp
 1 5 10 15
 Phe Ser Arg Thr Leu Met Ala Ala His Asn Leu Gln Gly Lys Asn Ala
 20 25 30
 Leu Ile Phe Arg Ala Asp Ala Leu Gln Pro Ala Ser Arg Gly Ala Asp
 35 40 45
 Val Ile Ile Ala Asp Pro Ala Arg Arg Ala Gly Gly Lys Arg Ile Thr
 50 55 60
 Asn Pro Ala Gln Leu Leu Pro Pro Leu Pro Ser Leu Leu Asp Ala Trp
 65 70 75 80
 Ile Asn Gln Pro Leu Ala Val Lys Cys Ala Pro Gly Leu Asp Phe Ser
 85 90 95
 Glu Trp Pro Gly Leu Val Ser Ile Ala Ser Val Asp Gly Gly Val Lys
 100 105 110
 Glu Ala Cys Leu Tyr Thr Thr Asp Leu Ala Asp Gly Glu Thr Arg Glu
 115 120 125
 Ala Ile Val Ile Lys Asp Gly Leu Ile Asp Arg Ile Thr Asn Phe Glu
 130 135 140
 Asp Asp Ala Thr Gly Gln Asp Leu Ala Ala Ala Pro Gly Glu Phe Ile
 145 150 155 160
 Ile Asp Pro Asp Gly Ala Ile Val Arg Ala Gly Leu Val Arg His Tyr
 165 170 175
 Ala Val Arg Glu Gln Leu Trp Met Leu Asp Glu Arg Ile Ala Tyr Leu
 180 185 190
 Thr Gly Asn Arg Ile Pro Glu Gly Thr Ser Gly Phe Arg Phe Ile Glu
 195 200 205
 Glu Val Pro Leu Lys Lys Leu Lys Ser Ala Met Ala Ala His Asp Ala
 210 215 220

Gly Ala Val Glu Ile Leu Val Arg Gly Val Asp Val Asp Pro Asp Gln
 225 230 235 240

Leu Arg Lys Arg Leu Gln Leu Lys Gly Thr Lys Ala Met Ser Val Val
 245 250 255

Ile Thr Arg Ile Gly Ser Arg Gly Val Ala Leu Ile Cys Gly Pro Arg
 260 265 270

Glu Arg Ala
 275

<210> 155
 <211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> RXN01885

<400> 155
 gtggcgctcgc aggggatgttc ctgcggcacc atttttgctg aggtggaact cacggattaa 60
 acacggattt ttctaagggtt aatcaagtaa ggtttacctt atg act acg aaa cct 115
 Met Thr Thr Lys Pro
 1 5

atc atc cca gaa tca acc cac tcc gca gaa cgt gct ggt gga cat tgg 163
 Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg Ala Gly Gly His Trp
 10 15 20

atc ctt gcc agg ctt gga aag aaa gtg ctg cgc cct gga ggt cgt gaa 211
 Ile Leu Ala Arg Leu Gly Lys Lys Val Leu Arg Pro Gly Gly Arg Glu
 25 30 35

aca acg cag ttc ctg ctg gag aac ctt tct ttg acc ggt gct acc gtg 259
 Thr Thr Gln Phe Leu Leu Glu Asn Leu Ser Leu Thr Gly Ala Thr Val
 40 45 50

gtg gaa ttt gct cca gga ctt ggc gtg act gca cgt gac atc ctt ggc 307
 Val Glu Phe Ala Pro Gly Leu Gly Val Thr Ala Arg Asp Ile Leu Gly
 55 60 65

aag ggt ccg gct cgc tac atc gga gtg gat agc gac gcg gat gca tgc 355
 Lys Gly Pro Ala Arg Tyr Ile Gly Val Asp Ser Asp Ala Asp Ala Cys
 70 75 80 85

gcg aat gta cgt gcg atc tta cct gct ggt cct cac gag gtg cgc aat 403
 Ala Asn Val Arg Ala Ile Leu Pro Ala Gly Pro His Glu Val Arg Asn
 90 95 100

aca aat gcc acc gat act ggc ctt gaa agc gac tcg ttt gat gtt gtc 451
 Thr Asn Ala Thr Asp Thr Gly Leu Glu Ser Asp Ser Phe Asp Val Val
 105 110 115

atc ggc gaa gcg atg ttg acc atg cag acc gat aag cac aag ttg gag 499
 Ile Gly Glu Ala Met Leu Thr Met Gln Thr Asp Lys His Lys Leu Glu
 120 125 130

ctg atg cgc gag gca gct cga att ctg aaa cca ggc ggg ctg tac ggc 547
 Leu Met Arg Glu Ala Ala Arg Ile Leu Lys Pro Gly Gly Leu Tyr Gly
 135 140 145

 att cac gag ctg tcg ctg gtg cct gac aat gtc tcc act gcg gtg aaa 595
 Ile His Glu Leu Ser Leu Val Pro Asp Asn Val Ser Thr Ala Val Lys
 150 155 160 165

 gag gat att gct aag gcg ctg gct cgt tcc atc aaa gtc aat gcc cgc 643
 Glu Asp Ile Ala Lys Ala Leu Ala Arg Ser Ile Lys Val Asn Ala Arg
 170 175 180

 ccc atc acg gtg ccg gaa tgg gct gcg ttg gcg cgt gag gca ggg ttc 691
 Pro Ile Thr Val Pro Glu Trp Ala Ala Leu Ala Arg Glu Ala Gly Phe
 185 190 195

 gat gtg att aat att cgc caa gcc gac atg gcc ctt cta tcc ctc aag 739
 Asp Val Ile Asn Ile Arg Gln Ala Asp Met Ala Leu Leu Ser Leu Lys
 200 205 210

 cgg aac ctg aag gat gaa ggg cta aaa ggt gtc ttc acg att gtg agg 787
 Arg Asn Leu Lys Asp Glu Gly Leu Lys Gly Val Phe Thr Ile Val Arg
 215 220 225

 aac gtg att agc caa ccg gat ctg cgc aag cga gtg ctc gga atg cga 835
 Asn Val Ile Ser Gln Pro Asp Leu Arg Lys Arg Val Leu Gly Met Arg
 230 235 240 245

 aag act ttc acc gag cat aaa gat cac tta ggt gcg gtt ggc atc att 883
 Lys Thr Phe Thr Glu His Lys Asp His Leu Gly Ala Val Gly Ile Ile
 250 255 260

 ttg cag aag aga gcc caa tagggatctg aaatggaggg gtg 924
 Leu Gln Lys Arg Ala Gln
 265

<210> 156

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Thr Thr Lys Pro Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg
 1 5 10 15

 Ala Gly Gly His Trp Ile Leu Ala Arg Leu Gly Lys Lys Val Leu Arg
 20 25 30

 Pro Gly Gly Arg Glu Thr Thr Gln Phe Leu Leu Glu Asn Leu Ser Leu
 35 40 45

 Thr Gly Ala Thr Val Val Glu Phe Ala Pro Gly Leu Gly Val Thr Ala
 50 55 60

 Arg Asp Ile Leu Gly Lys Gly Pro Ala Arg Tyr Ile Gly Val Asp Ser
 65 70 75 80

 Asp Ala Asp Ala Cys Ala Asn Val Arg Ala Ile Leu Pro Ala Gly Pro
 85 90 95

His Glu Val Arg Asn Thr Asn Ala Thr Asp Thr Gly Leu Glu Ser Asp
 100 105 110
 Ser Phe Asp Val Val Ile Gly Glu Ala Met Leu Thr Met Gln Thr Asp
 115 120 125
 Lys His Lys Lys Leu Glu Leu Met Arg Glu Ala Ala Arg Ile Leu Lys Pro
 130 135 140
 Gly Gly Leu Tyr Gly Ile His Glu Leu Ser Leu Val Pro Asp Asn Val
 145 150 155 160
 Ser Thr Ala Val Lys Glu Asp Ile Ala Lys Ala Leu Ala Arg Ser Ile
 165 170 175
 Lys Val Asn Ala Arg Pro Ile Thr Val Pro Glu Trp Ala Ala Leu Ala
 180 185 190
 Arg Glu Ala Gly Phe Asp Val Ile Asn Ile Arg Gln Ala Asp Met Ala
 195 200 205
 Leu Leu Ser Leu Lys Arg Asn Leu Lys Asp Glu Gly Leu Lys Gly Val
 210 215 220
 Phe Thr Ile Val Arg Asn Val Ile Ser Gln Pro Asp Leu Arg Lys Arg
 225 230 235 240
 Val Leu Gly Met Arg Lys Thr Phe Thr Glu His Lys Asp His Leu Gly
 245 250 255
 Ala Val Gly Ile Ile Leu Gln Lys Arg Ala Gln
 260 265

<210> 157
 <211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> FRXA01885

<400> 157
 gtggcgtcgc agggatgttc ctgoggcacc atttttgctg aggtggaact cacggattaa 60
 acacggattt ttctaagggtt aatcaagtaa ggtttacctt atg act acg aaa cct 115
 Met Thr Thr Lys Pro
 1 5
 atc atc cca gaa tca acc cac tcc gca gaa cgt gct ggt gga cat tgg 163
 Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg Ala Gly Gly His Trp
 10 15 20
 atc ctt gcc agg ctt gga aag aaa gtg ctg cgc cct gga ggt cgt gaa 211
 Ile Leu Ala Arg Leu Gly Lys Lys Val Leu Arg Pro Gly Gly Arg Glu
 25 30 35
 aca acg cag ttc ctg ctg gag aac ctt tct ttg acc ggt gct acc gtg 259

Thr	Thr	Gln	Phe	Leu	Leu	Glu	Asn	Leu	Ser	Leu	Thr	Gly	Ala	Thr	Val		
		40					45					50					
gtg	gaa	ttt	gct	cca	gga	ctt	ggc	gtg	act	gca	cgt	gac	atc	ctt	ggc	307	
Val	Glu	Phe	Ala	Pro	Gly	Leu	Gly	Val	Thr	Ala	Arg	Asp	Ile	Leu	Gly		
	55					60					65						
aag	ggt	ccg	gct	cgc	tac	atc	gga	gtg	gat	agc	gac	gcg	gat	gca	tgc	355	
Lys	Gly	Pro	Ala	Arg	Tyr	Ile	Gly	Val	Asp	Ser	Asp	Ala	Asp	Ala	Cys		
	70				75					80					85		
gcg	aat	gta	cgt	gcg	atc	tta	cct	gct	ggg	cct	cac	gag	gtg	cg	aat	403	
Ala	Asn	Val	Arg	Ala	Ile	Leu	Pro	Ala	Gly	Pro	His	Glu	Val	Arg	Asn		
				90					95					100			
aca	aat	gcc	acc	gat	act	ggc	ctt	gaa	agc	gac	tcg	ttt	gat	gtt	gtc	451	
Thr	Asn	Ala	Thr	Asp	Thr	Gly	Leu	Glu	Ser	Asp	Ser	Phe	Asp	Val	Val		
			105					110					115				
atc	ggc	gaa	gcg	atg	ttg	acc	atg	cag	acc	gat	aag	cac	aag	ttg	gag	499	
Ile	Gly	Glu	Ala	Met	Leu	Thr	Met	Gln	Thr	Asp	Lys	His	Lys	Leu	Glu		
		120					125					130					
ctg	atg	cgc	gag	gca	gct	cga	att	ctg	aaa	cca	ggc	ggg	ctg	tac	ggc	547	
Leu	Met	Arg	Glu	Ala	Ala	Arg	Ile	Leu	Lys	Pro	Gly	Gly	Leu	Tyr	Gly		
	135					140					145						
att	cac	gag	ctg	tcg	ctg	gtg	cct	gac	aat	gtc	tcc	act	gcg	gtg	aaa	595	
Ile	His	Glu	Leu	Ser	Leu	Val	Pro	Asp	Asn	Val	Ser	Thr	Ala	Val	Lys		
	150				155					160					165		
gag	gat	att	gct	aag	gcg	ctg	gct	cgt	tcc	atc	aaa	gtc	aat	gcc	cgc	643	
Glu	Asp	Ile	Ala	Lys	Ala	Leu	Ala	Arg	Ser	Ile	Lys	Val	Asn	Ala	Arg		
				170					175					180			
ccc	atc	acg	gtg	ccg	gaa	tgg	gct	gcg	ttg	gcg	cgt	gag	gca	ggg	ttc	691	
Pro	Ile	Thr	Val	Pro	Glu	Trp	Ala	Ala	Leu	Ala	Arg	Glu	Ala	Gly	Phe		
			185					190					195				
gat	gtg	att	aat	att	cgc	caa	gcc	gac	atg	gcc	ctt	cta	tcc	ctc	aag	739	
Asp	Val	Ile	Asn	Ile	Arg	Gln	Ala	Asp	Met	Ala	Leu	Leu	Ser	Leu	Lys		
		200					205					210					
cg	aac	ctg	aag	gat	gaa	ggg	cta	aaa	ggg	gtc	ttc	acg	att	gtg	agg	787	
Arg	Asn	Leu	Lys	Asp	Glu	Gly	Leu	Lys	Gly	Val	Phe	Thr	Ile	Val	Arg		
	215					220					225						
aac	gtg	att	agc	caa	ccg	gat	ctg	cgc	aag	cga	gtg	ctc	gga	atg	cga	835	
Asn	Val	Ile	Ser	Gln	Pro	Asp	Leu	Arg	Lys	Arg	Val	Leu	Gly	Met	Arg		
	230				235					240				245			
aag	act	ttc	acc	gag	cat	aaa	gat	cac	tta	ggg	gcg	gtt	ggc	atc	att	883	
Lys	Thr	Phe	Thr	Glu	His	Lys	Asp	His	Leu	Gly	Ala	Val	Gly	Ile	Ile		
				250				255					260				
ttg	cag	aag	aga	gcc	caa	taggg	gat	ctg	aaatg	ggagg	gtg					924	
Leu	Gln	Lys	Arg	Ala	Gln												
				265													

<210> 158

<211> 267

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 158

```

Met Thr Thr Lys Pro Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg
 1             5             10             15
Ala Gly Gly His Trp Ile Leu Ala Arg Leu Gly Lys Lys Val Leu Arg
          20             25             30
Pro Gly Gly Arg Glu Thr Thr Gln Phe Leu Leu Glu Asn Leu Ser Leu
      35             40             45
Thr Gly Ala Thr Val Val Glu Phe Ala Pro Gly Leu Gly Val Thr Ala
 50             55             60
Arg Asp Ile Leu Gly Lys Gly Pro Ala Arg Tyr Ile Gly Val Asp Ser
 65             70             75             80
Asp Ala Asp Ala Cys Ala Asn Val Arg Ala Ile Leu Pro Ala Gly Pro
          85             90             95
His Glu Val Arg Asn Thr Asn Ala Thr Asp Thr Gly Leu Glu Ser Asp
          100             105             110
Ser Phe Asp Val Val Ile Gly Glu Ala Met Leu Thr Met Gln Thr Asp
          115             120             125
Lys His Lys Leu Glu Leu Met Arg Glu Ala Ala Arg Ile Leu Lys Pro
 130             135             140
Gly Gly Leu Tyr Gly Ile His Glu Leu Ser Leu Val Pro Asp Asn Val
 145             150             155             160
Ser Thr Ala Val Lys Glu Asp Ile Ala Lys Ala Leu Ala Arg Ser Ile
          165             170             175
Lys Val Asn Ala Arg Pro Ile Thr Val Pro Glu Trp Ala Ala Leu Ala
          180             185             190
Arg Glu Ala Gly Phe Asp Val Ile Asn Ile Arg Gln Ala Asp Met Ala
          195             200             205
Leu Leu Ser Leu Lys Arg Asn Leu Lys Asp Glu Gly Leu Lys Gly Val
 210             215             220
Phe Thr Ile Val Arg Asn Val Ile Ser Gln Pro Asp Leu Arg Lys Arg
 225             230             235             240
Val Leu Gly Met Arg Lys Thr Phe Thr Glu His Lys Asp His Leu Gly
          245             250             255
Ala Val Gly Ile Ile Leu Gln Lys Arg Ala Gln
          260             265

```

<210> 159

<211> 894

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(871)

<223> RXA02592

<400> 159

aaacaccacc attgtttcct ccacgcacga tgccatcacc accattttgc gatggatgaa 60

cggcgaagac atccgcgacc tcaactggac ccgcgcataa atg gcc tca ttt ccg 115
 Met Ala Ser Phe Pro
 1 5

gag ctt ccg get ctt cgt cgc ttg gct acc ttg ggc agg tcg tgg ggt 163
 Glu Leu Pro Ala Leu Arg Arg Leu Ala Thr Leu Gly Arg Ser Trp Gly
 10 15 20

tta ctg tct gat ttc aaa tac gaa caa acc cga cct gac atc ttt tac 211
 Leu Leu Ser Asp Phe Lys Tyr Glu Gln Thr Arg Pro Asp Ile Phe Tyr
 25 30 35

gga aac ctg gcc ctc gat acc tcg agt ctg gtg gcg gct ttg tct gaa 259
 Gly Asn Leu Ala Leu Asp Thr Ser Ser Leu Val Ala Ala Leu Ser Glu
 40 45 50

gat att tct ggc gcc gga tta aat gac ctg aaa gtt ctc gac gtc ggc 307
 Asp Ile Ser Gly Ala Gly Leu Asn Asp Leu Lys Val Leu Asp Val Gly
 55 60 65

ggc gga ccc gga tac ttc gcc gaa gcc ttt gag aca ctg ggc gcc acc 355
 Gly Gly Pro Gly Tyr Phe Ala Glu Ala Phe Glu Thr Leu Gly Ala Thr
 70 75 80 85

tac ttc tcc gtc gaa ccc gac gtt ggc gaa atg tcc gca gct ggc atc 403
 Tyr Phe Ser Val Glu Pro Asp Val Gly Glu Met Ser Ala Ala Gly Ile
 90 95 100

gac gtc cac gga tca gtc cgc gga tcc ggc ctc gac ctg ccg ttt ctt 451
 Asp Val His Gly Ser Val Arg Gly Ser Gly Leu Asp Leu Pro Phe Leu
 105 110 115

ccc gat tcc ttt gac gtg gtg tac tcc tcc aac gtt gca gaa cat gtc 499
 Pro Asp Ser Phe Asp Val Val Tyr Ser Ser Asn Val Ala Glu His Val
 120 125 130

tcc gca ccg tgg gaa ttg gga gaa gaa atg ctc cgc gtc acc cgc agc 547
 Ser Ala Pro Trp Glu Leu Gly Glu Glu Met Leu Arg Val Thr Arg Ser
 135 140 145

ggc ggc ctg gca atc ctg agc tac acc att tgg tta ggg ccc ttc ggc 595
 Gly Gly Leu Ala Ile Leu Ser Tyr Thr Ile Trp Leu Gly Pro Phe Gly
 150 155 160 165

ggc cat gaa acc gga ctg tgg gaa cac tac gtt ggc gga gaa ttt gcc 643
 Gly His Glu Thr Gly Leu Trp Glu His Tyr Val Gly Gly Glu Phe Ala
 170 175 180

cgc gat cgc tac acg aag aaa cac ggc cac ccg cct aag aac gtt ttc 691
 Arg Asp Arg Tyr Thr Lys Lys His Gly His Pro Pro Lys Asn Val Phe
 185 190 195

ggg gag tca ctg ttt aat gtg tcc tgc cgg gag ggg ctg gaa tgg gga 739
 Gly Glu Ser Leu Phe Asn Val Ser Cys Arg Glu Gly Leu Glu Trp Gly
 200 205 210

gcc tcc gtg ggc aat gcg gaa ttg gtt gcc gct ttt ccc cgc tac cac 787
 Ala Ser Val Gly Asn Ala Glu Leu Val Ala Ala Phe Pro Arg Tyr His
 215 220 225

ccg tat tgg gtc tgg tgg atg gtt aaa gtc cca gtg ctc cga gaa ttc 835
 Pro Tyr Trp Val Trp Trp Met Val Lys Val Pro Val Leu Arg Glu Phe
 230 235 240 245

gcg gta agt aac ttg gtg ttg gtg ttt aaa aag cac tgaggttttg 881
 Ala Val Ser Asn Leu Val Leu Val Phe Lys Lys His
 250 255

aggaattcat cgc 894

<210> 160

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Ala Ser Phe Pro Glu Leu Pro Ala Leu Arg Arg Leu Ala Thr Leu
 1 5 10 15

Gly Arg Ser Trp Gly Leu Leu Ser Asp Phe Lys Tyr Glu Gln Thr Arg
 20 25 30

Pro Asp Ile Phe Tyr Gly Asn Leu Ala Leu Asp Thr Ser Ser Leu Val
 35 40 45

Ala Ala Leu Ser Glu Asp Ile Ser Gly Ala Gly Leu Asn Asp Leu Lys
 50 55 60

Val Leu Asp Val Gly Gly Gly Pro Gly Tyr Phe Ala Glu Ala Phe Glu
 65 70 75 80

Thr Leu Gly Ala Thr Tyr Phe Ser Val Glu Pro Asp Val Gly Glu Met
 85 90 95

Ser Ala Ala Gly Ile Asp Val His Gly Ser Val Arg Gly Ser Gly Leu
 100 105 110

Asp Leu Pro Phe Leu Pro Asp Ser Phe Asp Val Val Tyr Ser Ser Asn
 115 120 125

Val Ala Glu His Val Ser Ala Pro Trp Glu Leu Gly Glu Glu Met Leu
 130 135 140

Arg Val Thr Arg Ser Gly Gly Leu Ala Ile Leu Ser Tyr Thr Ile Trp
 145 150 155 160

Leu Gly Pro Phe Gly Gly His Glu Thr Gly Leu Trp Glu His Tyr Val
 165 170 175

Gly Gly Glu Phe Ala Arg Asp Arg Tyr Thr Lys Lys His Gly His Pro
 180 185 190

Pro Lys Asn Val Phe Gly Glu Ser Leu Phe Asn Val Ser Cys Arg Glu
 195 200 205

Gly Leu Glu Trp Gly Ala Ser Val Gly Asn Ala Glu Leu Val Ala Ala
 210 215 220

Phe Pro Arg Tyr His Pro Tyr Trp Val Trp Trp Met Val Lys Val Pro
 225 230 235 240

Val Leu Arg Glu Phe Ala Val Ser Asn Leu Val Leu Val Phe Lys Lys
 245 250 255

His

<210> 161
 <211> 720
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(697)
 <223> RXN01795

<400> 161
 agaccatatt gaagacctcg aagctgttga gcctggctac atcgtaagc ctcgcctgta 60

caacttcgct gaatacgggtg tcccacaatt ccgcgaacgt gtg ctc att gtt ggc 115
 Val Leu Ile Val Gly
 1 5

att cgc cgt gac acc ggc ttt gat ttc aag cac cca gct cct acc cat 163
 Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His Pro Ala Pro Thr His
 10 15 20

ggc cct cgc ggt gac atg ccg tat aag act gcc ggc gaa gcg ctc aaa 211
 Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala Gly Glu Ala Leu Lys
 25 30 35

ggc gtg aag gat gtc ccc aca aac aac aac cac atg aag atc atg cct 259
 Gly Val Lys Asp Val Pro Thr Asn Asn His Met Lys Ile Met Pro
 40 45 50

cgc acc gtt gaa gtg ctt aag cgc atc cct gag ggc gaa aac ttc acc 307
 Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu Gly Glu Asn Phe Thr
 55 60 65

gcg atc ccc aaa gat gac ccc tac tac gtc aag ggc atg att agt cac 355
 Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys Gly Met Ile Ser His
 70 75 80 85

gtt tac cgt cgc ttg cac cgt gat gag cca tcc aaa acc ctt atc gcc 403
 Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser Lys Thr Leu Ile Ala
 90 95 100

ggg ggc ggc ggc ggt aca tgg gga tac cat tat gaa aaa aat cga gca 451
 Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr Glu Lys Asn Arg Ala
 105 110 115

ttg acc aac cgc gag cgg gct aga att caa tgc ttc ccc gat gac ttt 499
 Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser Phe Pro Asp Asp Phe
 120 125 130
 gag ttt ttg gga tca aac acc gaa gtc cgc cgc caa atc ggt aat gct 547
 Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg Gln Ile Gly Asn Ala
 135 140 145
 gtt cct cct gta ggt atg cac gct gtg ggt gag cga ctg atg aac ctg 595
 Val Pro Pro Val Gly Met His Ala Val Gly Glu Arg Leu Met Asn Leu
 150 155 160 165
 tac acc ggg aat tac act ccc gtc gat cta gag gaa cag cac gcg tac 643
 Tyr Thr Gly Asn Tyr Thr Pro Val Asp Leu Glu Glu Gln His Ala Tyr
 170 175 180
 ctg cag acg ctc tcc att aag gaa cgt ctc gcg ctg gct gat cag gaa 691
 Leu Gln Thr Leu Ser Ile Lys Glu Arg Leu Ala Leu Ala Asp Gln Glu
 185 190 195
 gct gat taagtagata tatgaagccc acc 720
 Ala Asp

<210> 162

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Val Leu Ile Val Gly Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His
 1 5 10 15
 Pro Ala Pro Thr His Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala
 20 25 30
 Gly Glu Ala Leu Lys Gly Val Lys Asp Val Pro Thr Asn Asn Asn His
 35 40 45
 Met Lys Ile Met Pro Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu
 50 55 60
 Gly Glu Asn Phe Thr Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys
 65 70 75 80
 Gly Met Ile Ser His Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser
 85 90 95
 Lys Thr Leu Ile Ala Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr
 100 105 110
 Glu Lys Asn Arg Ala Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser
 115 120 125
 Phe Pro Asp Asp Phe Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg
 130 135 140
 Gln Ile Gly Asn Ala Val Pro Pro Val Gly Met His Ala Val Gly Glu
 145 150 155 160

<400> 163															
agaccatatt gaagacctcg aagctgttga gcctggctac atcgtcaagc ctcgcctgta 60															
caacttcgct gaatacggtg tcccacaatt ccgcgaacgt gtg ctc att gtt ggc 115															
Val Leu Ile Val Gly 5															
att cgc cgt gac acc ggc ttt gat ttc aag cac cca gct cct acc cat 163															
Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His Pro Ala Pro Thr His 10 15 20															
ggc cct cgc ggt gac atg ccg tat aag act gcc ggc gaa gcg ctc aaa 211															
Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala Gly Glu Ala Leu Lys 25 30 35															
ggc gtg aag gat gtc ccc aca aac aac aac cac atg aag atc atg cct 259															
Gly Val Lys Asp Val Pro Thr Asn Asn Asn His Met Lys Ile Met Pro 40 45 50															
cgc acc gtt gaa gtg ctt aag cgc atc cct gag ggc gaa aac ttc acc 307															
Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu Gly Glu Asn Phe Thr 55 60 65															
gcg atc ccc aaa gat gac ccc tac tac gtc aag ggc atg att agt cac 355															
Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys Gly Met Ile Ser His 70 75 80 85															
gtt tac cgt cgc ttg cac cgt gat gag cca tcc aaa acc ctt atc gcc 403															
Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser Lys Thr Leu Ile Ala 90 95 100															
ggt ggc ggc ggg ggt aca tgg gga tac cat tat gaa aaa aat cga gca 451															
Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr Glu Lys Asn Arg Ala 105 110 115															
ttg acc aac cgc gag cgg gct aga att caa tcg ttc ccc gat gac ttt 499															
Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser Phe Pro Asp Asp Phe 120 125 130															
gag ttt ttg gga tca aac acc caa gtc cgc cgc caa 535															
Glu Phe Leu Gly Ser Asn Thr Gln Val Arg Arg Gln															

135

140

145

<210> 164

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Val Leu Ile Val Gly Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His
 1 5 10 15

Pro Ala Pro Thr His Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala
 20 25 30

Gly Glu Ala Leu Lys Gly Val Lys Asp Val Pro Thr Asn Asn Asn His
 35 40 45

Met Lys Ile Met Pro Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu
 50 55 60

Gly Glu Asn Phe Thr Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys
 65 70 75 80

Gly Met Ile Ser His Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser
 85 90 95

Lys Thr Leu Ile Ala Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr
 100 105 110

Glu Lys Asn Arg Ala Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser
 115 120 125

Phe Pro Asp Asp Phe Glu Phe Leu Gly Ser Asn Thr Gln Val Arg Arg
 130 135 140

Gln

145

<210> 165

<211> 1614

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1591)

<223> RXA01214

<400> 165

gttgatatga tgtgggggtgt ttatgaaaat ttgtttgagg gagtgaaggc gcatgttggtt 60

gccagagttg aatcgctcgga cttttttcaa aggggccggg gtg ctg gca gca acg 115
 Val Leu Ala Ala Thr
 1 5

gtg gtg ggt gcg cag gtg ctg gtg gcg tgt tcc tca gat gat gtg cgt 163
 Val Val Gly Ala Gln Val Leu Val Ala Cys Ser Ser Asp Asp Val Arg
 10 15 20

ggt tat ggg gga gag ccg cgg acg ttg cct att cca cca gca gat tta	211
Gly Tyr Gly Gly Glu Pro Arg Thr Leu Pro Ile Pro Pro Ala Asp Leu	
25 30 35	
ggt acg cgt gag gga tct agc gtg cac ttt gcc ctg gag gct cag act	259
Gly Thr Arg Glu Gly Ser Ser Val His Phe Ala Leu Glu Ala Gln Thr	
40 45 50	
ggg gag agt cag att ttg ccg gat gtc aca acg aag acg tgg ggt ttc	307
Gly Glu Ser Gln Ile Leu Pro Asp Val Thr Thr Lys Thr Trp Gly Phe	
55 60 65	
aat ggc act cat ttg ggg ccg acg ttg gtg gtg aag aaa ggt gat gac	355
Asn Gly Thr His Leu Gly Pro Thr Leu Val Val Lys Lys Gly Asp Asp	
70 75 80 85	
gtc cac gtt gat gtg ata aac aat ttg gat gaa atg acc act gtg cac	403
Val His Val Asp Val Ile Asn Asn Leu Asp Glu Met Thr Thr Val His	
90 95 100	
tgg cat ggc atg aag ttg ccg gcg att gct gat ggt ggt ccg cac tca	451
Trp His Gly Met Lys Leu Pro Ala Ile Ala Asp Gly Gly Pro His Ser	
105 110 115	
ccg atc ggg cct ggg cag acg tgg tca cca acg tgg act gtg gcc aat	499
Pro Ile Gly Pro Gly Gln Thr Trp Ser Pro Thr Trp Thr Val Ala Asn	
120 125 130	
gat gca gcc act ttg tgg tac cac ccg cac act cat ggc ctg aca ggt	547
Asp Ala Ala Thr Leu Trp Tyr His Pro His Thr His Gly Leu Thr Gly	
135 140 145	
ttg cat gcg tac cgt ggt ttg gcg ggg atg atc att gtg gaa gat gaa	595
Leu His Ala Tyr Arg Gly Leu Ala Gly Met Ile Ile Val Glu Asp Glu	
150 155 160 165	
gca aca gac aag ctg gat ctg cca cgc gag tac ggt gtg gac gat att	643
Ala Thr Asp Lys Leu Asp Leu Pro Arg Glu Tyr Gly Val Asp Asp Ile	
170 175 180	
ccg ctg gtt tta atg gat cac cgc ttc tta gaa gac ggt tcc ctt gat	691
Pro Leu Val Leu Met Asp His Arg Phe Leu Glu Asp Gly Ser Leu Asp	
185 190 195	
gag gaa gac ctc ccc gat ctt ggg ctg ttg ggc gat acc ccc act gcc	739
Glu Glu Asp Leu Pro Asp Leu Gly Leu Leu Gly Asp Thr Pro Thr Ala	
200 205 210	
aat ggc att acc aat gcg cac ttt gat gcc acc acg cgc cgg gtt cgg	787
Asn Gly Ile Thr Asn Ala His Phe Asp Ala Thr Thr Arg Arg Val Arg	
215 220 225	
ttc cgc gtg ctc aac ggc tcc aat atg cgg ttc tat aac ttg gcg ttt	835
Phe Arg Val Leu Asn Gly Ser Asn Met Arg Phe Tyr Asn Leu Ala Phe	
230 235 240 245	
tca gac acg cgc acc ttc caa gtc att gcc agc gat tcc ggt ttg ctg	883
Ser Asp Thr Arg Thr Phe Gln Val Ile Ala Ser Asp Ser Gly Leu Leu	
250 255 260	
gat gaa cct caa gac cgc acc acc ttg gct att ggc cca ggc gag cgg	931

Asp	Glu	Pro	Gln	Asp	Arg	Thr	Thr	Leu	Ala	Ile	Gly	Pro	Gly	Glu	Arg		
			265					270					275				
tgg	gaa	atc	gtc	gtg	gag	cta	gag	ccc	ggc	gag	gac	gtc	acc	ttg	gaa	979	
Trp	Glu	Ile	Val	Val	Glu	Leu	Glu	Pro	Gly	Glu	Asp	Val	Thr	Leu	Glu		
			280					285				290					
tct	gta	ggt	ttt	gag	gac	aac	tac	ggc	gtc	cct	gat	gat	gag	ttc	gtg	1027	
Ser	Val	Gly	Phe	Glu	Asp	Asn	Tyr	Gly	Val	Pro	Asp	Asp	Glu	Phe	Val		
			295				300				305						
ccc	gat	ttc	ggc	atg	tca	gat	tcc	ttc	cag	ctg	ctc	acc	atc	acc	ggc	1075	
Pro	Asp	Phe	Gly	Met	Ser	Asp	Ser	Phe	Gln	Leu	Leu	Thr	Ile	Thr	Gly		
310						315				320					325		
cct	tcc	gat	gat	gct	gcg	caa	gca	cct	gct	ttg	ccg	ggc	gtg	ctg	gtg	1123	
Pro	Ser	Asp	Asp	Ala	Ala	Gln	Ala	Pro	Ala	Leu	Pro	Gly	Val	Leu	Val		
				330						335				340			
aaa	tcc	acc	gaa	cct	gac	gtc	atc	gat	gcc	act	gaa	cgc	acc	ttc	atc	1171	
Lys	Ser	Thr	Glu	Pro	Asp	Val	Ile	Asp	Ala	Thr	Glu	Arg	Thr	Phe	Ile		
			345					350				355					
atg	aac	acc	ttc	tcc	atc	aac	gat	cta	cag	atg	gac	atg	cag	cgc	gtt	1219	
Met	Asn	Thr	Phe	Ser	Ile	Asn	Asp	Leu	Gln	Met	Asp	Met	Gln	Arg	Val		
			360				365					370					
gac	gtg	gtg	att	gac	cat	gac	cag	cca	gaa	gtg	tgg	att	gtc	acc	aac	1267	
Asp	Val	Val	Ile	Asp	His	Asp	Gln	Pro	Glu	Val	Trp	Ile	Val	Thr	Asn		
			375				380				385						
gac	aac	tcc	gac	tgg	ccc	cac	aac	ttc	cat	gtc	cac	gac	gcc	cgg	ttt	1315	
Asp	Asn	Ser	Asp	Trp	Pro	His	Asn	Phe	His	Val	His	Asp	Ala	Arg	Phe		
390						395				400					405		
aag	gtg	ctg	aaa	ttt	gaa	ggc	acc	gac	gta	gag	ctc	ttc	aac	gac	ggc	1363	
Lys	Val	Leu	Lys	Phe	Glu	Gly	Thr	Asp	Val	Glu	Leu	Phe	Asn	Asp	Gly		
				410						415				420			
tgg	aaa	gac	acc	gtc	ggc	ctg	cca	ccg	gga	gca	acc	gca	act	tta	gcc	1411	
Trp	Lys	Asp	Thr	Val	Gly	Leu	Pro	Pro	Gly	Ala	Thr	Ala	Thr	Leu	Ala		
			425					430					435				
gtg	gaa	ttt	ggc	cac	tac	cca	gac	ccg	caa	tgg	ccc	tac	atg	tat	cac	1459	
Val	Glu	Phe	Gly	His	Tyr	Pro	Asp	Pro	Gln	Trp	Pro	Tyr	Met	Tyr	His		
			440				445					450					
tgc	cac	atg	ctc	tac	cac	gag	gat	caa	ggc	atg	atg	ggg	cag	ttc	gtc	1507	
Cys	His	Met	Leu	Tyr	His	Glu	Asp	Gln	Gly	Met	Met	Gly	Gln	Phe	Val		
			455				460					465					
atc	gtg	gag	cca	ggc	gac	gag	ccg	gcg	gcg	gtg	ctg	ggg	tcg	ggc	acg	1555	
Ile	Val	Glu	Pro	Gly	Asp	Glu	Pro	Ala	Ala	Val	Leu	Gly	Ser	Gly	Thr		
470					475					480					485		
ggc	tcc	agc	att	gac	tcc	gcc	ggc	gga	cat	gcg	cac	taggggcgtg				1601	
Gly	Ser	Ser	Ile	Asp	Ser	Ala	Gly	Gly	His	Ala	His						
				490						495							
gggcggcgctc	gat															1614	

<210> 166

<211> 497

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 166

Val	Leu	Ala	Ala	Thr	Val	Val	Gly	Ala	Gln	Val	Leu	Val	Ala	Cys	Ser	1	5	10	15
Ser	Asp	Asp	Val	Arg	Gly	Tyr	Gly	Gly	Glu	Pro	Arg	Thr	Leu	Pro	Ile	20	25	30	
Pro	Pro	Ala	Asp	Leu	Gly	Thr	Arg	Glu	Gly	Ser	Ser	Val	His	Phe	Ala	35	40	45	
Leu	Glu	Ala	Gln	Thr	Gly	Glu	Ser	Gln	Ile	Leu	Pro	Asp	Val	Thr	Thr	50	55	60	
Lys	Thr	Trp	Gly	Phe	Asn	Gly	Thr	His	Leu	Gly	Pro	Thr	Leu	Val	Val	65	70	75	80
Lys	Lys	Gly	Asp	Asp	Val	His	Val	Asp	Val	Ile	Asn	Asn	Leu	Asp	Glu	85	90	95	
Met	Thr	Thr	Val	His	Trp	His	Gly	Met	Lys	Leu	Pro	Ala	Ile	Ala	Asp	100	105	110	
Gly	Gly	Pro	His	Ser	Pro	Ile	Gly	Pro	Gly	Gln	Thr	Trp	Ser	Pro	Thr	115	120	125	
Trp	Thr	Val	Ala	Asn	Asp	Ala	Ala	Thr	Leu	Trp	Tyr	His	Pro	His	Thr	130	135	140	
His	Gly	Leu	Thr	Gly	Leu	His	Ala	Tyr	Arg	Gly	Leu	Ala	Gly	Met	Ile	145	150	155	160
Ile	Val	Glu	Asp	Glu	Ala	Thr	Asp	Lys	Leu	Asp	Leu	Pro	Arg	Glu	Tyr	165	170	175	
Gly	Val	Asp	Asp	Ile	Pro	Leu	Val	Leu	Met	Asp	His	Arg	Phe	Leu	Glu	180	185	190	
Asp	Gly	Ser	Leu	Asp	Glu	Glu	Asp	Leu	Pro	Asp	Leu	Gly	Leu	Leu	Gly	195	200	205	
Asp	Thr	Pro	Thr	Ala	Asn	Gly	Ile	Thr	Asn	Ala	His	Phe	Asp	Ala	Thr	210	215	220	
Thr	Arg	Arg	Val	Arg	Phe	Arg	Val	Leu	Asn	Gly	Ser	Asn	Met	Arg	Phe	225	230	235	240
Tyr	Asn	Leu	Ala	Phe	Ser	Asp	Thr	Arg	Thr	Phe	Gln	Val	Ile	Ala	Ser	245	250	255	
Asp	Ser	Gly	Leu	Leu	Asp	Glu	Pro	Gln	Asp	Arg	Thr	Thr	Leu	Ala	Ile	260	265	270	
Gly	Pro	Gly	Glu	Arg	Trp	Glu	Ile	Val	Val	Glu	Leu	Glu	Pro	Gly	Glu	275	280	285	

Asp Val Thr Leu Glu Ser Val Gly Phe Glu Asp Asn Tyr Gly Val Pro
 290 295 300
 Asp Asp Glu Phe Val Pro Asp Phe Gly Met Ser Asp Ser Phe Gln Leu
 305 310 315 320
 Leu Thr Ile Thr Gly Pro Ser Asp Asp Ala Ala Gln Ala Pro Ala Leu
 325 330 335
 Pro Gly Val Leu Val Lys Ser Thr Glu Pro Asp Val Ile Asp Ala Thr
 340 345 350
 Glu Arg Thr Phe Ile Met Asn Thr Phe Ser Ile Asn Asp Leu Gln Met
 355 360 365
 Asp Met Gln Arg Val Asp Val Val Ile Asp His Asp Gln Pro Glu Val
 370 375 380
 Trp Ile Val Thr Asn Asp Asn Ser Asp Trp Pro His Asn Phe His Val
 385 390 395 400
 His Asp Ala Arg Phe Lys Val Leu Lys Phe Glu Gly Thr Asp Val Glu
 405 410 415
 Leu Phe Asn Asp Gly Trp Lys Asp Thr Val Gly Leu Pro Pro Gly Ala
 420 425 430
 Thr Ala Thr Leu Ala Val Glu Phe Gly His Tyr Pro Asp Pro Gln Trp
 435 440 445
 Pro Tyr Met Tyr His Cys His Met Leu Tyr His Glu Asp Gln Gly Met
 450 455 460
 Met Gly Gln Phe Val Ile Val Glu Pro Gly Asp Glu Pro Ala Ala Val
 465 470 475 480
 Leu Gly Ser Gly Thr Gly Ser Ser Ile Asp Ser Ala Gly Gly His Ala
 485 490 495

His

<210> 167
 <211> 588
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(588)
 <223> RXA01250

<400> 167
 ctg gat atc ggc ggc atc gaa gcc aag acg tgg gga tac gtc tct gac 48
 Leu Asp Ile Gly Gly Ile Glu Ala Lys Thr Trp Gly Tyr Val Ser Asp
 1 5 10 15
 acc ggg gat gcg gcc att gag gcc acc gcc ggc gac gtc ctc cag gtc 96
 Thr Gly Asp Ala Ala Ile Glu Ala Thr Ala Gly Asp Val Leu Gln Val
 20 25 30

gat atc acc aat gac ctg cct gag agc acc tcc atc cac tgg cat ggc 144
Asp Ile Thr Asn Asp Leu Pro Glu Ser Thr Ser Ile His Trp His Gly
35 40 45

atc gca ctc cac aac gca gcc gac ggt gtg ccc ggc atg acc cag gac 192
Ile Ala Leu His Asn Ala Ala Asp Gly Val Pro Gly Met Thr Gln Asp
50 55 60

ccc att gaa cct ggc gag tct ttc tcc tat gtt ttt gaa gtc ccc cac 240
Pro Ile Glu Pro Gly Glu Ser Phe Ser Tyr Val Phe Glu Val Pro His
65 70 75 80

ggt ggc acc tac ttc tac cat tcc cac acc ggc ctg cag ctt gat cgc 288
Gly Gly Thr Tyr Phe Tyr His Ser His Thr Gly Leu Gln Leu Asp Arg
85 90 95

ggc ctc cac gcc cca ctg atc atc cgt gac ccg caa gac gct gag gac 336
Gly Leu His Ala Pro Leu Ile Ile Arg Asp Pro Gln Asp Ala Glu Asp
100 105 110

cag gac gtc gag tgg acc atc gtg ctc gac gac tgg gtc gat ggc att 384
Gln Asp Val Glu Trp Thr Ile Val Leu Asp Asp Trp Val Asp Gly Ile
115 120 125

cag ggc act ccc gac gat gag ctc gac aag ctc acc gga atg ggt tcg 432
Gln Gly Thr Pro Asp Asp Glu Leu Asp Lys Leu Thr Gly Met Gly Ser
130 135 140

ggc gac cat aac ggg agg atg gga atg gga ggt cac ggc cag atg atg 480
Gly Asp His Asn Gly Arg Met Gly Met Gly Gly His Gly Gln Met Met
145 150 155 160

cac ggc acc ccg gac cgg gta ctg ggc ggg gat gtc ggc gat gtg atg 528
His Gly Thr Pro Asp Arg Val Leu Gly Gly Asp Val Gly Asp Val Met
165 170 175

tat ccg cac tac ctc atc aac gga cgt atc ccc cgt gct cac cgg acc 576
Tyr Pro His Tyr Leu Ile Asn Gly Arg Ile Pro Arg Ala His Arg Thr
180 185 190

ttc gag gct cgc 588
Phe Glu Ala Arg
195

<210> 168

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Leu Asp Ile Gly Gly Ile Glu Ala Lys Thr Trp Gly Tyr Val Ser Asp
1 5 10 15

Thr Gly Asp Ala Ala Ile Glu Ala Thr Ala Gly Asp Val Leu Gln Val
20 25 30

Asp Ile Thr Asn Asp Leu Pro Glu Ser Thr Ser Ile His Trp His Gly
35 40 45

Ile Ala Leu His Asn Ala Ala Asp Gly Val Pro Gly Met Thr Gln Asp
 50 55 60

Pro Ile Glu Pro Gly Glu Ser Phe Ser Tyr Val Phe Glu Val Pro His
 65 70 75 80

Gly Gly Thr Tyr Phe Tyr His Ser His Thr Gly Leu Gln Leu Asp Arg
 85 90 95

Gly Leu His Ala Pro Leu Ile Ile Arg Asp Pro Gln Asp Ala Glu Asp
 100 105 110

Gln Asp Val Glu Trp Thr Ile Val Leu Asp Asp Trp Val Asp Gly Ile
 115 120 125

Gln Gly Thr Pro Asp Asp Glu Leu Asp Lys Leu Thr Gly Met Gly Ser
 130 135 140

Gly Asp His Asn Gly Arg Met Gly Met Gly Gly His Gly Gln Met Met
 145 150 155 160

His Gly Thr Pro Asp Arg Val Leu Gly Gly Asp Val Gly Asp Val Met
 165 170 175

Tyr Pro His Tyr Leu Ile Asn Gly Arg Ile Pro Arg Ala His Arg Thr
 180 185 190

Phe Glu Ala Arg
 195

<210> 169

<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(721)

<223> RXA02477

<400> 169

cgagcagggc tgtttgaaaa gctgtaaatg acatgacctt aatgattgta ctgactggca 60

cttttaggtca tatgtcacac cgagtggaat aataaagctt atg cct ttg cgt aat 115
 Met Pro Leu Arg Asn
 1 5

gtt gat aga act ccg ccc gca gta tgg gaa gca ttg ctt gcc gga aac 163
 Val Asp Arg Thr Pro Pro Ala Val Trp Glu Ala Leu Leu Ala Gly Asn
 10 15 20

gaa aga ttc atc agt ttc aac gaa gat cga cca aac cag gac gcc ccg 211
 Glu Arg Phe Ile Ser Phe Asn Glu Asp Arg Pro Asn Gln Asp Ala Pro
 25 30 35

cgc aga aga gaa ctt cgc aat gga caa acg cct gca gct gtt gtt att 259
 Arg Arg Arg Glu Leu Arg Asn Gly Gln Thr Pro Ala Ala Val Val Ile
 40 45 50

tcc tgt tca gat tct cga gtg cca gtt gag att att ttt gac gtc ggt 307

Ser Cys Ser Asp Ser Arg Val Pro Val Glu Ile Ile Phe Asp Val Gly
55 60 65

ctc ggt gac ctc ttt gtt gtc cgt act gcc gga gaa atc ctc gac caa 355
Leu Gly Asp Leu Phe Val Val Arg Thr Ala Gly Glu Ile Leu Asp Gln
70 75 80 85

gca gtg ctt gcg tcc atc gaa tac gcc act gaa tcc atc ggc gtt cca 403
Ala Val Leu Ala Ser Ile Glu Tyr Ala Thr Glu Ser Ile Gly Val Pro
90 95 100

ttg gtt atc gtc atg ggc cac gaa tcc tgt ggt gca gtt gca gca act 451
Leu Val Ile Val Met Gly His Glu Ser Cys Gly Ala Val Ala Ala Thr
105 110 115

gca gca gca ctt gaa ggc ggt gca ctt ccc gga ggc tac caa cga gtt 499
Ala Ala Ala Leu Glu Gly Gly Ala Leu Pro Gly Gly Tyr Gln Arg Val
120 125 130

ttg gtt gaa aag gtt gca cca tcc att cta gaa gcc aag gca gag ggc 547
Leu Val Glu Lys Val Ala Pro Ser Ile Leu Glu Ala Lys Ala Glu Gly
135 140 145

ctg agc tcc atc aag gaa ttc gag gaa cac cac gtt gtg gca acg gta 595
Leu Ser Ser Ile Lys Glu Phe Glu Glu His His Val Val Ala Thr Val
150 155 160 165

aac caa ctg ttg tcc cgt tct cca gag att cat cag aag gtc gaa acc 643
Asn Gln Leu Leu Ser Arg Ser Pro Glu Ile His Gln Lys Val Glu Thr
170 175 180

ggt gag ttg gga atc att ggt ttg cgc tac cga ctc tct gac ggt cgt 691
Gly Glu Leu Gly Ile Ile Gly Leu Arg Tyr Arg Leu Ser Asp Gly Arg
185 190 195

act gaa cct gta att agc aag aac gtg ggt tagtttttcgg tctgagattg 741
Thr Glu Pro Val Ile Ser Lys Asn Val Gly
200 205

cct 744

<210> 170

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Pro Leu Arg Asn Val Asp Arg Thr Pro Pro Ala Val Trp Glu Ala
1 5 10 15

Leu Leu Ala Gly Asn Glu Arg Phe Ile Ser Phe Asn Glu Asp Arg Pro
20 25 30

Asn Gln Asp Ala Pro Arg Arg Arg Glu Leu Arg Asn Gly Gln Thr Pro
35 40 45

Ala Ala Val Val Ile Ser Cys Ser Asp Ser Arg Val Pro Val Glu Ile
50 55 60

Ile Phe Asp Val Gly Leu Gly Asp Leu Phe Val Val Arg Thr Ala Gly

65	70	75	80
Glu Ile Leu Asp	Gln Ala Val Leu Ala Ser Ile Glu Tyr Ala Thr Glu		
	85	90	95
Ser Ile Gly Val	Pro Leu Val Ile Val Met Gly His Glu Ser Cys Gly		
	100	105	110
Ala Val Ala Ala Thr Ala Ala Ala Leu Glu Gly Gly Ala Leu Pro Gly			
	115	120	125
Gly Tyr Gln Arg Val Leu Val Glu Lys Val Ala Pro Ser Ile Leu Glu			
	130	135	140
Ala Lys Ala Glu Gly Leu Ser Ser Ile Lys Glu Phe Glu Glu His His			
	145	150	155
Val Val Ala Thr Val Asn Gln Leu Leu Ser Arg Ser Pro Glu Ile His			
	165	170	175
Gln Lys Val Glu Thr Gly Glu Leu Gly Ile Ile Gly Leu Arg Tyr Arg			
	180	185	190
Leu Ser Asp Gly Arg Thr Glu Pro Val Ile Ser Lys Asn Val Gly			
	195	200	205

<210> 171
 <211> 618
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> RXN00833

<400> 171
 agcttttttgc atgtgtcata tcgtaccggt tgcataaggcc tgttcgcgct tgggtgaacct 60

 tttctagcac caaaacaaaa ctctccctag tatgggggtcc atg gct aaa aca cat 115
 Met Ala Lys Thr His
 1 5

 ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163
 Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
 10 15 20

 gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
 Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
 25 30 35

 tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
 Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
 40 45 50

 tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
 Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
 55 60 65

 gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355

Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
 70 75 80 85

ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
 Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
 90 95 100

gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
 Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
 105 110 115

atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499
 Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val
 120 125 130

atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547
 Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp
 135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
 Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Leu Ala Gly Leu Asn
 150 155 160 165

taatttactt cgctcagggg aat 618

<210> 172

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
 1 5 10 15

Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
 20 25 30

Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45

Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60

Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80

Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95

Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110

Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
 115 120 125

Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
 130 135 140

Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
 145 150 155 160

Leu Ala Gly Leu Asn
165

<210> 173
<211> 469
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(469)
<223> FRXA00833

<400> 173
agcttttttgc atgtgtcata tcgtaccgtt tgcataaggcc tgttcgcgct tgggtgaacct 60
tttctagcac caaaacaaaa ctctccctag tatgggggtcc atg gct aaa aca cat 115
Met Ala Lys Thr His
1 5
ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163
Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
10 15 20
gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
25 30 35
tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
40 45 50
tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
55 60 65
gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355
Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
70 75 80 85
ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
90 95 100
gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
105 110 115
atc gtg ctc gaa ggc tca 469
Ile Val Leu Glu Gly Ser
120

<210> 174
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 174

Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
 1 5 10 15
 Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
 20 25 30
 Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45
 Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60
 Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80
 Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95
 Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110
 Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser
 115 120

<210> 175

<211> 1146

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1123)

<223> RXA01224

<400> 175

ttggcggcgg gaagttcagg cttgggggca aacagtgcctt ggattttaga caaaaaactc 60
 acggaagtca tcctatggca ggcgcgccta ggatggtgcc atg agc atc ctt gac 115
 Met Ser Ile Leu Asp
 1 5
 acg ttg aaa act ccc gtg att gtc gcc ccg atg gct ggc ggc ccg tcc 163
 Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met Ala Gly Gly Pro Ser
 10 15 20
 act ccc gcg ttg gtc aat gca gca gca gag gca ggt tcc ctc ggg ttc 211
 Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala Gly Ser Leu Gly Phe
 25 30 35
 ttg gct ggt ggc gtc atg cct ctt gag cag ctg aaa cag gaa ttg tca 259
 Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu Lys Gln Glu Leu Ser
 40 45 50
 gag gta aaa ggc gtc ttt ggc gtc aac ctg ttt cgc ccg cag acg gat 307
 Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe Arg Pro Gln Thr Asp
 55 60 65
 gcg cct aag cct tca gac att gat gag ctg gcg gga ttg ttg tcc tcg 355
 Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala Gly Leu Leu Ser Ser
 70 75 80 85

gcg ttt cgg caa ttt ggc ctc gat gag ccg acg gtg cct acg ccg gat	403
Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr Val Pro Thr Pro Asp	
90 95 100	
ttg agc aat ggg tgg gag gct aaa ttt gag gcc gtt ctt gcc gct aag	451
Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala Val Leu Ala Ala Lys	
105 110 115	
ccc gcc gtt ttt tcc tgc acc ttt ggt att ttt agc gct gaa gaa ttc	499
Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe Ser Ala Glu Glu Phe	
120 125 130	
gcc cgg atc aaa gcc acc gga att gag gcg tgg gtg acg gtg acc aat	547
Ala Arg Ile Lys Ala Thr Gly Ile Glu Ala Trp Val Thr Val Thr Asn	
135 140 145	
ccg gag gac gcg ctg gct gcg cag aaa gct ggc gcc aac gcg ctt gtc	595
Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly Ala Asn Ala Leu Val	
150 155 160 165	
gtg caa ggc ccc gag gcg ggt ggg cac cgc tct acc tgg tcc att gaa	643
Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser Thr Trp Ser Ile Glu	
170 175 180	
gtg gag ccg gac gag cgc gac ctg aaa acc ctc ctc gca gct gtc aaa	691
Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu Leu Ala Ala Val Lys	
185 190 195	
caa gcg ggc gtt tac ctc ccg ctc atc gca gcc ggc ggc ctt tca acc	739
Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala Gly Gly Leu Ser Thr	
200 205 210	
tcc gca gac gtg gca gca att tta gaa gcc ggc gcc agc gct gcc tcc	787
Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly Ala Ser Ala Ala Ser	
215 220 225	
tgt ggt tcc gcc ttt ttg ctt agc gac gaa gcc ggc acc agc tca ctt	835
Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala Gly Thr Ser Ser Leu	
230 235 240 245	
aac cgc gag atc ttg gac gcc gcc cca gca ctt ggt ttg gaa tcg gtg	883
Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu Gly Leu Glu Ser Val	
250 255 260	
tca tct cgc gca ttt tcg ggc cgt tat gcc agg gga gtg gaa acc agg	931
Ser Ser Arg Ala Phe Ser Gly Arg Tyr Ala Arg Gly Val Glu Thr Arg	
265 270 275	
ttc acc cgt tcg aac gag ggg tta ccc ccg ttg tac cca tac ctc aac	979
Phe Thr Arg Ser Asn Glu Gly Leu Pro Pro Leu Tyr Pro Tyr Leu Asn	
280 285 290	
cca atg atc aca tct tta cgt aag gtg gcg gga agt gca ggg aac tgg	1027
Pro Met Ile Thr Ser Leu Arg Lys Val Ala Gly Ser Ala Gly Asn Trp	
295 300 305	
gat tac gcc tac tgc ctg gta gga gtc ggc ctg gaa tcg att gcg aag	1075
Asp Tyr Ala Tyr Cys Leu Val Gly Val Gly Leu Glu Ser Ile Ala Lys	
310 315 320 325	

ggt agt gca aag cag ata ctg gaa tca tta aca cct tcc gct ttg ggc 1123
 Gly Ser Ala Lys Gln Ile Leu Glu Ser Leu Thr Pro Ser Ala Leu Gly
 330 335 340

taatgttggg gggagtgcctt tca 1146

<210> 176

<211> 341

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 176

Met Ser Ile Leu Asp Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met
 1 5 10 15

Ala Gly Gly Pro Ser Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala
 20 25 30

Gly Ser Leu Gly Phe Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu
 35 40 45

Lys Gln Glu Leu Ser Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe
 50 55 60

Arg Pro Gln Thr Asp Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala
 65 70 75 80

Gly Leu Leu Ser Ser Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr
 85 90 95

Val Pro Thr Pro Asp Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala
 100 105 110

Val Leu Ala Ala Lys Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe
 115 120 125

Ser Ala Glu Glu Phe Ala Arg Ile Lys Ala Thr Gly Ile Glu Ala Trp
 130 135 140

Val Thr Val Thr Asn Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly
 145 150 155 160

Ala Asn Ala Leu Val Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser
 165 170 175

Thr Trp Ser Ile Glu Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu
 180 185 190

Leu Ala Ala Val Lys Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala
 195 200 205

Gly Gly Leu Ser Thr Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly
 210 215 220

Ala Ser Ala Ala Ser Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala
 225 230 235 240

Gly Thr Ser Ser Leu Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu
 245 250 255

gtt	aaa	cgg	aaactaatac	cccaaaggat	accgattcaa	tttgtgatgt	gtgggtgttcg		60							
gg	tcatatca	agctaaacag	atgcccccta	caataggctt	gtg Val	ttc Phe	aat Asn	tta Leu	ttt Phe	115						
					1				5							
ggt	cgt	aaa	act	cct	cgc	tct	aac	ctc	cgc	cca	cca	cgc	ggt	ccg	ggc	163
Gly	Arg	Lys	Thr	Pro	Arg	Ser	Asn	Leu	Arg	Pro	Pro	Arg	Gly	Pro	Gly	
				10					15					20		
gat	act	gtg	cgc	ccg	gaa	gat	tta	aaa	ttc	ttg	atg	caa	tgg	gtg	cag	211
Asp	Thr	Val	Arg	Pro	Glu	Asp	Leu	Lys	Phe	Leu	Met	Gln	Trp	Val	Gln	
				25				30					35			
gat	aag	cca	ttt	gtt	gag	gca	ttc	gtt	gaa	ccg	gaa	acg	ctg	gtc	aat	259
Asp	Lys	Pro	Phe	Val	Glu	Ala	Phe	Val	Glu	Pro	Glu	Thr	Leu	Val	Asn	
		40					45					50				
gag	atg	tct	gtc	gtt	ttg	gtt	gat	gct	cat	ggg	gtt	ttt	gtc	cgc	cga	307
Glu	Met	Ser	Val	Val	Leu	Val	Asp	Ala	His	Gly	Val	Phe	Val	Arg	Arg	
	55					60					65					
agg	atc	ggc	ggt	ccc	aaa	ggg	att	gat	gtt	atc	gcg	aaa	aag	ctc	ggc	355
Arg	Ile	Gly	Gly	Pro	Lys	Gly	Ile	Asp	Val	Ile	Ala	Lys	Lys	Leu	Gly	
	70				75					80					85	
gtt	ccg	gtt	tat	gat	gtt	gag	gag	acc	ggt	tac	ccc	caa	agg	atg	cgc	403
Val	Pro	Val	Tyr	Asp	Val	Glu	Glu	Thr	Gly	Tyr	Pro	Gln	Arg	Met	Arg	
				90					95					100		
gaa	cgc	att	gaa	tat	gag	cgc	atc	tta	aga	aag	cgt	gag	qaa	caa	aaa	451

Glu Arg Ile Glu Tyr Glu Arg Ile Leu Arg Lys Arg Glu Glu Gln Lys
 105 110 115
 gct cgc cgc gct aaa ttt gag cgc ggc gag aat cct. gat ctt 493
 Ala Arg Arg Ala Lys Phe Glu Arg Gly Glu Asn Pro Asp Leu
 120 125 130
 taactagcgt ttagctttcc gac 516

<210> 178
 <211> 131
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 178
 Val Phe Asn Leu Phe Gly Arg Lys Thr Pro Arg Ser Asn Leu Arg Pro
 1 5 10 15
 Pro Arg Gly Pro Gly Asp Thr Val Arg Pro Glu Asp Leu Lys Phe Leu
 20 25 30
 Met Gln Trp Val Gln Asp Lys Pro Phe Val Glu Ala Phe Val Glu Pro
 35 40 45
 Glu Thr Leu Val Asn Glu Met Ser Val Val Leu Val Asp Ala His Gly
 50 55 60
 Val Phe Val Arg Arg Arg Ile Gly Gly Pro Lys Gly Ile Asp Val Ile
 65 70 75 80
 Ala Lys Lys Leu Gly Val Pro Val Tyr Asp Val Glu Glu Thr Gly Tyr
 85 90 95
 Pro Gln Arg Met Arg Glu Arg Ile Glu Tyr Glu Arg Ile Leu Arg Lys
 100 105 110
 Arg Glu Glu Gln Lys Ala Arg Arg Ala Lys Phe Glu Arg Gly Glu Asn
 115 120 125
 Pro Asp Leu
 130

<210> 179
 <211> 834
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(811)
 <223> RXA02531

<400> 179
 cacttcgctc cccaaggtac atccccgatg ccacttcttg gagccatcat cggtgccacc 60
 aaacacattg aagtgggcac tggagtagtg gatatgcgtt atg aaa atc cct ttg 115
 Met Lys Ile Pro Leu
 1 5

tat	atg	gcc	gag	gaa	gca	gct	gct	ctc	aat	ctg	ctt	gcc	gac	ggc	cga	163
Tyr	Met	Ala	Glu	Glu	Ala	Ala	Ala	Leu	Asn	Leu	Leu	Ala	Asp	Gly	Arg	
				10					15					20		
cta	gcc	ctc	gga	gtt	tcc	agg	gga	tca	ccc	gaa	cca	gcc	gag	aag	ggc	211
Leu	Ala	Leu	Gly	Val	Ser	Arg	Gly	Ser	Pro	Glu	Pro	Ala	Glu	Lys	Gly	
			25					30					35			
tgg	gaa	gct	ttc	ggc	tac	gac	ggc	ggc	gat	gat	cct	aaa	gct	gca	ggc	259
Trp	Glu	Ala	Phe	Gly	Tyr	Asp	Gly	Gly	Asp	Asp	Pro	Lys	Ala	Ala	Gly	
		40					45					50				
atg	gca	cgg	gag	aaa	ttc	ctt	cgc	ttc	ctc	gat	gcc	atc	gat	ggc	cgc	307
Met	Ala	Arg	Glu	Lys	Phe	Leu	Arg	Phe	Leu	Asp	Ala	Ile	Asp	Gly	Arg	
	55					60					65					
ccc	atg	tcc	atc	gct	tcc	gag	aat	caa	tac	cca	cgc	ctc	tac	cat	ccg	355
Pro	Met	Ser	Ile	Ala	Ser	Glu	Asn	Gln	Tyr	Pro	Arg	Leu	Tyr	His	Pro	
	70				75					80					85	
ggc	act	ccc	ctg	ccg	atc	ttc	ccg	cat	gat	ctt	gac	ttg	ggc	aaa	tcc	403
Gly	Thr	Pro	Leu	Pro	Ile	Phe	Pro	His	Asp	Leu	Asp	Leu	Gly	Lys	Ser	
				90					95					100		
att	tgg	tgg	ggc	gcc	ggc	tcc	cac	aac	acc	gcc	gaa	caa	gca	gca	cgc	451
Ile	Trp	Trp	Gly	Ala	Gly	Ser	His	Asn	Thr	Ala	Glu	Gln	Ala	Ala	Arg	
			105					110					115			
gat	ggc	gtt	aac	ttg	atg	agc	tcc	acc	ctc	gtc	gcc	gaa	gcc	acc	ggc	499
Asp	Gly	Val	Asn	Leu	Met	Ser	Ser	Thr	Leu	Val	Ala	Glu	Ala	Thr	Gly	
		120					125					130				
caa	tcc	ttc	ggg	gat	ctg	caa	gcc	gat	caa	atc	gcg	ttc	tac	cgc	caa	547
Gln	Ser	Phe	Gly	Asp	Leu	Gln	Ala	Asp	Gln	Ile	Ala	Phe	Tyr	Arg	Gln	
	135					140					145					
gct	tgg	aaa	gaa	gcc	gga	cac	gat	tgg	acc	cca	cgt	gtg	tct	gtc	tcc	595
Ala	Trp	Lys	Glu	Ala	Gly	His	Asp	Trp	Thr	Pro	Arg	Val	Ser	Val	Ser	
	150				155					160					165	
agg	tcc	atc	ttt	ccg	atc	gtc	acc	gac	cgc	gac	cgt	gag	ctt	ttc	gga	643
Arg	Ser	Ile	Phe	Pro	Ile	Val	Thr	Asp	Arg	Asp	Arg	Glu	Leu	Phe	Gly	
				170					175					180		
ctt	cag	gga	caa	ggc	ggc	gac	caa	gta	gga	atc	ctg	gat	gat	acc	cga	691
Leu	Gln	Gly	Gln	Gly	Gly	Asp	Gln	Val	Gly	Ile	Leu	Asp	Asp	Thr	Arg	
			185					190					195			
tcc	acg	ttc	ggc	cgc	agc	tac	gcc	gga	agt	ccc	gat	gaa	ctc	atc	gac	739
Ser	Thr	Phe	Gly	Arg	Ser	Tyr	Ala	Gly	Ser	Pro	Asp	Glu	Leu	Ile	Asp	
		200					205					210				
cag	ctc	caa	gga	aga	caa	agc	tgt	gat	gga	agc	cga	cac	ctt	gat	gct	787
Gln	Leu	Gln	Gly	Arg	Gln	Ser	Cys	Asp	Gly	Ser	Arg	His	Leu	Asp	Ala	
	215					220					225					
cac	cgc	ccc	caa	cca	aat	ggg	tgt	tgagatcaac	gcgtcgatcc	tga						834
His	Arg	Pro	Gln	Pro	Asn	Gly	Cys									
	230				235											

<210> 180
 <211> 237
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 180
 Met Lys Ile Pro Leu Tyr Met Ala Glu Glu Ala Ala Ala Leu Asn Leu
 1 5 10 15
 Leu Ala Asp Gly Arg Leu Ala Leu Gly Val Ser Arg Gly Ser Pro Glu
 20 25 30
 Pro Ala Glu Lys Gly Trp Glu Ala Phe Gly Tyr Asp Gly Gly Asp Asp
 35 40 45
 Pro Lys Ala Ala Gly Met Ala Arg Glu Lys Phe Leu Arg Phe Leu Asp
 50 55 60
 Ala Ile Asp Gly Arg Pro Met Ser Ile Ala Ser Glu Asn Gln Tyr Pro
 65 70 75 80
 Arg Leu Tyr His Pro Gly Thr Pro Leu Pro Ile Phe Pro His Asp Leu
 85 90 95
 Asp Leu Gly Lys Ser Ile Trp Trp Gly Ala Gly Ser His Asn Thr Ala
 100 105 110
 Glu Gln Ala Ala Arg Asp Gly Val Asn Leu Met Ser Ser Thr Leu Val
 115 120 125
 Ala Glu Ala Thr Gly Gln Ser Phe Gly Asp Leu Gln Ala Asp Gln Ile
 130 135 140
 Ala Phe Tyr Arg Gln Ala Trp Lys Glu Ala Gly His Asp Trp Thr Pro
 145 150 155 160
 Arg Val Ser Val Ser Arg Ser Ile Phe Pro Ile Val Thr Asp Arg Asp
 165 170 175
 Arg Glu Leu Phe Gly Leu Gln Gly Gln Gly Gly Asp Gln Val Gly Ile
 180 185 190
 Leu Asp Asp Thr Arg Ser Thr Phe Gly Arg Ser Tyr Ala Gly Ser Pro
 195 200 205
 Asp Glu Leu Ile Asp Gln Leu Gln Gly Arg Gln Ser Cys Asp Gly Ser
 210 215 220
 Arg His Leu Asp Ala His Arg Pro Gln Pro Asn Gly Cys
 225 230 235

<210> 181
 <211> 1614
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1591)
 <223> RXN00689

<400> 181

```

acagggaaat cctcccagaa ttaatcaccg aagctgcaca ccagatggct actgcagacc 60

tcaatcgtgc aaaggccctg ttaagaacgg atgcatccg atg aat gct gca acc 115
                               Met Asn Ala Ala Thr
                               1           5

agg cgt gct tct ctg caa ctc ccc tat acc cat gtc gat gat ttc tac 163
Arg Arg Ala Ser Leu Gln Leu Pro Tyr Thr His Val Asp Asp Phe Tyr
                10                15                20

atc aac ggt tcc tgg gtt aaa gca gaa gga aca caa cgc aac ccc gta 211
Ile Asn Gly Ser Trp Val Lys Ala Glu Gly Thr Gln Arg Asn Pro Val
                25                30                35

gtt gat cct gcg gtc ggt caa gaa tgg gga tct gtt cca gaa gca acc 259
Val Asp Pro Ala Val Gly Gln Glu Trp Gly Ser Val Pro Glu Ala Thr
                40                45                50

gca tct gaa ttg gac tct gcg gtg gga gct gca cgt aca gcg cta aag 307
Ala Ser Glu Leu Asp Ser Ala Val Gly Ala Ala Arg Thr Ala Leu Lys
                55                60                65

tcg tgg agt gca ctt aca ggt gcg gaa cga aca ggc tac ctc ctg aaa 355
Ser Trp Ser Ala Leu Thr Gly Ala Glu Arg Thr Gly Tyr Leu Leu Lys
                70                75                80                85

atc gcg acg gaa att gaa tcc cgt tct gaa gct cta gca ctt act aat 403
Ile Ala Thr Glu Ile Glu Ser Arg Ser Glu Ala Leu Ala Leu Thr Asn
                90                95                100

acc cgc gaa aat ggt tcc ccc att tcc gag acc cgt gga gct gcg tcc 451
Thr Arg Glu Asn Gly Ser Pro Ile Ser Glu Thr Arg Gly Ala Ala Ser
                105                110                115

aat gca gca gga att ttc cgt tac ttt gcc act ctc gcg cct tgg tta 499
Asn Ala Ala Gly Ile Phe Arg Tyr Phe Ala Thr Leu Ala Pro Trp Leu
                120                125                130

gac ggc gaa gac atc cgc cca ttt cct gcc ggt agc gcc gaa tcc atc 547
Asp Gly Glu Asp Ile Arg Pro Phe Pro Ala Gly Ser Ala Glu Ser Ile
                135                140                145

gtg gat aaa gat ccc atc ggt gtc tgc gca ctc atc gcc cca tgg aat 595
Val Asp Lys Asp Pro Ile Gly Val Cys Ala Leu Ile Ala Pro Trp Asn
                150                155                160                165

ttc ccg atc aac ctt gta gtc atc aaa ctg gca cca gca ctt ctt gcc 643
Phe Pro Ile Asn Leu Val Val Ile Lys Leu Ala Pro Ala Leu Leu Ala
                170                175                180

ggc tgt acc gtc atc atc aaa cca gcc tcc ccc acc cca ctg tcg atc 691
Gly Cys Thr Val Ile Ile Lys Pro Ala Ser Pro Thr Pro Leu Ser Ile
                185                190                195

cgt ttc atc atc gaa gcc atc gaa gcc gcc gga gtg cca gca ggc gta 739
Arg Phe Ile Ile Glu Ala Ile Glu Ala Ala Gly Val Pro Ala Gly Val
                200                205                210

gtc aac cta ctc acc ggt tca ggg cgt ttc ggt gat gcc ctt gtc cgc 787

```

Val	Asn	Leu	Leu	Thr	Gly	Ser	Gly	Arg	Phe	Gly	Asp	Ala	Leu	Val	Arg	
215						220					225					
cac	ccc	gga	gta	gac	aag	gta	gcg	ttt	acc	gga	tca	acg	cct	gtt	gga	835
His	Pro	Gly	Val	Asp	Lys	Val	Ala	Phe	Thr	Gly	Ser	Thr	Pro	Val	Gly	
230					235					240					245	
aag	aag	atc	gct	gcc	gcc	tcg	gga	gaa	cta	ctc	cga	cca	gtg	act	tta	883
Lys	Lys	Ile	Ala	Ala	Ala	Cys	Gly	Glu	Leu	Leu	Arg	Pro	Val	Thr	Leu	
				250					255					260		
gag	cta	ggc	gga	aaa	tct	tcc	gcg	att	atc	ctt	cct	gat	gca	gac	atg	931
Glu	Leu	Gly	Gly	Lys	Ser	Ser	Ala	Ile	Ile	Leu	Pro	Asp	Ala	Asp	Met	
			265					270					275			
tca	gta	ctc	tcg	acg	cgg	ttg	att	cga	tcc	tgt	atg	cgc	aac	act	gga	979
Ser	Val	Leu	Ser	Thr	Arg	Leu	Ile	Arg	Ser	Cys	Met	Arg	Asn	Thr	Gly	
			280				285					290				
caa	acc	tcg	tac	atc	agt	acc	cgg	att	att	gcc	cct	agc	tca	cgc	tat	1027
Gln	Thr	Cys	Tyr	Ile	Ser	Thr	Arg	Ile	Ile	Ala	Pro	Ser	Ser	Arg	Tyr	
	295					300					305					
gcg	gaa	gtc	gta	caa	aca	gtg	gca	agc	act	atc	gct	gca	ggg	aga	caa	1075
Ala	Glu	Val	Val	Gln	Thr	Val	Ala	Ser	Thr	Ile	Ala	Ala	Gly	Arg	Gln	
310					315					320					325	
ggt	gac	ccc	tat	gat	gaa	gaa	acg	gtt	ttt	ggg	cca	gtt	gcc	agc	gcc	1123
Gly	Asp	Pro	Tyr	Asp	Glu	Glu	Thr	Val	Phe	Gly	Pro	Val	Ala	Ser	Ala	
				330					335					340		
tct	cag	tac	tca	acc	gtc	atg	tct	tac	att	gac	tcc	gca	cga	gag	gaa	1171
Ser	Gln	Tyr	Ser	Thr	Val	Met	Ser	Tyr	Ile	Asp	Ser	Ala	Arg	Glu	Glu	
			345					350				355				
ggt	gca	cga	gtg	gtt	gca	ggg	gga	acc	cgg	tca	atc	agc	ctt	tct	gaa	1219
Gly	Ala	Arg	Val	Val	Ala	Gly	Gly	Thr	Arg	Ser	Ile	Ser	Leu	Ser	Glu	
		360					365					370				
ggt	tta	gaa	tca	ggc	gag	ttt	atc	caa	cca	acc	gtg	ttt	gcc	gat	gtc	1267
Gly	Leu	Glu	Ser	Gly	Glu	Phe	Ile	Gln	Pro	Thr	Val	Phe	Ala	Asp	Val	
	375					380					385					
acc	ccc	gac	atg	cgg	ata	tca	cgc	gaa	gaa	atc	ttc	ggc	cct	gtt	att	1315
Thr	Pro	Asp	Met	Arg	Ile	Ser	Arg	Glu	Glu	Ile	Phe	Gly	Pro	Val	Ile	
390					395					400					405	
tcc	atc	cta	aag	tac	gac	gat	aca	aac	ggt	gtt	tcc	gaa	gca	atc	gca	1363
Ser	Ile	Leu	Lys	Tyr	Asp	Asp	Thr	Asn	Gly	Val	Ser	Glu	Ala	Ile	Ala	
				410					415					420		
cta	gcc	aac	aac	acg	aaa	ttc	ggt	ctc	ggt	ggc	ttg	gta	ttt	ggt	gcg	1411
Leu	Ala	Asn	Asn	Thr	Lys	Phe	Gly	Leu	Gly	Gly	Leu	Val	Phe	Gly	Ala	
				425				430					435			
gat	gag	gaa	caa	gca	cta	gaa	gtc	gcc	cgt	caa	gtg	gat	tct	ggt	tcc	1459
Asp	Glu	Glu	Gln	Ala	Leu	Glu	Val	Ala	Arg	Gln	Val	Asp	Ser	Gly	Ser	
		440					445					450				
gta	ggc	atc	aac	ttc	ttc	ggt	tcc	aac	cat	tcc	gcc	cca	ttt	gga	gga	1507
Val	Gly	Ile	Asn	Phe	Phe	Gly	Ser	Asn	His	Ser	Ala	Pro	Phe	Gly	Gly	

455 460 465
 cgc cac gaa tcc ggt atg gga gtg gaa tac ggc atc gaa ggc ctc agt 1555
 Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly Ile Glu Gly Leu Ser
 470 475 480 485

 gct tac ctg aca tac aag agt att cac cga acc att tagttactga 1601
 Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr Ile
 490 495

 aagttctcag cta 1614

 <210> 182
 <211> 497
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 182
 Met Asn Ala Ala Thr Arg Arg Ala Ser Leu Gln Leu Pro Tyr Thr His
 1 5 10 15
 Val Asp Asp Phe Tyr Ile Asn Gly Ser Trp Val Lys Ala Glu Gly Thr
 20 25 30
 Gln Arg Asn Pro Val Val Asp Pro Ala Val Gly Gln Glu Trp Gly Ser
 35 40 45
 Val Pro Glu Ala Thr Ala Ser Glu Leu Asp Ser Ala Val Gly Ala Ala
 50 55 60
 Arg Thr Ala Leu Lys Ser Trp Ser Ala Leu Thr Gly Ala Glu Arg Thr
 65 70 75 80
 Gly Tyr Leu Leu Lys Ile Ala Thr Glu Ile Glu Ser Arg Ser Glu Ala
 85 90 95
 Leu Ala Leu Thr Asn Thr Arg Glu Asn Gly Ser Pro Ile Ser Glu Thr
 100 105 110
 Arg Gly Ala Ala Ser Asn Ala Ala Gly Ile Phe Arg Tyr Phe Ala Thr
 115 120 125
 Leu Ala Pro Trp Leu Asp Gly Glu Asp Ile Arg Pro Phe Pro Ala Gly
 130 135 140
 Ser Ala Glu Ser Ile Val Asp Lys Asp Pro Ile Gly Val Cys Ala Leu
 145 150 155 160
 Ile Ala Pro Trp Asn Phe Pro Ile Asn Leu Val Val Ile Lys Leu Ala
 165 170 175
 Pro Ala Leu Leu Ala Gly Cys Thr Val Ile Ile Lys Pro Ala Ser Pro
 180 185 190
 Thr Pro Leu Ser Ile Arg Phe Ile Ile Glu Ala Ile Glu Ala Ala Gly
 195 200 205
 Val Pro Ala Gly Val Val Asn Leu Leu Thr Gly Ser Gly Arg Phe Gly
 210 215 220

Asp Ala Leu Val Arg His Pro Gly Val Asp Lys Val Ala Phe Thr Gly
 225 230 235 240
 Ser Thr Pro Val Gly Lys Lys Ile Ala Ala Ala Cys Gly Glu Leu Leu
 245 250 255
 Arg Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Ser Ala Ile Ile Leu
 260 265 270
 Pro Asp Ala Asp Met Ser Val Leu Ser Thr Arg Leu Ile Arg Ser Cys
 275 280 285
 Met Arg Asn Thr Gly Gln Thr Cys Tyr Ile Ser Thr Arg Ile Ile Ala
 290 295 300
 Pro Ser Ser Arg Tyr Ala Glu Val Val Gln Thr Val Ala Ser Thr Ile
 305 310 315 320
 Ala Ala Gly Arg Gln Gly Asp Pro Tyr Asp Glu Glu Thr Val Phe Gly
 325 330 335
 Pro Val Ala Ser Ala Ser Gln Tyr Ser Thr Val Met Ser Tyr Ile Asp
 340 345 350
 Ser Ala Arg Glu Glu Gly Ala Arg Val Val Ala Gly Gly Thr Arg Ser
 355 360 365
 Ile Ser Leu Ser Glu Gly Leu Glu Ser Gly Glu Phe Ile Gln Pro Thr
 370 375 380
 Val Phe Ala Asp Val Thr Pro Asp Met Arg Ile Ser Arg Glu Glu Ile
 385 390 395 400
 Phe Gly Pro Val Ile Ser Ile Leu Lys Tyr Asp Asp Thr Asn Gly Val
 405 410 415
 Ser Glu Ala Ile Ala Leu Ala Asn Asn Thr Lys Phe Gly Leu Gly Gly
 420 425 430
 Leu Val Phe Gly Ala Asp Glu Glu Gln Ala Leu Glu Val Ala Arg Gln
 435 440 445
 Val Asp Ser Gly Ser Val Gly Ile Asn Phe Phe Gly Ser Asn His Ser
 450 455 460
 Ala Pro Phe Gly Gly Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly
 465 470 475 480
 Ile Glu Gly Leu Ser Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr
 485 490 495
 Ile

<210> 183

<211> 750

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(727)

<223> FRXA00689

<400> 183

```

actccgacca gtgactttag agctaggcgg aaaatcttcc gcgattatcc ttcctgatgc 60

agacatgtca gtactctcga cgcggttgat tcgatcctgt atg cgc aac act gga 115
Met Arg Asn Thr Gly
1 5

caa acc tgc tac atc agt acc cgg att att gcc cct agc tca cgc tat 163
Gln Thr Cys Tyr Ile Ser Thr Arg Ile Ile Ala Pro Ser Ser Arg Tyr
10 15 20

gcg gaa gtc gta caa aca gtg gca agc act atc gct gca ggt aga caa 211
Ala Glu Val Val Gln Thr Val Ala Ser Thr Ile Ala Ala Gly Arg Gln
25 30 35

ggg gac ccc tat gat gaa gaa acg gtt ttt ggg cca gtt gcc agc gcc 259
Gly Asp Pro Tyr Asp Glu Glu Thr Val Phe Gly Pro Val Ala Ser Ala
40 45 50

tct cag tac tca acc gtc atg tct tac att gac tcc gca cga gag gaa 307
Ser Gln Tyr Ser Thr Val Met Ser Tyr Ile Asp Ser Ala Arg Glu Glu
55 60 65

ggg gca cga gtg gtt gca ggt gga acc cgg tca atc agc ctt tct gaa 355
Gly Ala Arg Val Val Ala Gly Gly Thr Arg Ser Ile Ser Leu Ser Glu
70 75 80 85

ggg tta gaa tca ggc gag ttt atc caa cca acc gtg ttt gcc gat gtc 403
Gly Leu Glu Ser Gly Glu Phe Ile Gln Pro Thr Val Phe Ala Asp Val
90 95 100

acc ccc gac atg cgg ata tca cgc gaa gaa atc ttc ggc cct gtt att 451
Thr Pro Asp Met Arg Ile Ser Arg Glu Glu Ile Phe Gly Pro Val Ile
105 110 115

tcc atc cta aag tac gac gat aca aac ggt gtt tcc gaa gca atc gca 499
Ser Ile Leu Lys Tyr Asp Asp Thr Asn Gly Val Ser Glu Ala Ile Ala
120 125 130

cta gcc aac aac acg aaa ttc ggt ctc ggt ggc ttg gta ttt ggt gcg 547
Leu Ala Asn Asn Thr Lys Phe Gly Leu Gly Gly Leu Val Phe Gly Ala
135 140 145

gat gag gaa caa gca cta gaa gtc gcc cgt caa gtg gat tct ggt tcc 595
Asp Glu Glu Gln Ala Leu Glu Val Ala Arg Gln Val Asp Ser Gly Ser
150 155 160 165

gta ggc atc aac ttc ttc ggt tcc aac cat tcc gcc cca ttt gga gga 643
Val Gly Ile Asn Phe Phe Gly Ser Asn His Ser Ala Pro Phe Gly Gly
170 175 180

cgc cac gaa tcc ggt atg gga gtg gaa tac ggc atc gaa ggc ctc agt 691
Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly Ile Glu Gly Leu Ser
185 190 195

gct tac ctg aca tac aag agt att cac cga acc att tagttactga 737
Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr Ile

```


200

205

aagttctcag cta

750

<210> 184

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

Met Arg Asn Thr Gly Gln Thr Cys Tyr Ile Ser Thr Arg Ile Ile Ala
 1 5 10 15

Pro Ser Ser Arg Tyr Ala Glu Val Val Gln Thr Val Ala Ser Thr Ile
 20 25 30

Ala Ala Gly Arg Gln Gly Asp Pro Tyr Asp Glu Glu Thr Val Phe Gly
 35 40 45

Pro Val Ala Ser Ala Ser Gln Tyr Ser Thr Val Met Ser Tyr Ile Asp
 50 55 60

Ser Ala Arg Glu Glu Gly Ala Arg Val Val Ala Gly Gly Thr Arg Ser
 65 70 75 80

Ile Ser Leu Ser Glu Gly Leu Glu Ser Gly Glu Phe Ile Gln Pro Thr
 85 90 95

Val Phe Ala Asp Val Thr Pro Asp Met Arg Ile Ser Arg Glu Glu Ile
 100 105 110

Phe Gly Pro Val Ile Ser Ile Leu Lys Tyr Asp Asp Thr Asn Gly Val
 115 120 125

Ser Glu Ala Ile Ala Leu Ala Asn Asn Thr Lys Phe Gly Leu Gly Gly
 130 135 140

Leu Val Phe Gly Ala Asp Glu Glu Gln Ala Leu Glu Val Ala Arg Gln
 145 150 155 160

Val Asp Ser Gly Ser Val Gly Ile Asn Phe Phe Gly Ser Asn His Ser
 165 170 175

Ala Pro Phe Gly Gly Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly
 180 185 190

Ile Glu Gly Leu Ser Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr
 195 200 205

Ile

<210> 185

<211> 878

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(855)

<223> RXN03128

<400> 185

aac gga ctc gcc att ccc gac att gga ttt ggt gta ttc caa acc cca	48
Asn Gly Leu Ala Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro	
1 5 10 15	
ccc gat gaa acc cga aac tcc gtt aac gct gct ctt gaa gcc ggc tat	96
Pro Asp Glu Thr Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr	
20 25 30	
cgc cac atc gac acc gcc gcc gca tac ggc aat gaa cgt gaa gtc ggt	144
Arg His Ile Asp Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly	
35 40 45	
gaa gca atc gca gca tcc ggc att ggc cgc gac gag atc acc atc gaa	192
Glu Ala Ile Ala Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu	
50 55 60	
acc aaa atc tgg gtg acc gac tac ggc ttc gag gaa act ctc cac gca	240
Thr Lys Ile Trp Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala	
65 70 75 80	
ttc gac aag gcc aca ggc aag ctt ggt gtc gat aca ctg gac att ttg	288
Phe Asp Lys Ala Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu	
85 90 95	
atc ttg cac cag gca gtg cca agc agc ttt gat cgc acc atc gcc gcc	336
Ile Leu His Gln Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala	
100 105 110	
tac aag gcg cta gag aag ctg ctt ttc gac ggc gcg gtg cgg gca atc	384
Tyr Lys Ala Leu Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile	
115 120 125	
gga gtc agt aat ttc atg cca gag cac ctg gac aaa ctc ctt ttg gaa	432
Gly Val Ser Asn Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu	
130 135 140	
acc tcc att gtc cca gct ctg aac caa atc gaa tgc cac ccc tac ttc	480
Thr Ser Ile Val Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe	
145 150 155 160	
cag cag cgt gac gtg ctt gcc cgc aat gag cag ctt ggc att ttg act	528
Gln Gln Arg Asp Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr	
165 170 175	
cag gcg tgg tca cca atc ggt ggc atc acc ttc tac cgc gac gga cag	576
Gln Ala Trp Ser Pro Ile Gly Gly Ile Thr Phe Tyr Arg Asp Gly Gln	
180 185 190	
ctt cca agc act cta gaa aat gag gtc atc gct gga atc gcc gca gaa	624
Leu Pro Ser Thr Leu Glu Asn Glu Val Ile Ala Gly Ile Ala Ala Glu	
195 200 205	
gtt ggc aaa aca cca gct caa gta atg ctg cgc tgg cac cta cag cgt	672
Val Gly Lys Thr Pro Ala Gln Val Met Leu Arg Trp His Leu Gln Arg	
210 215 220	
aga cgt cac gca att cca aag tct gtg acc cca tca cgc att gtg gaa	720

Arg Arg His Ala Ile Pro Lys Ser Val Thr Pro Ser Arg Ile Val Glu
 225 230 235 240

aac ttt gag atc ttt gat ttc gaa ctc tcc gat gag caa cta cag caa 768
 Asn Phe Glu Ile Phe Asp Phe Glu Leu Ser Asp Glu Gln Leu Gln Gln
 245 250 255

atc gat gcc ctc aac acc gat ctg cgc ggt ggc cca gaa cca gag aac 816
 Ile Asp Ala Leu Asn Thr Asp Leu Arg Gly Gly Pro Glu Pro Glu Asn
 260 265 270

atc acc atg gaa aac tac tac cga gaa atc cca gaa gcc taaaggccct 865
 Ile Thr Met Glu Asn Tyr Tyr Arg Glu Ile Pro Glu Ala
 275 280 285

tagaggcgaa tgt 878

<210> 186
 <211> 285
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 186
 Asn Gly Leu Ala Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro
 1 5 10 15

Pro Asp Glu Thr Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr
 20 25 30

Arg His Ile Asp Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly
 35 40 45

Glu Ala Ile Ala Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu
 50 55 60

Thr Lys Ile Trp Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala
 65 70 75 80

Phe Asp Lys Ala Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu
 85 90 95

Ile Leu His Gln Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala
 100 105 110

Tyr Lys Ala Leu Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile
 115 120 125

Gly Val Ser Asn Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu
 130 135 140

Thr Ser Ile Val Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe
 145 150 155 160

Gln Gln Arg Asp Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr
 165 170 175

Gln Ala Trp Ser Pro Ile Gly Gly Ile Thr Phe Tyr Arg Asp Gly Gln
 180 185 190

Leu Pro Ser Thr Leu Glu Asn Glu Val Ile Ala Gly Ile Ala Ala Glu

195	200	205
Val Gly Lys Thr Pro Ala Gln Val Met Leu Arg Trp His Leu Gln Arg		
210	215	220
Arg Arg His Ala Ile Pro Lys Ser Val Thr Pro Ser Arg Ile Val Glu		
225	230	235
Asn Phe Glu Ile Phe Asp Phe Glu Leu Ser Asp Glu Gln Leu Gln Gln		
245	250	255
Ile Asp Ala Leu Asn Thr Asp Leu Arg Gly Gly Pro Glu Pro Glu Asn		
260	265	270
Ile Thr Met Glu Asn Tyr Tyr Arg Glu Ile Pro Glu Ala		
275	280	285

<210> 187

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(522)

<223> FRXA02192

<400> 187

att ccc gac att gga ttt ggt gtc ttc caa acc cca ccc gat gaa acc	48
Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro Pro Asp Glu Thr	
1 5 10 15	
cga aac tcc gtt aac gct gct ctt gaa gcc ggc tat cgc cac atc gac	96
Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr Arg His Ile Asp	
20 25 30	
acc gcg gcc gca tac ggc aat gaa cgt gaa gtc ggt gaa gca atc gca	144
Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly Glu Ala Ile Ala	
35 40 45	
gca tcc ggc att ggc cgc gac gag atc acc atc gaa acc aaa atc tgg	192
Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu Thr Lys Ile Trp	
50 55 60	
gtg acc gac tac ggc ttc gag gaa act ctc cac gca ttc gac aag gcc	240
Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala Phe Asp Lys Ala	
65 70 75 80	
aca ggc aag ctt ggt gtc gat aca ctg gac att ttg atc ttg cac cag	288
Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu Ile Leu His Gln	
85 90 95	
gca gtg cca agc agc ttt gat cgc acc atc gcc gcc tac aag gcg cta	336
Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala Tyr Lys Ala Leu	
100 105 110	
gag aag ctg ctt ttc gac ggc gcg gtg cgg gca atc gga gtc agt aat	384
Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile Gly Val Ser Asn	
115 120 125	

ttc atg cca gag cac ctg gac aaa ctc ctt ttg gaa acc tcc att gtc 432
 Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu Thr Ser Ile Val
 130 135 140

cca gct ctg aac caa atc gaa tgc cac ccc tac ttc cag cag cgt gac 480
 Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe Gln Gln Arg Asp
 145 150 155 160

gtg ctt gcc cgc aat gag cag ctt ggc att ttg act cag gcg 522
 Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr Gln Ala
 165 170

<210> 188

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro Pro Asp Glu Thr
 1 5 10 15

Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr Arg His Ile Asp
 20 25 30

Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly Glu Ala Ile Ala
 35 40 45

Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu Thr Lys Ile Trp
 50 55 60

Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala Phe Asp Lys Ala
 65 70 75 80

Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu Ile Leu His Gln
 85 90 95

Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala Tyr Lys Ala Leu
 100 105 110

Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile Gly Val Ser Asn
 115 120 125

Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu Thr Ser Ile Val
 130 135 140

Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe Gln Gln Arg Asp
 145 150 155 160

Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr Gln Ala
 165 170

<210> 189

<211> 1039

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1039)

<223> RXA02351

<400> 189

```

tgacacttta cagactgggt ttcaactaat gacaccgaaa gaaatacacc tcaacctttt 60

tgcttttcggt gccgggcacc acgcggcggc gtggcgagcg gtg gag gga agc gtc 115
                               Val Glu Gly Ser Val
                               1                               5

gaa aag ctg ggt tta att tcc tgg tgg gag gaa ctc gcg cgc acc gct 163
Glu Lys Leu Gly Leu Ile Ser Trp Trp Glu Glu Leu Ala Arg Thr Ala
                        10                        15                        20

gag cgg ggc aag ctg gat gcg gtc ttt ttg gcc gat ggg cag gcg att 211
Glu Arg Gly Lys Leu Asp Ala Val Phe Leu Ala Asp Gly Gln Ala Ile
                        25                        30                        35

aat ccg gtc ggt ctg gag aat ggg ccg gcc tgg ttt ttg gag ccg gtg 259
Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp Phe Leu Glu Pro Val
                        40                        45                        50

acc gcg ttg act gcg atg gcg ccg gcg acg aac aat att ggg ttg atc 307
Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn Asn Ile Gly Leu Ile
                        55                        60                        65

agc aca att tcc agt acg ttt tgg cag ccg ttt cat gcg gcg ccg atg 355
Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe His Ala Ala Arg Met
                        70                        75                        80                        85

atc gcc agc ttg gat cat att tcg ggt ggg cgt gct gga atc aat gtg 403
Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg Ala Gly Ile Asn Val
                        90                        95                        100

gtg aca tcg atg acc gat gcg gag gcg cgt aac cac ggg atg gat gcg 451
Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn His Gly Met Asp Ala
                        105                        110                        115

ttg ccg ggt cac gat gtt cgc tat gcg cgc gct gcg gaa ttt att gaa 499
Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala Ala Glu Phe Ile Glu
                        120                        125                        130

acc atc act gcg ctg tgg gat tct tgg cct gcg gaa agt ttg gtg atg 547
Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala Glu Ser Leu Val Met
                        135                        140                        145

gat cgt gct gga aaa ttt gcg gac tcc tcg ctc att aaa tct atc gat 595
Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu Ile Lys Ser Ile Asp
                        150                        155                        160                        165

cat gat ggt gag ttc ttc caa gtc gct ggt ccg ctg aat atc ccc agt 643
His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro Leu Asn Ile Pro Ser
                        170                        175                        180

cct ccg cag ggt cga ccc gta ctt ttt cag gct gga tcc tca ccg caa 691
Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala Gly Ser Pro Gln
                        185                        190                        195

gga cgg gaa atc gct gcg aaa tac gcc gag gca att tac tct gtg gcg 739
Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala Ile Tyr Ser Val Ala
                        200                        205                        210

```

tgg gat ttg gag caa gcg caa gat tat cgc tct gat att cat gct cgt 787
 Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser Asp Ile His Ala Arg
 215 220 225

 gcc act gcc cag ggt cgc gag ccc atg ccg gtg ctt cct ggt ttg gtg 835
 Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val Leu Pro Gly Leu Val
 230 235 240 245

 act ttt gtt ggc acg acc gtg gaa gaa gcg cgt gca aaa cag cag gct 883
 Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg Ala Lys Gln Gln Ala
 250 255 260

 ctt aat gcg ttg ctg ccg gtc aaa gac tca cta aat cag ttg agt ttc 931
 Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu Asn Gln Leu Ser Phe
 265 270 275

 ttt gtg ggt caa gat tgc tcg acg tgg gat ttg gat gca cct ccc cca 979
 Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu Asp Ala Pro Pro Pro
 280 285 290

 cca ctg cca ccg cta gaa gag ttt tcc ggt cct aaa ggc agg tac gaa 1027
 Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro Lys Gly Arg Tyr Glu
 295 300 305

 acg gtc ctg cgg 1039
 Thr Val Leu Arg
 310

<210> 190
 <211> 313
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 190
 Val Glu Gly Ser Val Glu Lys Leu Gly Leu Ile Ser Trp Trp Glu Glu
 1 5 10 15

 Leu Ala Arg Thr Ala Glu Arg Gly Lys Leu Asp Ala Val Phe Leu Ala
 20 25 30

 Asp Gly Gln Ala Ile Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp
 35 40 45

 Phe Leu Glu Pro Val Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn
 50 55 60

 Asn Ile Gly Leu Ile Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe
 65 70 75 80

 His Ala Ala Arg Met Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg
 85 90 95

 Ala Gly Ile Asn Val Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn
 100 105 110

 His Gly Met Asp Ala Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala
 115 120 125

 Ala Glu Phe Ile Glu Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala
 130 135 140

Glu Ser Leu Val Met Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu
 145 150 155 160
 Ile Lys Ser Ile Asp His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro
 165 170 175
 Leu Asn Ile Pro Ser Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala
 180 185 190
 Gly Ser Ser Pro Gln Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala
 195 200 205
 Ile Tyr Ser Val Ala Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser
 210 215 220
 Asp Ile His Ala Arg Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val
 225 230 235 240
 Leu Pro Gly Leu Val Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg
 245 250 255
 Ala Lys Gln Gln Ala Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu
 260 265 270
 Asn Gln Leu Ser Phe Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu
 275 280 285
 Asp Ala Pro Pro Pro Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro
 290 295 300
 Lys Gly Arg Tyr Glu Thr Val Leu Arg
 305 310

<210> 191
 <211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> RXN00905

<400> 191
 cgctgcccct ctatgctgct cctagttacc cctgcacaaa tagcggtttt tctcacgcat 60
 tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
 Met Thr Gln Phe Glu
 1 5
 aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20
 ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
 25 30 35
 cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259

Pro	Asn	Leu	Leu	Glu	Asp	Tyr	Ala	Gly	Ala	Lys	Glu	Trp	Val	Lys	Glu		
	40						45					50					
aca	ctg	acc	aac	gca	ggg	ctc	acc	gtc	agc	gaa	ttc	gct	gcc	gaa	gat	307	
Thr	Leu	Thr	Asn	Ala	Gly	Leu	Thr	Val	Ser	Glu	Phe	Ala	Ala	Glu	Asp		
	55					60					65						
gga	acc	acc	aac	ttc	atc	ggc	acc	cgc	aag	ggc	tcc	gaa	ggg	gca	cca	355	
Gly	Thr	Thr	Asn	Phe	Ile	Gly	Thr	Arg	Lys	Gly	Ser	Glu	Gly	Ala	Pro		
	70				75					80					85		
aag	gta	ctg	ctg	tac	agc	cac	ttc	gac	gtt	gtc	cca	tcc	ggc	cct	ttg	403	
Lys	Val	Leu	Leu	Tyr	Ser	His	Phe	Asp	Val	Val	Pro	Ser	Gly	Pro	Leu		
				90					95					100			
gat	ctc	tgg	gac	acc	aat	cct	ttt	gaa	ctc	acc	gag	cgc	gac	gct	ggc	451	
Asp	Leu	Trp	Asp	Thr	Asn	Pro	Phe	Glu	Leu	Thr	Glu	Arg	Asp	Ala	Gly		
			105					110					115				
cac	ggc	acc	cgc	tgg	tac	ggc	cgc	ggc	gcc	gct	gac	tgc	aag	ggc	aac	499	
His	Gly	Thr	Arg	Trp	Tyr	Gly	Arg	Gly	Ala	Ala	Asp	Cys	Lys	Gly	Asn		
		120					125					130					
ctg	gtc	atg	cac	ctc	gca	gca	ctg	cgc	gcc	gtc	gaa	gcc	agc	ggc	gac	547	
Leu	Val	Met	His	Leu	Ala	Ala	Leu	Arg	Ala	Val	Glu	Ala	Ser	Gly	Asp		
		135				140					145						
acc	aca	ctc	aac	ctc	acc	tac	gtg	gtc	gag	ggc	tcc	gag	gaa	atg	gga	595	
Thr	Thr	Leu	Asn	Leu	Thr	Tyr	Val	Val	Glu	Gly	Ser	Glu	Glu	Met	Gly		
					155				160						165		
ggc	gga	gcg	ctc	agc	gcg	ctc	atc	aag	gac	aag	cct	gag	ctt	ttc	gac	643	
Gly	Gly	Ala	Leu	Ser	Ala	Leu	Ile	Lys	Asp	Lys	Pro	Glu	Leu	Phe	Asp		
				170				175						180			
gca	gat	gtc	atc	ttg	att	gca	gac	agc	gga	aac	gct	tcc	gtg	ggc	acc	691	
Ala	Asp	Val	Ile	Leu	Ile	Ala	Asp	Ser	Gly	Asn	Ala	Ser	Val	Gly	Thr		
				185				190					195				
cca	acc	ttg	acc	act	acc	ctg	cgc	ggg	ggc	gga	cag	gtc	acc	gtc	acc	739	
Pro	Thr	Leu	Thr	Thr	Thr	Leu	Arg	Gly	Gly	Gly	Gln	Val	Thr	Val	Thr		
		200					205					210					
gtg	gac	acc	ctt	gaa	ggc	gct	gtt	cac	tcc	ggc	cag	aac	ggg	ggc	gct	787	
Val	Asp	Thr	Leu	Glu	Gly	Ala	Val	His	Ser	Gly	Gln	Asn	Gly	Gly	Ala		
		215				220					225						
gcc	cca	gat	gct	gtt	gct	gct	ctc	gtg	cgc	gtt	ctg	gat	act	ttg	cgc	835	
Ala	Pro	Asp	Ala	Val	Ala	Ala	Leu	Val	Arg	Val	Leu	Asp	Thr	Leu	Arg		
		230			235					240					245		
gat	gaa	cac	gga	cgc	acc	gtt	atc	gac	ggc	tgt	caa	cac	cac	cgc	aaa	883	
Asp	Glu	His	Gly	Arg	Thr	Val	Ile	Asp	Gly	Cys	Gln	His	His	Arg	Lys		
				250				255						260			
ctg	gaa	ggg	cga	gcc	tta	tgatccagag	actttccgca	gcg								924	
Leu	Glu	Gly	Arg	Ala	Leu												
				265													

<210> 192

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

```

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn
 1           5           10           15

Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn
          20           25           30

Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
          35           40           45

Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
          50           55           60

Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
          65           70           75           80

Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
          85           90           95

Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
          100          105          110

Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
          115          120          125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
          130          135          140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
          145          150          155          160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys
          165          170          175

Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn
          180          185          190

Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly
          195          200          205

Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly
          210          215          220

Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val
          225          230          235          240

Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys
          245          250          255

Gln His His Arg Lys Leu Glu Gly Arg Ala Leu
          260          265

```

<210> 193

<211> 716

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(693)

<223> FRXA00905

<400> 193

gat cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa	48
Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys	
1 5 10 15	
 gaa aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa	96
Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu	
20 25 30	
 gat gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca	144
Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala	
35 40 45	
 cca aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct	192
Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro	
50 55 60	
 ttg gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct	240
Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala	
65 70 75 80	
 ggc cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc	288
Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly	
85 90 95	
 aac ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc	336
Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly	
100 105 110	
 gac acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg	384
Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met	
115 120 125	
 gga ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc	432
Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe	
130 135 140	
 gac gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc	480
Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly	
145 150 155 160	
 acc cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc	528
Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val	
165 170 175	
 acc gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc	576
Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly	
180 185 190	
 gct gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg	624
Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu	
195 200 205	
 cgc gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc	672
Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg	

210

215

220

aaa ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg

716

Lys Leu Glu Gly Arg Ala Leu

225

230

<210> 194

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys
1 5 10 15Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu
20 25 30Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala
35 40 45Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro
50 55 60Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala
65 70 75 80Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly
85 90 95Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly
100 105 110Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met
115 120 125Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe
130 135 140Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly
145 150 155 160Thr Pro Thr Leu Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val
165 170 175Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly
180 185 190Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu
195 200 205Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg
210 215 220Lys Leu Glu Gly Arg Ala Leu
225 230

<210> 195

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXA00906

<400> 195

accgtggaca cccttgaagg cgctgttcac tccggccaga acggtggcgc tgccccagat 60

gctgttgctg	ctctcgtg	cg	ttctggat	actttgcgcg	atg	aac	acg	gac	gca	115
					Met	Asn	Thr	Asp	Ala	
					1				5	

ccg	tta	tcg	acg	gct	gtc	aac	acc	acc	gca	aac	tgg	aag	ggc	gag	cct	163
Pro	Leu	Ser	Thr	Ala	Val	Asn	Thr	Thr	Ala	Asn	Trp	Lys	Gly	Glu	Pro	
			10						15					20		

tat	gat	cca	gag	act	ttc	cgc	agc	gat	gcc	ggc	atc	ctc	gac	ggg	gta	211
Tyr	Asp	Pro	Glu	Thr	Phe	Arg	Ser	Asp	Ala	Gly	Ile	Leu	Asp	Gly	Val	
			25					30					35			

gac	atc	atg	ggc	gac	ggc	gac	aac	cca	gca	agc	atg	ctg	tgg	tcc	agg	259
Asp	Ile	Met	Gly	Asp	Gly	Asp	Asn	Pro	Ala	Ser	Met	Leu	Trp	Ser	Arg	
		40					45					50				

cct	gca	atc	tcc	atc	acc	gga	ttc	act	tcc	acc	cca	gtg	gca	gaa	gca	307
Pro	Ala	Ile	Ser	Ile	Thr	Gly	Phe	Thr	Ser	Thr	Pro	Val	Ala	Glu	Ala	
		55				60					65					

ctc	aac	gca	gtg	ccc	gca	acg	gcg	tcc	gcc	aag	cta	aac	ctt	cgc	gtg	355
Leu	Asn	Ala	Val	Pro	Ala	Thr	Ala	Ser	Ala	Lys	Leu	Asn	Leu	Arg	Val	
	70					75				80					85	

cca	gca	ggc	ctg	gaa	gca	aac	gat	gtg	gcc	gag	aag	ctg	aag	cag	cac	403
Pro	Ala	Gly	Leu	Glu	Ala	Asn	Asp	Val	Ala	Glu	Lys	Leu	Lys	Gln	His	
			90						95					100		

ctg	atc	aat	cac	aca	cct	tgg	ggc	gca	aag	atc	acg	gtg	gag	atc	gat	451
Leu	Ile	Asn	His	Thr	Pro	Trp	Gly	Ala	Lys	Ile	Thr	Val	Glu	Ile	Asp	
			105					110					115			

gac	att	aac	caa	ccg	ttc	tcc	acc	gat	att	acc	ggc	cct	gca	atg	tcc	499
Asp	Ile	Asn	Gln	Pro	Phe	Ser	Thr	Asp	Ile	Thr	Gly	Pro	Ala	Met	Ser	
			120				125					130				

acc	ctg	gcg	tcc	tgc	ctg	agc	gct	gcg	tac	gag	ggc	aag	gat	ctt	gtc	547
Thr	Leu	Ala	Ser	Cys	Leu	Ser	Ala	Ala	Tyr	Glu	Gly	Lys	Asp	Leu	Val	
	135					140					145					

acc	gaa	ggc	agc	ggc	gga	tcc	att	cca	ctg	tgt	acc	gaa	ctg	att	gag	595
Thr	Glu	Gly	Ser	Gly	Gly	Ser	Ile	Pro	Leu	Cys	Thr	Glu	Leu	Ile	Glu	
	150				155					160					165	

gtc	aac	cca	taagcagaat	tggcactcta	cgg	627
Val	Asn	Pro				

<210> 196

<211> 168
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 196
 Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn
 1 5 10 15
 Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly
 20 25 30
 Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser
 35 40 45
 Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
 50 55 60
 Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
 65 70 75 80
 Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
 85 90 95
 Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
 100 105 110
 Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
 115 120 125
 Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu
 130 135 140
 Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys
 145 150 155 160
 Thr Glu Leu Ile Glu Val Asn Pro
 165

<210> 197
 <211> 246
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(223)
 <223> RXA00907

<400> 197
 cctgagcgct gcgtacgagg gcaaggatct tgtcaccgaa ggcagcggcg gatccattcc 60
 actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115
 Leu Ala Leu Tyr Gly
 1 5
 gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
 10 15 20
 ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211

Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
 25 30 35

aac tac acc aag tagaccctaaa agcaggcggtt aac 246
 Asn Tyr Thr Lys
 40

<210> 198
 <211> 41
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 198
 Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala
 1 5 10 15
 Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu
 20 25 30
 Ala Leu Phe Leu Leu Asn Tyr Thr Lys
 35 40

<210> 199
 <211> 1386
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1363)
 <223> RXA02101

<400> 199
 gccatggaat gctccggtga acgcaacagc cttaaataca atccccctcct ataagccaag 60

agtttttagtg tcgctgcgca ggtactctac tatctaatacc atg agc cgc att tca 115
 Met Ser Arg Ile Ser
 1 5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163
 Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala
 10 15 20

tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag 211
 Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu
 25 30 35

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259
 Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val
 40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307
 Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly
 55 60 65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355
 Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp
 70 75 80 85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt	403
Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg	
90 95 100	
atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc	451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly	
105 110 115	
cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat	499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp	
120 125 130	
gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca	547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro	
135 140 145	
tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta	595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu	
150 155 160 165	
gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc	643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val	
170 175 180	
ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct	691
Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala	
185 190 195	
gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt	739
Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
200 205 210	
tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att	787
Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat	835
Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac	883
Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt	979
Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
280 285 290	
ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac	1027
Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr	
295 300 305	
ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act	1075
Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr	
310 315 320 325	
gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct	1123

Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala
 330 335 340
 tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc 1171
 Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe
 345 350 355
 aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag 1219
 Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln
 360 365 370
 tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc 1267
 Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala
 375 380 385
 aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct 1315
 Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala
 390 395 400 405
 gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac 1363
 Ala Thr Arg Ala Ala Ala Ala Leu Leu Thr Tyr Leu Gly Thr Asn
 410 415 420
 taatcatcta gttttctgcg acg 1386

 <210> 200
 <211> 421
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 200
 Met Ser Arg Ile Ser Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser
 1 5 10 15
 Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser
 20 25 30
 Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg
 35 40 45
 Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala
 50 55 60
 Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met
 65 70 75 80
 Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro
 85 90 95
 Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val
 100 105 110
 Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala
 115 120 125
 Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile
 130 135 140
 Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met
 145 150 155 160

Val Ala Gly Gly Leu Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe
 165 170 175
 Gly Gln His Val Val Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro
 180 185 190
 Gly Gly Ala Leu Ala Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly
 195 200 205
 Arg Ser Ala His Gly Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr
 210 215 220
 Val Ala Ala Met Ile Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu
 225 230 235 240
 Val Ser Pro Glu Asp Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser
 245 250 255
 Gly Asn Thr Asn Asn Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn
 260 265 270
 Cys Arg Phe Tyr Asn Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile
 275 280 285
 Glu Arg Val Val Arg Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu
 290 295 300
 Pro Val Ile Glu Tyr Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro
 305 310 315 320
 Val Val Phe Asp Thr Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu
 325 330 335
 Asp Ser Ile Asp Ala Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser
 340 345 350
 Ile Pro Lys Ala Phe Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val
 355 360 365
 Thr Pro Arg Asp Gln Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala
 370 375 380
 Ser Asp Val Pro Ala Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala
 385 390 395 400
 Pro Thr Met Ser Ala Ala Thr Arg Ala Ala Ala Ala Leu Leu Thr
 405 410 415
 Tyr Leu Gly Thr Asn
 420

<210> 201
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)

<223> RXN02565

<400> 201

```

ggaaattcga tacagtgcga tgacgcgata ttagaaagaa aaagatgcgc ttacgacga 60
aaccctcacc ctccttcagg aacttatccg caacgcctgc gtg aat gat cta acc 115
                                         Val Asn Asp Leu Thr
                                         1           5

cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
              10              15              20

ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
              25              30              35

ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
              40              45              50

gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
              55              60              65

cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
              70              75              80              85

att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
              90              95              100

gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
              105              110              115

ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
              120              125              130

gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
              135              140              145

tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
              150              155              160              165

gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643
Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg
              170              175              180

att cac gtc aat ggc gat gct ggt cat ggt tcc att cct ttc gac cgt 691
Ile His Val Asn Gly Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg
              185              190              195

gac agc gct att gtc aag atc ggt gaa gtc gcc cgc cga atc gct gcc 739
Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala Arg Arg Ile Ala Ala
              200              205              210

```

gcc gat ctg aag gta gcc aag gac gat atc tgg caa ggc ttc gtc caa	787
Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp Gln Gly Phe Val Gln	
215 220 225	
gcg cac cgt ttc gac cca gaa acg gag cag gcg ctt ctt agc ggg acc	835
Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala Leu Leu Ser Gly Thr	
230 235 240 245	
tcc cct gag gcc tac gca gag ttc ggc gga ctc tcc cgc ttc gcc cac	883
Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu Ser Arg Phe Ala His	
250 255 260	
gcg gtg tct cat ctc acg atc gcc caa act gtg gtt cgt gca ggt caa	931
Ala Val Ser His Leu Thr Ile Ala Gln Thr Val Val Arg Ala Gly Gln	
265 270 275	
gcc atc aat gta ttg cca tcg cat gcg tac ttg gaa ctg gat atc cgt	979
Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu Glu Leu Asp Ile Arg	
280 285 290	
acc ctt cca ggc caa acc aat gac tat gtt gat gac acc ctg cgt gct	1027
Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp Asp Thr Leu Arg Ala	
295 300 305	
gct ctg ggc gat ctt gcc gat gaa gta gaa atc gaa cac ctc atc tct	1075
Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile Glu His Leu Ile Ser	
310 315 320 325	
gaa gaa gca acg gtg agc cca act gat tcc agg ttg tat aac acc ttg	1123
Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg Leu Tyr Asn Thr Leu	
330 335 340	
gaa aaa gtt ctt ggt gat ttc ttc ccc gat gcg cct gtg gtc cca att	1171
Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro Ile	
345 350 355	
att tcc tct ggt ggc tct gac ctg cgc ttt ggt cgt cga cta ggc ggt	1219
Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly Gly	
360 365 370	
gtt ggt tat ggt ttt gca gtt cat gca cgt gaa cga act ttg gcg gaa	1267
Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala Glu	
375 380 385	
gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat	1315
Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp	
390 395 400 405	
ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta	1363
Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu	
410 415 420	
ggc taaaaacatg aagcaggagt ctt	1389
Gly	

<210> 202

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu
 1 5 10 15
 Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys
 20 25 30
 Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
 35 40 45
 Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
 50 55 60
 Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
 65 70 75 80
 Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
 85 90 95
 Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
 100 105 110
 Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
 115 120 125
 Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
 130 135 140
 Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
 145 150 155 160
 Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
 165 170 175
 Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
 180 185 190
 Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
 195 200 205
 Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320

<400> 203																	
gct	gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	48	
Ala	Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile		
1				5				10				15					
.																	
tct	gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	96	
Ser	Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr		
20				25				30									
.																	
ttg	gaa	aaa	gtt	ctt	ggg	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	144	
Leu	Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro		
35				40				45									
.																	
att	att	tcc	tct	ggg	ggc	tct	gac	ctg	cgc	ttt	ggg	cgt	cga	cta	ggc	192	
Ile	Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly		
50				55				60									
.																	
ggg	gtt	ggg	tat	ggg	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	240	
Gly	Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala		
65				70				75				80					
.																	
gaa	gca	atg	ggg	caa	ctt	cac	tcc	cat	gac	gag	gcg	ctg	tac	ctg	gaa	288	
Glu	Ala	Met	Gly	Gln	Leu	His	Ser	His	Asp	Glu	Ala	Leu	Tyr	Leu	Glu		
85				90				95									
.																	
gat	ctt	gaa	ctg	act	gtt	cgg	ggg	tat	gac	tcc	gtc	gtg	cgt	gaa	ttc	336	
Asp	Leu	Glu	Leu	Thr	Val	Arg	Gly	Tyr	Asp	Ser	Val	Val	Arg	Glu	Phe		
100				105				110									

cta ggc taaaaacatg aagcaggagt ctt
Leu Gly

365

<210> 204
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 204
Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile Glu His Leu Ile
1 5 10 15
Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg Leu Tyr Asn Thr
20 25 30
Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro
35 40 45
Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly
50 55 60
Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala
65 70 75 80
Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu
85 90 95
Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe
100 105 110
Leu Gly

<210> 205
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(738)
<223> FRXA02567

<400> 205
ctt atc cgc aac gcc tgc gtg aat gat cta acc cca gat tca ggt cag 48
Leu Ile Arg Asn Ala Cys Val Asn Asp Leu Thr Pro Asp Ser Gly Gln
1 5 10 15
gaa att aga aac gcg gaa agc cta gaa cgt ttc ttt gaa gga acc ccc 96
Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro
20 25 30
aac gtt aaa atc acc aag ctg gaa ccg cat ccg ggc cgg acc tca att 144
Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro Gly Arg Thr Ser Ile
35 40 45
atc gtg act gtt cca ggc agc gat cca gat gct gag cct tta aca ctg 192

Ile	Val	Thr	Val	Pro	Gly	Ser	Asp	Pro	Asp	Ala	Glu	Pro	Leu	Thr	Leu	
50						55					60					
ctt	gga	cat	act	gat	gtt	gtg	cct	gtt	gat	ctg	cct	aaa	tgg	act	aaa	240
Leu	Gly	His	Thr	Asp	Val	Val	Pro	Val	Asp	Leu	Pro	Lys	Trp	Thr	Lys	
65					70					75					80	
gat	cca	ttc	ggt	gcg	gag	att	tcg	gat	gga	cag	att	tgg	ggt	aga	ggg	288
Asp	Pro	Phe	Gly	Ala	Glu	Ile	Ser	Asp	Gly	Gln	Ile	Trp	Gly	Arg	Gly	
				85					90					95		
tcc	gtc	gat	atg	ctc	ttt	att	acc	gca	acc	caa	gcg	gcc	gtc	acc	cgt	336
Ser	Val	Asp	Met	Leu	Phe	Ile	Thr	Ala	Thr	Gln	Ala	Ala	Val	Thr	Arg	
			100					105					110			
caa	gta	gcc	cgt	gaa	ggc	ggc	ctg	cgt	ggc	acg	ctg	aca	ttc	gtt	ggc	384
Gln	Val	Ala	Arg	Glu	Gly	Gly	Leu	Arg	Gly	Thr	Leu	Thr	Phe	Val	Gly	
		115					120					125				
gtt	gct	gat	gag	gaa	gcc	cgc	ggc	gga	ctc	gga	gcg	aag	tgg	ctt	tcc	432
Val	Ala	Asp	Glu	Glu	Ala	Arg	Gly	Gly	Leu	Gly	Ala	Lys	Trp	Leu	Ser	
		130				135					140					
gaa	gaa	cac	caa	aac	ctc	ttc	agc	tgg	aaa	aac	tgc	ctc	tcc	gaa	tcc	480
Glu	Glu	His	Gln	Asn	Leu	Phe	Ser	Trp	Lys	Asn	Cys	Leu	Ser	Glu	Ser	
145					150					155					160	
ggt	gga	tcg	cac	ctt	cca	gtc	cac	gac	ggc	agc	gac	gca	gta	gta	att	528
Gly	Gly	Ser	His	Leu	Pro	Val	His	Asp	Gly	Ser	Asp	Ala	Val	Val	Ile	
				165					170					175		
aac	gtt	gga	gaa	aaa	ggt	gca	gct	caa	cgt	cgt	att	cac	gtc	aat	ggc	576
Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg	Ile	His	Val	Asn	Gly	
			180					185					190			
gat	gct	ggt	cat	ggt	tcc	att	cct	ttc	gac	cgt	gac	agc	gct	att	gtc	624
Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg	Asp	Ser	Ala	Ile	Val	
		195				200						205				
aag	atc	ggt	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	gcc	gat	ctg	aag	gta	672
Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala	Ala	Asp	Leu	Lys	Val	
	210					215					220					
gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	gcg	cac	cgt	ttc	gac	720
Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln	Ala	His	Arg	Phe	Asp	
225					230					235					240	
cca	gaa	acg	gag	cag	gcg											738
Pro	Glu	Thr	Glu	Gln	Ala											
				245												

<210> 206

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Leu	Ile	Arg	Asn	Ala	Cys	Val	Asn	Asp	Leu	Thr	Pro	Asp	Ser	Gly	Gln	
1				5					10					15		


```

<400> 207
accccgatcc tttgttttcg tgggatcact attagactcg actctaccgc gctgcaggtt 60
ttcctgatac gcctgcggac aaaacagaaa ggtatttcac gtg atg gaa att ggt 115
                               Val Met Glu Ile Gly

```

																1	5	
gtg	cag	ggt	gcc	tca	tgg	atg	gac	cgc	cac	cat	gac	gag	gtc	ata	aag	163		
Val	Gln	Val	Ala	Ser	Trp	Met	Asp	Arg	His	His	Asp	Glu	Val	Ile	Lys			
				10					15					20				
tgg	cgc	agg	cat	ttg	cac	agc	cat	cct	gag	ctc	tcc	cac	atg	gaa	tac	211		
Trp	Arg	Arg	His	Leu	His	Ser	His	Pro	Glu	Leu	Ser	His	Met	Glu	Tyr			
				25					30					35				
cgc	acg	act	gag	tat	ttg	gcc	tcg	gtt	ctg	aaa	gat	cac	ggc	atg	gaa	259		
Arg	Thr	Thr	Glu	Tyr	Leu	Ala	Ser	Val	Leu	Lys	Asp	His	Gly	Met	Glu			
				40					45					50				
cca	cac	ctg	ttc	cca	gga	acc	ggt	ttg	atg	gtg	gat	atc	gga	cca	gaa	307		
Pro	His	Leu	Phe	Pro	Gly	Thr	Gly	Leu	Met	Val	Asp	Ile	Gly	Pro	Glu			
				55					60					65				
ggg	gac	tcc	cgc	ctg	gcg	ttt	cgc	gct	gat	atc	gat	gcc	ctt	ccg	ctg	355		
Gly	Asp	Ser	Arg	Leu	Ala	Phe	Arg	Ala	Asp	Ile	Asp	Ala	Leu	Pro	Leu			
				70					75					80				
ctt	gaa	tca	acc	ggc	tta	gag	ttc	tct	tcc	aca	gcc	act	ggc	gtt	gcg	403		
Leu	Glu	Ser	Thr	Gly	Leu	Glu	Phe	Ser	Ser	Thr	Ala	Thr	Gly	Val	Ala			
				90					95					100				
cat	gcc	tgc	gga	cat	gac	gtg	cac	acg	gtg	atc	gct	ttg	gca	ctt	gcc	451		
His	Ala	Cys	Gly	His	Asp	Val	His	Thr	Val	Ile	Ala	Leu	Ala	Leu	Ala			
				105					110					115				
tgt	gca	ctg	aac	acc	atc	gaa	ctg	ccc	atc	ggc	att	cgg	gtg	att	ttc	499		
Cys	Ala	Leu	Asn	Thr	Ile	Glu	Leu	Pro	Ile	Gly	Ile	Arg	Val	Ile	Phe			
				120					125					130				
cag	ccg	gca	gaa	gaa	gtc	atg	act	ggt	ggc	gca	acg	gac	gtc	att	gcc	547		
Gln	Pro	Ala	Glu	Glu	Val	Met	Thr	Gly	Gly	Ala	Thr	Asp	Val	Ile	Ala			
				135					140					145				
cac	ggt	ggc	ctt	gat	ggt	gtg	gat	gcg	att	tac	gcc	atc	cac	gtt	gaa	595		
His	Gly	Gly	Leu	Asp	Gly	Val	Asp	Ala	Ile	Tyr	Ala	Ile	His	Val	Glu			
				150					155					160				
ccc	aaa	ttg	aag	gtc	ggt	cgc	gtc	ggt	gta	cgc	gct	ggc	gcg	att	act	643		
Pro	Lys	Leu	Lys	Val	Gly	Arg	Val	Gly	Val	Arg	Ala	Gly	Ala	Ile	Thr			
				170					175					180				
tct	gcc	tca	gat	gtg	atc	gaa	atc	aga	gtc	aag	ggt	gaa	gga	gga	cat	691		
Ser	Ala	Ser	Asp	Val	Ile	Glu	Ile	Arg	Val	Lys	Gly	Glu	Gly	Gly	His			
				185					190					195				
agc	gca	cgt	cca	cac	ctc	tcc	gct	gat	gtt	gtt	tac	gcc	ttg	agc	aaa	739		
Ser	Ala	Arg	Pro	His	Leu	Ser	Ala	Asp	Val	Val	Tyr	Ala	Leu	Ser	Lys			
				200					205					210				
ttg	gtc	gtt	gat	ctt	ccc	ggt	ttg	ctg	tcc	agg	cgc	gtc	gat	cca	cgc	787		
Leu	Val	Val	Asp	Leu	Pro	Gly	Leu	Leu	Ser	Arg	Arg	Val	Asp	Pro	Arg			
				215					220					225				
acc	ggc	acc	gtg	ctt	gtt	ttc	ggc	acc	atc	aac	gcc	ggc	tat	gcg	ccc	835		
Thr	Gly	Thr	Val	Leu	Val	Phe	Gly	Thr	Ile	Asn	Ala	Gly	Tyr	Ala	Pro			
				230					235					240				

aac gcg atc cca gat tcc ggc atc gtg tca ggc acc ttg cgt aca gcc 883
 Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala
 250 255 260
 gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg 931
 Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val
 265 270 275
 gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat 979
 Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn
 280 285 290
 ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg 1027
 Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu
 295 300 305
 gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg 1075
 Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro
 310 315 320 325
 cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca 1123
 Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro
 330 335 340
 gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa 1171
 Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln
 345 350 355
 gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt 1219
 Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val
 360 365 370
 ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct 1267
 Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser
 375 380 385
 gaa gct ttc tta aat tcc taatgggggt agtgtgtagg gct 1308
 Glu Ala Phe Leu Asn Ser
 390 395

<210> 208

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
 1 5 10 15

Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
 20 25 30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
 35 40 45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
 50 55 60

Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile

65	70	75	80
Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr	85	90	95
Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile	100	105	110
Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly	115	120	125
Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala	130	135	140
Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr	145	150	155
Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg	165	170	175
Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys	180	185	190
Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val	195	200	205
Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg	210	215	220
Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn	225	230	235
Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly	245	250	255
Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu	260	265	270
Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His	275	280	285
Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val	290	295	300
Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser	305	310	315
Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr	325	330	335
Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly	340	345	350
His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu	355	360	365
Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln	370	375	380
Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser	385	390	395

```
<220>  
<221> CDS  
<222> (101)..(1285)  
<223> FRXA02855
```

289

170										175					180					
tct	gcc	tca	gat	gtg	atc	gaa	atc	aga	gtc	aag	ggt	gaa	gga	gga	cat	691				
Ser	Ala	Ser	Asp	Val	Ile	Glu	Ile	Arg	Val	Lys	Gly	Glu	Gly	Gly	His					
			185					190					195							
agc	gca	cgt	cca	cac	ctc	tcc	gct	gat	gtt	gtt	tac	gcc	ttg	agc	aaa	739				
Ser	Ala	Arg	Pro	His	Leu	Ser	Ala	Asp	Val	Val	Tyr	Ala	Leu	Ser	Lys					
		200					205					210								
ttg	gtc	gtt	gat	ctt	ccc	ggt	ttg	ctg	tcc	agg	cgc	gtc	gat	cca	cgc	787				
Leu	Val	Val	Asp	Leu	Pro	Gly	Leu	Leu	Ser	Arg	Arg	Val	Asp	Pro	Arg					
	215					220				225										
acc	ggc	acc	gtg	ctt	gtt	ttc	ggc	acc	atc	aac	gcc	ggc	tat	gcg	ccc	835				
Thr	Gly	Thr	Val	Leu	Val	Phe	Gly	Thr	Ile	Asn	Ala	Gly	Tyr	Ala	Pro					
230				235				240							245					
aac	gcg	atc	cca	gat	tcc	ggc	atc	gtg	tca	ggc	acc	ttg	cgt	aca	gcc	883				
Asn	Ala	Ile	Pro	Asp	Ser	Gly	Ile	Val	Ser	Gly	Thr	Leu	Arg	Thr	Ala					
			250					255						260						
gac	atc	tct	acc	tgg	cgt	gac	atg	cgt	ccg	ctt	atc	tct	gag	ctg	gtg	931				
Asp	Ile	Ser	Thr	Trp	Arg	Asp	Met	Arg	Pro	Leu	Ile	Ser	Glu	Leu	Val					
			265					270					275							
gaa	cag	gtg	ctc	gca	ccc	acc	gga	gtc	acc	cat	gaa	ctg	atc	tac	aat	979				
Glu	Gln	Val	Leu	Ala	Pro	Thr	Gly	Val	Thr	His	Glu	Leu	Ile	Tyr	Asn					
		280					285				290									
ccg	ggt	gtt	cca	cca	gtg	ctt	aac	gac	gat	gtc	gcc	acc	gct	ttg	ttg	1027				
Pro	Gly	Val	Pro	Pro	Val	Leu	Asn	Asp	Asp	Val	Ala	Thr	Ala	Leu	Leu					
	295				300					305										
gca	agc	gca	gca	cgc	gac	atg	gac	aca	caa	tct	gtt	gtc	caa	gcg	ccg	1075				
Ala	Ser	Ala	Ala	Arg	Asp	Met	Asp	Thr	Gln	Ser	Val	Val	Gln	Ala	Pro					
310				315				320							325					
cag	tca	tcc	ggt	gga	gaa	gac	ttc	tcg	tgg	tac	ctt	gaa	cac	gtc	cca	1123				
Gln	Ser	Ser	Gly	Gly	Glu	Asp	Phe	Ser	Trp	Tyr	Leu	Glu	His	Val	Pro					
			330					335						340						
gga	tca	atg	gcc	cgg	ttg	ggt	tgc	tgg	ccg	ggg	cac	gga	ccc	aag	caa	1171				
Gly	Ser	Met	Ala	Arg	Leu	Gly	Cys	Trp	Pro	Gly	His	Gly	Pro	Lys	Gln					
			345				350						355							
gac	ctc	cat	caa	agt	gac	ctg	gtt	gtg	gat	gag	cga	gcc	atc	gga	gtt	1219				
Asp	Leu	His	Gln	Ser	Asp	Leu	Val	Val	Asp	Glu	Arg	Ala	Ile	Gly	Val					
			360				365					370								
ggc	gtc	agg	ctc	ttt	ggc	tcc	ctt	gtg	cag	cag	tac	agt	agc	cga	tct	1267				
Gly	Val	Arg	Leu	Phe	Gly	Ser	Leu	Val	Gln	Gln	Tyr	Ser	Ser	Arg	Ser					
	375					380					385									
gaa	gct	ttc	tta	aat	tcc	taatgggggt	agtgtgtagg	gct								1308				
Glu	Ala	Phe	Leu	Asn	Ser															
390				395																

<210> 210

<211> 395

<213> Corynebacterium glutamicum

Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
1 5 10 15

Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
20 25 30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
35 40 45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
50 55 60

Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile
65 70 75 80

Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr
85 90 95

Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile
100 105 110

Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly
115 120 125

Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala
130 135 140

Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr
145 150 155 160

Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg
165 170 175

Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys
180 185 190

Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val
195 200 205

Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg
210 215 220

Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn
225 230 235 240

Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly
245 250 255

Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu
260 265 270

Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His
275 280 285

Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val
290 295 300

Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser
 305 310 315 320

Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr
 325 330 335

Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly
 340 345 350

His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu
 355 360 365

Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln
 370 375 380

Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser
 385 390 395

<210> 211
 <211> 1509
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1486)
 <223> RXA00026

<400> 211
 ccctttctgg ctagcctggg ctacattggt ggcaatttgg ttctacgccg atttgccgct 60

tggacctggc tctgcgatct tcctcgaagg ataagttttc atg agt act gac aat 115
 Met Ser Thr Asp Asn
 1 5

ttt tct cca caa gtt ccg tcg act gtg tat ttg gat tac atg gag caa 163
 Phe Ser Pro Gln Val Pro Ser Thr Val Tyr Leu Asp Tyr Met Glu Gln
 10 15 20

ggg att gcc gcg cgc aaa gcg gag gca gaa tct aac gcc agc acg aag 211
 Gly Ile Ala Ala Arg Lys Ala Glu Ala Glu Ser Asn Ala Ser Thr Lys
 25 30 35

ggg gag agc ccg gat tat cca ggc cag cag gtt att tgg cgc ctg atc 259
 Gly Glu Ser Pro Asp Tyr Pro Gly Gln Gln Val Ile Trp Arg Leu Ile
 40 45 50

cag gaa gca ggg gag tcg ttg cgt gat gaa ctg cgc aca ctg gct ttc 307
 Gln Glu Ala Gly Glu Ser Leu Arg Asp Glu Leu Arg Thr Leu Ala Phe
 55 60 65

acg ctg cac gac cat ccg gaa gaa gcg ttc gag gag gtg ttc gcc acc 355
 Thr Leu His Asp His Pro Glu Glu Ala Phe Glu Glu Val Phe Ala Thr
 70 75 80 85

gag gaa atc aca aaa ctt ctg caa aat cat ggt ttt gag gtt cag agt 403
 Glu Glu Ile Thr Lys Leu Leu Gln Asn His Gly Phe Glu Val Gln Ser
 90 95 100

gga gtt tat ggt gtt aaa acc gct cta gaa act agt ttt gaa acc cct 451

Gly	Val	Tyr	Gly	Val	Lys	Thr	Ala	Leu	Glu	Thr	Ser	Phe	Glu	Thr	Pro	
			105					110					115			
ggt	tat	gat	cca	gcg	cag	cac	cca	agc	att	gcg	atc	ttg	gcg	gaa	tac	499
Gly	Tyr	Asp	Pro	Ala	Gln	His	Pro	Ser	Ile	Ala	Ile	Leu	Ala	Glu	Tyr	
		120					125					130				
gat	gcc	ctt	cca	gag	atc	ggc	cat	gca	tgc	ggg	cac	aat	atc	atc	gca	547
Asp	Ala	Leu	Pro	Glu	Ile	Gly	His	Ala	Cys	Gly	His	Asn	Ile	Ile	Ala	
	135					140					145					
gca	gct	ggt	gtt	ggc	gca	ttt	tta	gct	gtc	acc	aac	atg	atc	aaa	act	595
Ala	Ala	Gly	Val	Gly	Ala	Phe	Leu	Ala	Val	Thr	Asn	Met	Ile	Lys	Thr	
150					155				160						165	
gcc	gaa	gtg	aaa	ggc	gtg	gat	cac	ctc	gac	ttt	gaa	ggc	cgg	atc	gtg	643
Ala	Glu	Val	Lys	Gly	Val	Asp	His	Leu	Asp	Phe	Glu	Gly	Arg	Ile	Val	
				170					175					180		
ctg	ttg	gga	aca	cct	gct	gag	gag	ggg	cat	tcc	ggc	aag	gaa	tac	atg	691
Leu	Leu	Gly	Thr	Pro	Ala	Glu	Glu	Gly	His	Ser	Gly	Lys	Glu	Tyr	Met	
			185					190						195		
atc	cga	aat	ggc	gca	ttc	gat	ggc	att	gat	gcg	tcg	att	atg	atg	cac	739
Ile	Arg	Asn	Gly	Ala	Phe	Asp	Gly	Ile	Asp	Ala	Ser	Ile	Met	Met	His	
		200					205					210				
ccc	ttt	ggc	ttc	gat	ctg	gcg	gag	cat	gtt	tgg	gtg	ggc	aga	cgt	acc	787
Pro	Phe	Gly	Phe	Asp	Leu	Ala	Glu	His	Val	Trp	Val	Gly	Arg	Arg	Thr	
	215					220					225					
atg	acg	gcg	acg	ttc	cac	ggt	gtc	tct	gca	cac	gcg	tct	tcg	cag	cct	835
Met	Thr	Ala	Thr	Phe	His	Gly	Val	Ser	Ala	His	Ala	Ser	Ser	Gln	Pro	
230					235				240						245	
ttc	atg	ggt	aaa	aat	gcc	ctc	gac	gct	gca	agt	ttg	gcg	tac	cag	ggc	883
Phe	Met	Gly	Lys	Asn	Ala	Leu	Asp	Ala	Ala	Ser	Leu	Ala	Tyr	Gln	Gly	
				250					255					260		
ttc	gga	gtt	ttg	cgt	cag	caa	atg	cca	ccg	agc	gac	cgc	ctt	cac	gcc	931
Phe	Gly	Val	Leu	Arg	Gln	Gln	Met	Pro	Pro	Ser	Asp	Arg	Leu	His	Ala	
			265					270					275			
att	att	acg	gaa	ggc	gga	aac	cgg	cca	agc	atc	att	cca	gac	act	gca	979
Ile	Ile	Thr	Glu	Gly	Gly	Asn	Arg	Pro	Ser	Ile	Ile	Pro	Asp	Thr	Ala	
		280					285					290				
acg	atg	tcg	ctg	tac	gtg	cgt	tct	ttg	ttg	ccg	gaa	gca	ctc	aaa	gac	1027
Thr	Met	Ser	Leu	Tyr	Val	Arg	Ser	Leu	Leu	Pro	Glu	Ala	Leu	Lys	Asp	
	295					300					305					
ata	tcg	aaa	cgc	gtg	gat	gat	gtg	ctc	gat	ggg	gcg	gcc	ttg	atg	gcg	1075
Ile	Ser	Lys	Arg	Val	Asp	Asp	Val	Leu	Asp	Gly	Ala	Ala	Leu	Met	Ala	
310					315					320					325	
ggg	gtt	ggc	gtc	gaa	aag	caa	tgg	gat	gtg	cac	cca	gct	agc	ttg	ccc	1123
Gly	Val	Gly	Val	Glu	Lys	Gln	Trp	Asp	Val	His	Pro	Ala	Ser	Leu	Pro	
				330					335					340		
gtg	cgc	aac	aat	cat	gtg	ttg	gcg	cgg	cgt	tgg	gca	aaa	acg	cag	aat	1171
Val	Arg	Asn	Asn	His	Val	Leu	Ala	Arg	Arg	Trp	Ala	Lys	Thr	Gln	Asn	

345										350										355										
ctg	cgt	ggt	cga	acg	gcg	ctt	tcg	gag	ggt	att	ttg	ccc	gac	act	ctg	1219														
Leu	Arg	Gly	Arg	Thr	Ala	Leu	Ser	Glu	Gly	Ile	Leu	Pro	Asp	Thr	Leu															
		360					365					370																		
gca	gca	tcg	act	gat	ttt	ggc	aat	gtc	tcg	cac	ctg	ggt	ccg	ggc	att	1267														
Ala	Ala	Ser	Thr	Asp	Phe	Gly	Asn	Val	Ser	His	Leu	Val	Pro	Gly	Ile															
		375				380					385																			
cat	ccg	atg	gtg	aaa	att	tct	ccg	gaa	aac	gtt	gcg	ctc	cac	acc	aag	1315														
His	Pro	Met	Val	Lys	Ile	Ser	Pro	Glu	Asn	Val	Ala	Leu	His	Thr	Lys															
390					395					400					405															
gaa	ttc	gcc	gct	tat	gcg	cgc	acg	gaa	gag	gcc	atc	gac	gca	gcc	gtc	1363														
Glu	Phe	Ala	Ala	Tyr	Ala	Arg	Thr	Glu	Glu	Ala	Ile	Asp	Ala	Ala	Val															
				410					415					420																
gac	gcc	gca	atc	ggg	ctg	gcg	caa	gtc	gcc	gtt	gac	gcg	ctt	gca	gat	1411														
Asp	Ala	Ala	Ile	Gly	Leu	Ala	Gln	Val	Ala	Val	Asp	Ala	Leu	Ala	Asp															
				425				430					435																	
ccg	caa	atg	ctt	atc	gac	gcg	acc	ctc	gag	ttc	acc	aac	tcc	ggc	gac	1459														
Pro	Gln	Met	Leu	Ile	Asp	Ala	Thr	Leu	Glu	Phe	Thr	Asn	Ser	Gly	Asp															
		440					445					450																		
gta	ctt	aaa	gta	ggg	gac	tat	ttg	gct	taggcaacga	ctccgaaacc						1506														
Val	Leu	Lys	Val	Gly	Asp	Tyr	Leu	Ala																						
		455				460																								
ttc																1509														

<210> 212

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Met	Ser	Thr	Asp	Asn	Phe	Ser	Pro	Gln	Val	Pro	Ser	Thr	Val	Tyr	Leu
1				5					10					15	

Asp	Tyr	Met	Glu	Gln	Gly	Ile	Ala	Ala	Arg	Lys	Ala	Glu	Ala	Glu	Ser
			20					25					30		

Asn	Ala	Ser	Thr	Lys	Gly	Glu	Ser	Pro	Asp	Tyr	Pro	Gly	Gln	Gln	Val
		35					40					45			

Ile	Trp	Arg	Leu	Ile	Gln	Glu	Ala	Gly	Glu	Ser	Leu	Arg	Asp	Glu	Leu
	50					55					60				

Arg	Thr	Leu	Ala	Phe	Thr	Leu	His	Asp	His	Pro	Glu	Glu	Ala	Phe	Glu
	65				70					75					80

Glu	Val	Phe	Ala	Thr	Glu	Glu	Ile	Thr	Lys	Leu	Leu	Gln	Asn	His	Gly
				85					90					95	

Phe	Glu	Val	Gln	Ser	Gly	Val	Tyr	Gly	Val	Lys	Thr	Ala	Leu	Glu	Thr
			100					105					110		

Ser	Phe	Glu	Thr	Pro	Gly	Tyr	Asp	Pro	Ala	Gln	His	Pro	Ser	Ile	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115					120					125					
Ile	Leu	Ala	Glu	Tyr	Asp	Ala	Leu	Pro	Glu	Ile	Gly	His	Ala	Cys	Gly
130					135					140					
His	Asn	Ile	Ile	Ala	Ala	Ala	Gly	Val	Gly	Ala	Phe	Leu	Ala	Val	Thr
145				150						155					160
Asn	Met	Ile	Lys	Thr	Ala	Glu	Val	Lys	Gly	Val	Asp	His	Leu	Asp	Phe
				165					170					175	
Glu	Gly	Arg	Ile	Val	Leu	Leu	Gly	Thr	Pro	Ala	Glu	Glu	Gly	His	Ser
			180					185					190		
Gly	Lys	Glu	Tyr	Met	Ile	Arg	Asn	Gly	Ala	Phe	Asp	Gly	Ile	Asp	Ala
		195					200					205			
Ser	Ile	Met	Met	His	Pro	Phe	Gly	Phe	Asp	Leu	Ala	Glu	His	Val	Trp
		210				215					220				
Val	Gly	Arg	Arg	Thr	Met	Thr	Ala	Thr	Phe	His	Gly	Val	Ser	Ala	His
225				230						235					240
Ala	Ser	Ser	Gln	Pro	Phe	Met	Gly	Lys	Asn	Ala	Leu	Asp	Ala	Ala	Ser
				245					250					255	
Leu	Ala	Tyr	Gln	Gly	Phe	Gly	Val	Leu	Arg	Gln	Gln	Met	Pro	Pro	Ser
			260					265					270		
Asp	Arg	Leu	His	Ala	Ile	Ile	Thr	Glu	Gly	Gly	Asn	Arg	Pro	Ser	Ile
		275					280					285			
Ile	Pro	Asp	Thr	Ala	Thr	Met	Ser	Leu	Tyr	Val	Arg	Ser	Leu	Leu	Pro
		290				295					300				
Glu	Ala	Leu	Lys	Asp	Ile	Ser	Lys	Arg	Val	Asp	Asp	Val	Leu	Asp	Gly
305				310						315					320
Ala	Ala	Leu	Met	Ala	Gly	Val	Gly	Val	Glu	Lys	Gln	Trp	Asp	Val	His
			325						330					335	
Pro	Ala	Ser	Leu	Pro	Val	Arg	Asn	Asn	His	Val	Leu	Ala	Arg	Arg	Trp
			340					345					350		
Ala	Lys	Thr	Gln	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Leu	Ser	Glu	Gly	Ile
		355					360					365			
Leu	Pro	Asp	Thr	Leu	Ala	Ala	Ser	Thr	Asp	Phe	Gly	Asn	Val	Ser	His
		370				375					380				
Leu	Val	Pro	Gly	Ile	His	Pro	Met	Val	Lys	Ile	Ser	Pro	Glu	Asn	Val
385				390						395					400
Ala	Leu	His	Thr	Lys	Glu	Phe	Ala	Ala	Tyr	Ala	Arg	Thr	Glu	Glu	Ala
			405						410					415	
Ile	Asp	Ala	Ala	Val	Asp	Ala	Ala	Ile	Gly	Leu	Ala	Gln	Val	Ala	Val
			420					425					430		
Asp	Ala	Leu	Ala	Asp	Pro	Gln	Met	Leu	Ile	Asp	Ala	Thr	Leu	Glu	Phe
		435					440					445			

Thr Asn Ser Gly Asp Val Leu Lys Val Gly Asp Tyr Leu Ala
 450 455 460

<210> 213
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXA01971

<400> 213
 aggtcttggt tatttcggct actgattcag tagctgcgct ccgataggat tcttagtttt 60
 cagttcagta tctttgagcc acggctagaa tgtgaatcct atg tct aag aag aag 115
 Met Ser Lys Lys Lys
 1 5
 cct cgc ccc att ccg gtt cct gcc caa ttt atc cct ggt ctc att gat 163
 Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile Pro Gly Leu Ile Asp
 10 15 20
 gcg cat aca cat ttg gca tcg tgt gga gga gat ctt gca ggg ttg gtg 211
 Ala His Thr His Leu Ala Ser Cys Gly Gly Asp Leu Ala Gly Leu Val
 25 30 35
 gaa agg gcc aag gag gcg ggc gtc gaa aag ctt tgt acc gtc ggt gat 259
 Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu Cys Thr Val Gly Asp
 40 45 50
 ggt ttg gct gag gcc gag ctt gcg ctg gag gcc gcg caa cag ttt ggc 307
 Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala Ala Gln Gln Phe Gly
 55 60 65
 aat gtg ttt gct gcg tgt gcg att cat ccg acg aag gct gat cag ttg 355
 Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr Lys Ala Asp Gln Leu
 70 75 80 85
 gat ggg gct gcg cgt gcg cgg ctg acg cag atg gcg gcg gat ccg aat 403
 Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met Ala Ala Asp Pro Asn
 90 95 100
 tgt gtg gcc att ggt gag act ggt ttg gat tcg tat tgg atc aag cac 451
 Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser Tyr Trp Ile Lys His
 105 110 115
 gat cca gag gac acg gcg gcg ttg gat gtg caa gag gag gcg ctg cgc 499
 Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln Glu Glu Ala Leu Arg
 120 125 130
 tgg cat att gat ttg gca att agt gcg gat aag ccg ttg atg att cac 547
 Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys Pro Leu Met Ile His
 135 140 145
 aat cgt gag gcg gat gct gat ttg atg cga gtg ttg gcg gat gct cca 595
 Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val Leu Ala Asp Ala Pro
 150 155 160 165

cct cca aaa gat acg att ctg cat tgt ttt tct tcg ccg ttg gac gtg 643
 Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser Ser Pro Leu Asp Val
 170 175 180

gcg aag gaa gcg ttg gat cgt gga tat gtg ttg agt ttt gcg ggc aat 691
 Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu Ser Phe Ala Gly Asn
 185 190 195

gtg acg ttt aag cgt aat gag gag ttg cgg gag gct gct cgt att gcg 739
 Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu Ala Ala Arg Ile Ala
 200 205 210

ccg att tcc cag att ttg att gaa acc gat gcg ccg tat atg acg ccg 787
 Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala Pro Tyr Met Thr Pro
 215 220 225

gag ccg ttt cgg ggg agt agg aat gag ccg tcg ttg att ggt cat acg 835
 Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser Leu Ile Gly His Thr
 230 235 240 245

gcg cta tgc att gcg gag gtt cgg ggg atg gct gtg gag gat gtt gcg 883
 Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala Val Glu Asp Val Ala
 250 255 260

gcg gct ttg aat gag aat ttt gat cgc gtt tat ggg gtc aca aat cta 931
 Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr Gly Val Thr Asn Leu
 265 270 275

taacgtgagg tagctcacag tca 954

<210> 214
 <211> 277
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 214
 Met Ser Lys Lys Lys Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile
 1 5 10 15

Pro Gly Leu Ile Asp Ala His Thr His Leu Ala Ser Cys Gly Gly Asp
 20 25 30

Leu Ala Gly Leu Val Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu
 35 40 45

Cys Thr Val Gly Asp Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala
 50 55 60

Ala Gln Gln Phe Gly Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr
 65 70 75 80

Lys Ala Asp Gln Leu Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met
 85 90 95

Ala Ala Asp Pro Asn Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser
 100 105 110

Tyr Trp Ile Lys His Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln
 115 120 125

Glu Glu Ala Leu Arg Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys
 130 135 140
 Pro Leu Met Ile His Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val
 145 150 155 160
 Leu Ala Asp Ala Pro Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser
 165 170 175
 Ser Pro Leu Asp Val Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu
 180 185 190
 Ser Phe Ala Gly Asn Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu
 195 200 205
 Ala Ala Arg Ile Ala Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala
 210 215 220
 Pro Tyr Met Thr Pro Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser
 225 230 235 240
 Leu Ile Gly His Thr Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala
 245 250 255
 Val Glu Asp Val Ala Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr
 260 265 270
 Gly Val Thr Asn Leu
 275

<210> 215
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXA01802

<400> 215
 ggaattcttg acaaaagtgt tcactacgtt agacatgaga accagtgtgg cacatcacag 60
 gaaatcttcg cgggtgttta gacaaccggt atgtgacaga atg ggc gat caa gac 115
 Met Gly Asp Gln Asp
 1 5
 ata atc gga aag gaa tcc aaa caa atg gac ttt cgc ctc gtc gcg aca 163
 Ile Ile Gly Lys Glu Ser Lys Gln Met Asp Phe Arg Leu Val Ala Thr
 10 15 20
 gac atg gac ggc aca ctt tta aac acc cac cac gaa gtc cca gag aaa 211
 Asp Met Asp Gly Thr Leu Leu Asn Thr His His Glu Val Pro Glu Lys
 25 30 35
 ttt tgg gac atc ctg gaa caa atg cgt gcc aaa gga atc gcc ttc gca 259
 Phe Trp Asp Ile Leu Glu Gln Met Arg Ala Lys Gly Ile Ala Phe Ala
 40 45 50

```

cca gcc agc ggc cgt caa tta gcc acc ttg caa aaa caa ttc ggg cac 307
Pro Ala Ser Gly Arg Gln Leu Ala Thr Leu Gln Lys Gln Phe Gly His
    55                                60                                65

gcg ggt gaa ccc att tct tac atc gca gaa aac ggc acc gtg gta gtc 355
Ala Gly Glu Pro Ile Ser Tyr Ile Ala Glu Asn Gly Thr Val Val Val
    70                                75                                80                                85

cac gac ggc gaa att atc tcc ctg acc acc atc gac tcc gac acc gta 403
His Asp Gly Glu Ile Ile Ser Leu Thr Thr Ile Asp Ser Asp Thr Val
                                90                                95                                100

cac tcc atc atc gat gcc gtg cgc gca tcc gac atc gat atg gga gta 451
His Ser Ile Ile Asp Ala Val Arg Ala Ser Asp Ile Asp Met Gly Val
                                105                                110                                115

gtg gtc tgc cga cca gaa cgc gcc tac gtc gaa cgc aac gac gaa gct 499
Val Val Cys Arg Pro Glu Arg Ala Tyr Val Glu Arg Asn Asp Glu Ala
    120                                125                                130

ttc cgc gcc gaa ggc ctg aaa tac tac gtc tcc atc gag gaa gtc caa 547
Phe Arg Ala Glu Gly Leu Lys Tyr Tyr Val Ser Ile Glu Glu Val Gln
    135                                140                                145

gac ctc cac gaa gca gtc aac aat gaa gta atc aag gta gcg atc ttt 595
Asp Leu His Glu Ala Val Asn Asn Glu Val Ile Lys Val Ala Ile Phe
    150                                155                                160                                165

aca ttc caa gat gcc gaa aag gac tgt gcc ccc atc atc cgc gca gcc 643
Thr Phe Gln Asp Ala Glu Lys Asp Cys Ala Pro Ile Ile Arg Ala Ala
                                170                                175                                180

tcc ccc aac gcc aac gtt gtt gtc tcc ggc cag cac tgg gtc gat gtc 691
Ser Pro Asn Ala Asn Val Val Val Ser Gly Gln His Trp Val Asp Val
                                185                                190                                195

atg gat cct tca gcc aac aag ggc caa gct ttg gct gct ctc cgc gat 739
Met Asp Pro Ser Ala Asn Lys Gly Gln Ala Leu Ala Ala Leu Arg Asp
    200                                205                                210

gcc ctc gga ttg gaa gaa tcc caa act ctc gtg ttt ggc gac tac ctc 787
Ala Leu Gly Leu Glu Glu Ser Gln Thr Leu Val Phe Gly Asp Tyr Leu
    215                                220                                225

aac gac act gaa ttg atc aag gcc gcc ggc aag tct tac gcc atg tcc 835
Asn Asp Thr Glu Leu Ile Lys Ala Ala Gly Lys Ser Tyr Ala Met Ser
    230                                235                                240                                245

aat gcc cac ccg gac att ttg gaa ttg gcc gac gaa att gca cca tcc 883
Asn Ala His Pro Asp Ile Leu Glu Leu Ala Asp Glu Ile Ala Pro Ser
                                250                                255                                260

aac att gaa gag ggc gtt att gtg gtg ctg gag aag ttg ctt aac ggt 931
Asn Ile Glu Glu Gly Val Ile Val Val Leu Glu Lys Leu Leu Asn Gly
    265                                270                                275

taacgattgc aggacgagg ttc 954

```

<210> 216

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

```

Met Gly Asp Gln Asp Ile Ile Gly Lys Glu Ser Lys Gln Met Asp Phe
  1           5           10           15

Arg Leu Val Ala Thr Asp Met Asp Gly Thr Leu Leu Asn Thr His His
          20           25           30

Glu Val Pro Glu Lys Phe Trp Asp Ile Leu Glu Gln Met Arg Ala Lys
          35           40           45

Gly Ile Ala Phe Ala Pro Ala Ser Gly Arg Gln Leu Ala Thr Leu Gln
          50           55           60

Lys Gln Phe Gly His Ala Gly Glu Pro Ile Ser Tyr Ile Ala Glu Asn
          65           70           75           80

Gly Thr Val Val Val His Asp Gly Glu Ile Ile Ser Leu Thr Thr Ile
          85           90           95

Asp Ser Asp Thr Val His Ser Ile Ile Asp Ala Val Arg Ala Ser Asp
          100          105          110

Ile Asp Met Gly Val Val Val Cys Arg Pro Glu Arg Ala Tyr Val Glu
          115          120          125

Arg Asn Asp Glu Ala Phe Arg Ala Glu Gly Leu Lys Tyr Tyr Val Ser
          130          135          140

Ile Glu Glu Val Gln Asp Leu His Glu Ala Val Asn Asn Glu Val Ile
          145          150          155          160

Lys Val Ala Ile Phe Thr Phe Gln Asp Ala Glu Lys Asp Cys Ala Pro
          165          170          175

Ile Ile Arg Ala Ala Ser Pro Asn Ala Asn Val Val Val Ser Gly Gln
          180          185          190

His Trp Val Asp Val Met Asp Pro Ser Ala Asn Lys Gly Gln Ala Leu
          195          200          205

Ala Ala Leu Arg Asp Ala Leu Gly Leu Glu Glu Ser Gln Thr Leu Val
          210          215          220

Phe Gly Asp Tyr Leu Asn Asp Thr Glu Leu Ile Lys Ala Ala Gly Lys
          225          230          235          240

Ser Tyr Ala Met Ser Asn Ala His Pro Asp Ile Leu Glu Leu Ala Asp
          245          250          255

Glu Ile Ala Pro Ser Asn Ile Glu Glu Gly Val Ile Val Val Leu Glu
          260          265          270

Lys Leu Leu Asn Gly
          275

```

<210> 217

<211> 1066

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1066)

<223> RXN00866

<400> 217

```

gcatcaacgt aggagatcct cgacttccaa ttatggctcc aaatgagcag gaacttgagg 60

ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115
                                         Met Asn Asp Ser Arg
                                         1 5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt 163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly
                        10 15 20

cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc 211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser
                        25 30 35

tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg 259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg
                        40 45 50

gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln
                        55 60 65

aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn
                        70 75 80 85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly
                        90 95 100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln
                        105 110 115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys
                        120 125 130

tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag 547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys
                        135 140 145

gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa 595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu
                        150 155 160 165

atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc 643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile
                        170 175 180

gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac 691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp

```

185										190					195					
ctg	att	ctt	cct	gac	ttc	ggc	cca	att	gag	gat	cac	ctg	cac	cgc	gtc	739				
Leu	Ile	Leu	Pro	Asp	Phe	Gly	Pro	Ile	Glu	Asp	His	Leu	His	Arg	Val					
		200					205					210								
gat	gca	ttg	gtg	gtt	act	cac	gga	cac	gaa	gac	cac	att	ggg	gct	att	787				
Asp	Ala	Leu	Val	Val	Thr	His	Gly	His	Glu	Asp	His	Ile	Gly	Ala	Ile					
	215					220					225									
ccc	tgg	ctg	ctg	aag	ctg	cgc	aac	gat	atc	cca	atc	ttg	gca	tcc	cgt	835				
Pro	Trp	Leu	Leu	Lys	Leu	Arg	Asn	Asp	Ile	Pro	Ile	Leu	Ala	Ser	Arg					
230					235					240				245						
ttc	acc	ttg	gct	ctg	att	gca	gct	aag	tgt	aag	gaa	cac	cgt	cag	cgt	883				
Phe	Thr	Leu	Ala	Leu	Ile	Ala	Ala	Lys	Cys	Lys	Glu	His	Arg	Gln	Arg					
				250					255					260						
ccg	aag	ctg	atc	gag	gtc	aac	gag	cag	tcc	aat	gag	gac	cgc	gga	ccg	931				
Pro	Lys	Leu	Ile	Glu	Val	Asn	Glu	Gln	Ser	Asn	Glu	Asp	Arg	Gly	Pro					
			265					270					275							
ttc	aac	att	cgc	ttc	tgg	gct	gtt	aac	cac	tcc	atc	cca	gac	tgc	ctt	979				
Phe	Asn	Ile	Arg	Phe	Trp	Ala	Val	Asn	His	Ser	Ile	Pro	Asp	Cys	Leu					
		280					285					290								
ggg	ctt	gct	atc	aag	act	cct	gct	ggg	ttg	gtc	atc	cac	acc	ggg	gac	1027				
Gly	Leu	Ala	Ile	Lys	Thr	Pro	Ala	Gly	Leu	Val	Ile	His	Thr	Gly	Asp					
	295					300				305										
atc	aag	ctg	gat	cag	act	cct	cct	gat	gga	cgc	cca	act				1066				
Ile	Lys	Leu	Asp	Gln	Thr	Pro	Pro	Asp	Gly	Arg	Pro	Thr								
310					315					320										

<210> 218

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
1				5					10					15	

Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20						25					30		

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55					60				

Ser	Gln	Gly	Ser	Gln	Asn	Ala	Gln	Gly	Ser	Gln	Asn	Arg	Glu	Ser	Gly
	65				70					75					80

Asn	Asn	Asn	Arg	Asn	Arg	Ser	Asn	Asn	Asn	Arg	Arg	Gly	Gly	Arg	Gly
				85					90					95	

Arg	Arg	Gly	Ser	Gly	Asn	Ala	Asn	Glu	Gly	Ala	Asn	Asn	Asn	Ser	Gly
			100					105					110		

Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
 115 120 125
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
 130 135 140
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
 145 150 155 160
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
 165 170 175
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
 180 185 190
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
 245 250 255
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
 290 295 300
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg
 305 310 315 320
 Pro Thr

<210> 219
 <211> 1045
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1045)
 <223> FRXA00866

<400> 219
 gcacaaacgt aggagatcct cgacttccaa ttatggctcc aaatgagcag gaacttgagg 60
 ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115
 Met Asn Asp Ser Arg
 1 5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt	163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly	
10 15 20	
cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc	211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser	
25 30 35	
tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg	259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg	
40 45 50	
gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag	307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln	
55 60 65	
aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac	355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn	
70 75 80 85	
cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga	403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly	
90 95 100	
aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag	451
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln	
105 110 115	
ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag	499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys	
120 125 130	
tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag	547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys	
135 140 145	
gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa	595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu	
150 155 160 165	
atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc	643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile	
170 175 180	
gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac	691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp	
185 190 195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc	739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val	
200 205 210	
gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att	787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile	
215 220 225	
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt	835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg	
230 235 240 245	
ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt	883

<400> 220															
Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
1				5					10					15	
Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
			20					25					30		
Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			
Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55					60				
Ser	Gln	Gly	Ser	Gln	Asn	Ala	Gln	Gly	Ser	Gln	Asn	Arg	Glu	Ser	Gly
65					70					75					80
Asn	Asn	Asn	Arg	Asn	Arg	Ser	Asn	Asn	Asn	Arg	Arg	Gly	Gly	Arg	Gly
				85					90					95	
Arg	Arg	Gly	Ser	Gly	Asn	Ala	Asn	Glu	Gly	Ala	Asn	Asn	Asn	Ser	Gly
			100					105					110		
Asn	Gln	Asn	Arg	Gln	Gly	Gly	Asn	Arg	Gly	Asn	Arg	Gly	Gly	Gly	Arg
		115					120					125			
Arg	Asn	Val	Val	Lys	Ser	Met	Gln	Gly	Ala	Asp	Leu	Thr	Gln	Arg	Leu
	130					135					140				
Pro	Glu	Pro	Pro	Lys	Ala	Pro	Ala	Asn	Gly	Leu	Arg	Ile	Tyr	Ala	Leu
145					150					155					160
Gly	Gly	Ile	Ser	Glu	Ile	Gly	Arg	Asn	Met	Thr	Val	Phe	Glu	Tyr	Asn
				165					170					175	
Asn	Arg	Leu	Leu	Ile	Val	Asp	Cys	Gly	Val	Leu	Phe	Pro	Ser	Ser	Gly
			180					185					190		

Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
 245 250 255
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
 290 295 300
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr
 305 310 315

<210> 221
 <211> 789
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXA02410

<400> 221
 tatgagactg accatccttg gaagctctgg tagcgtgccc gctccaggta accccgcatac 60
 cgatatctg ttaacttctc cggacgcccc tgccgtgatt atg gac atg ggc cca 115
 Met Asp Met Gly Pro
 1 5
 ggt gtc ctt gca gca gtt caa gaa att caa gat cct gct gat gcg cat 163
 Gly Val Leu Ala Ala Val Gln Glu Ile Gln Asp Pro Ala Asp Ala His
 10 15 20
 gtt att ttc tcc cat ttg cac acc gat cac tgc gct gat ttt gcg tcc 211
 Val Ile Phe Ser His Leu His Thr Asp His Cys Ala Asp Phe Ala Ser
 25 30 35
 ttg atg gtg tgg cgc agg ttc cac cca acg ctg gcc gcc aag agc cgc 259
 Leu Met Val Trp Arg Arg Phe His Pro Thr Leu Ala Ala Lys Ser Arg
 40 45 50
 aat ctt ttg ttt gga cct gaa gat acc ccc aac agg ctt ggt cgt ttg 307
 Asn Leu Leu Phe Gly Pro Glu Asp Thr Pro Asn Arg Leu Gly Arg Leu
 55 60 65
 agc tcc gat gag cct gat ggc gtt gac gat atg tca gat act ttt gct 355
 Ser Ser Asp Glu Pro Asp Gly Val Asp Asp Met Ser Asp Thr Phe Ala

70	75	80	85	
ttc gac gcc tgg gaa gag cgc aag cca gag ctc att gat aat ttc acg				403
Phe Asp Ala Trp	Glu Glu Arg Lys Pro	Glu Leu Ile Asp Asn Phe Thr		
	90	95	100	
gtc acg ccg ttc cgc gtt gtg cac ccc att gag acc tac gcg ctt cgc				451
Val Thr Pro Phe Arg Val Val His Pro Ile Glu Thr Tyr Ala Leu Arg				
	105	110	115	
gta gag gag cac cgc acc ggc gcc tca att acg tat tcc ggt gac agc				499
Val Glu Glu His Arg Thr Gly Ala Ser Ile Thr Tyr Ser Gly Asp Ser				
	120	125	130	
gcg tac acc gaa gcg ctt atc gac gcc gcc cgc aac gtt gac att ttc				547
Ala Tyr Thr Glu Ala Leu Ile Asp Ala Ala Arg Asn Val Asp Ile Phe				
	135	140	145	
ttg tgc gag gca act tgg ggc acc tct tgc gat gac aaa gca cca gga				595
Leu Cys Glu Ala Thr Trp Gly Thr Ser Cys Asp Asp Lys Ala Pro Gly				
	150	155	160	165
atg cat atg tgt ggc caa gac gcc gga aga att gcg gca gca gct ggc				643
Met His Met Cys Gly Gln Asp Ala Gly Arg Ile Ala Ala Ala Ala Gly				
	170	175	180	
gta aag aaa ctg att atc act cat gtt cca cca tgg att gat gca gag				691
Val Lys Lys Leu Ile Ile Thr His Val Pro Pro Trp Ile Asp Ala Glu				
	185	190	195	
gcc aca gtg gca gca gct gcg gaa cac ttt gat ggt cct atc gaa ttg				739
Ala Thr Val Ala Ala Ala Ala Glu His Phe Asp Gly Pro Ile Glu Leu				
	200	205	210	
gca cga tca gga atg gtt atc gag ttt tagtccgttt gtactaataa				786
Ala Arg Ser Gly Met Val Ile Glu Phe				
	215	220		
ggt				789
<210> 222				
<211> 222				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 222				
Met Asp Met Gly Pro Gly Val Leu Ala Ala Val Gln Glu Ile Gln Asp				
1	5	10	15	
Pro Ala Asp Ala His Val Ile Phe Ser His Leu His Thr Asp His Cys				
	20	25	30	
Ala Asp Phe Ala Ser Leu Met Val Trp Arg Arg Phe His Pro Thr Leu				
	35	40	45	
Ala Ala Lys Ser Arg Asn Leu Leu Phe Gly Pro Glu Asp Thr Pro Asn				
	50	55	60	
Arg Leu Gly Arg Leu Ser Ser Asp Glu Pro Asp Gly Val Asp Asp Met				
	65	70	75	80

Ser Asp Thr Phe Ala Phe Asp Ala Trp Glu Glu Arg Lys Pro Glu Leu
 85 90 95

Ile Asp Asn Phe Thr Val Thr Pro Phe Arg Val Val His Pro Ile Glu
 100 105 110

Thr Tyr Ala Leu Arg Val Glu Glu His Arg Thr Gly Ala Ser Ile Thr
 115 120 125

Tyr Ser Gly Asp Ser Ala Tyr Thr Glu Ala Leu Ile Asp Ala Ala Arg
 130 135 140

Asn Val Asp Ile Phe Leu Cys Glu Ala Thr Trp Gly Thr Ser Cys Asp
 145 150 155 160

Asp Lys Ala Pro Gly Met His Met Cys Gly Gln Asp Ala Gly Arg Ile
 165 170 175

Ala Ala Ala Ala Gly Val Lys Lys Leu Ile Ile Thr His Val Pro Pro
 180 185 190

Trp Ile Asp Ala Glu Ala Thr Val Ala Ala Ala Ala Glu His Phe Asp
 195 200 205

Gly Pro Ile Glu Leu Ala Arg Ser Gly Met Val Ile Glu Phe
 210 215 220

<210> 223

<211> 455

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(432)

<223> RXA00961

<400> 223

cta gag aac tgg cgt atc ggc cgc atg ttg ctg ctt ggc gac gcc gcc 48
 Leu Glu Asn Trp Arg Ile Gly Arg Met Leu Leu Leu Gly Asp Ala Ala
 1 5 10 15

cac gca ccc ctc cag tac ctc gcc tca ggc gcg gtc atg gcc atg gaa 96
 His Ala Pro Leu Gln Tyr Leu Ala Ser Gly Ala Val Met Ala Met Glu
 20 25 30

gac gcc gag gct gtc gcc ctc ttc gct gcc gac gct gcg cgt gct ggc 144
 Asp Ala Glu Ala Val Ala Leu Phe Ala Ala Asp Ala Ala Arg Ala Gly
 35 40 45

aac ctc gat tgg gaa gag gta ctc gca gag gtg gaa gct gaa cgc cga 192
 Asn Leu Asp Trp Glu Glu Val Leu Ala Glu Val Glu Ala Glu Arg Arg
 50 55 60

cca cgc tgc agc cgc atc caa acc gta ggc cgt ttc tgg gga gag ctc 240
 Pro Arg Cys Ser Arg Ile Gln Thr Val Gly Arg Phe Trp Gly Glu Leu
 65 70 75 80

tgg cat gtg gaa ggc acc gca cgt ctc atc cgc aac gaa gtt ttc cgc 288

Trp His Val Glu Gly Thr Ala Arg Leu Ile Arg Asn Glu Val Phe Arg
 85 90 95

caa gca gac cgc aat ggc tgg ttc atc tat gca gac tgg ctg tgg ggt 336
 Gln Ala Asp Arg Asn Gly Trp Phe Ile Tyr Ala Asp Trp Leu Trp Gly
 100 105 110

tac gat gca tcc aag cgt gcc cac atc gcc aac cct gag ctc gga gaa 384
 Tyr Asp Ala Ser Lys Arg Ala His Ile Ala Asn Pro Glu Leu Gly Glu
 115 120 125

atg cca caa gca ctg aag gaa tgg cgc tac gcc ctc ctc gaa cag aaa 432
 Met Pro Gln Ala Leu Lys Glu Trp Arg Tyr Ala Leu Leu Glu Gln Lys
 130 135 140

tagcagcctc acctgttaag gga 455

<210> 224
 <211> 144
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 224
 Leu Glu Asn Trp Arg Ile Gly Arg Met Leu Leu Leu Gly Asp Ala Ala
 1 5 10 15

His Ala Pro Leu Gln Tyr Leu Ala Ser Gly Ala Val Met Ala Met Glu
 20 25 30

Asp Ala Glu Ala Val Ala Leu Phe Ala Ala Asp Ala Ala Arg Ala Gly
 35 40 45

Asn Leu Asp Trp Glu Glu Val Leu Ala Glu Val Glu Ala Glu Arg Arg
 50 55 60

Pro Arg Cys Ser Arg Ile Gln Thr Val Gly Arg Phe Trp Gly Glu Leu
 65 70 75 80

Trp His Val Glu Gly Thr Ala Arg Leu Ile Arg Asn Glu Val Phe Arg
 85 90 95

Gln Ala Asp Arg Asn Gly Trp Phe Ile Tyr Ala Asp Trp Leu Trp Gly
 100 105 110

Tyr Asp Ala Ser Lys Arg Ala His Ile Ala Asn Pro Glu Leu Gly Glu
 115 120 125

Met Pro Gln Ala Leu Lys Glu Trp Arg Tyr Ala Leu Leu Glu Gln Lys
 130 135 140

<210> 225
 <211> 1116
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1093)

<223> RXA00111

<400> 225

```

ccgagaagct ggagaaggcc aacaagcgtg gcctctacac ctccgcgtcc ttccacagcc 60

ccggcgccat cactggcgac cactaaaaaa ggagacttcg atg gcc ttt ttt agc 115
                                         Met Ala Phe Phe Ser
                                         1                               5

ttt tcg acg tct ccc ctc acc cgc ctc atc ccc ggc agc cgc tcc aaa 163
Phe Ser Thr Ser Pro Leu Thr Arg Leu Ile Pro Gly Ser Arg Ser Lys
                        10                               15                               20

gcc aca ggc gcc aaa cgg cgc ctg agc agc aca atc gcg tcg att gaa 211
Ala Thr Gly Ala Lys Arg Arg Leu Ser Ser Thr Ile Ala Ser Ile Glu
                        25                               30                               35

cgc tcc ccc ggc atc att gcc cta gac gga ccg ttc acc cac gat cac 259
Arg Ser Pro Gly Ile Ile Ala Leu Asp Gly Pro Phe Thr His Asp His
                        40                               45                               50

gtc tcc gta cgt ggc att cgc ctc cat tta gca gag gca ggc tcc ccc 307
Val Ser Val Arg Gly Ile Arg Leu His Leu Ala Glu Ala Gly Ser Pro
                        55                               60                               65

acc aaa ccc ctg gtt ctt ctg atc cac ggg gct ttc ggc ggt tgg tac 355
Thr Lys Pro Leu Val Leu Leu Ile His Gly Ala Phe Gly Gly Trp Tyr
                        70                               75                               80                               85

gac tac cgc gaa gtc atc ggc cca ctc gca gat gcc ggc ttc cac gtc 403
Asp Tyr Arg Glu Val Ile Gly Pro Leu Ala Asp Ala Gly Phe His Val
                        90                               95                               100

gcc gcc atc gat cta cgc ggc tac ggc atg tcc gac aaa ccc cca aca 451
Ala Ala Ile Asp Leu Arg Gly Tyr Gly Met Ser Asp Lys Pro Pro Thr
                        105                               110                               115

ggc tac gac ctc cgc cac gca gcc gga gaa ctc agc agc gtt atc gca 499
Gly Tyr Asp Leu Arg His Ala Ala Gly Glu Leu Ser Ser Val Ile Ala
                        120                               125                               130

gct ctc ggc cac gat gac gca ctt ctt gtc ggc tcc gac acc ggc gcc 547
Ala Leu Gly His Asp Asp Ala Leu Leu Val Gly Ser Asp Thr Gly Ala
                        135                               140                               145

agc atc gcc tgg gct atc gct tcc atg tac ccc gaa cgg gtc cgc ggc 595
Ser Ile Ala Trp Ala Ile Ala Ser Met Tyr Pro Glu Arg Val Arg Gly
                        150                               155                               160                               165

cta att tcc ctc ggc gcg atc cac ccc ctt gac atg cga cgc gcc atc 643
Leu Ile Ser Leu Gly Ala Ile His Pro Leu Asp Met Arg Arg Ala Ile
                        170                               175                               180

cga cga aaa ccc cac cta cac gtc tct gac ctc agc cga ctt gct cct 691
Arg Arg Lys Pro His Leu His Val Ser Asp Leu Ser Arg Leu Ala Pro
                        185                               190                               195

ttt cgg ttg ccc tca ttc ctg cat aac ctc ttc cac ttc gga atc acc 739
Phe Arg Leu Pro Ser Phe Leu His Asn Leu Phe His Phe Gly Ile Thr

```

200	205	210	
agc gaa gct cga cgt gag atc gtc aac aac acg tcc tcg tcc tac cag Ser Glu Ala Arg Arg Glu Ile Val Asn Asn Thr Ser Ser Ser Tyr Gln 215 220 225			787
cgc agc aac gca ttc aca gag aca gtg ctc ctc cgc aaa aaa gca cta Arg Ser Asn Ala Phe Thr Glu Thr Val Leu Leu Arg Lys Lys Ala Leu 230 235 240 245			835
tcg atc gac cac acc atc acc ccg atc atc cgc acc aac cgc tac ctc Ser Ile Asp His Thr Ile Thr Pro Ile Ile Arg Thr Asn Arg Tyr Leu 250 255 260			883
gtt ggg tcg atc ccc agc aaa aca gtc tcc gca ccg gtg tgg ctg ctc Val Gly Ser Ile Pro Ser Lys Thr Val Ser Ala Pro Val Trp Leu Leu 265 270 275			931
aga acc aac act cga cgc tgg gaa cat cta gcc aat act gcg cgc act Arg Thr Asn Thr Arg Arg Trp Glu His Leu Ala Asn Thr Ala Arg Thr 280 285 290			979
cga acg aca ggg cca ttc acc acc atc gcg atc ccc ggc ggc tac gaa Arg Thr Thr Gly Pro Phe Thr Thr Ile Ala Ile Pro Gly Gly Tyr Glu 295 300 305			1027
ctc ccc tac ctc gag aac cct tcc gaa ttt gca gca acc atc gca gag Leu Pro Tyr Leu Glu Asn Pro Ser Glu Phe Ala Ala Thr Ile Ala Glu 310 315 320 325			1075
ttc gcg cgc acc acg ttt taagcactgt ggctgaggcg ctg Phe Ala Arg Thr Thr Phe 330			1116

<210> 226

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met	Ala	Phe	Phe	Ser	Phe	Ser	Thr	Ser	Pro	Leu	Thr	Arg	Leu	Ile	Pro
1				5					10					15	

Gly	Ser	Arg	Ser	Lys	Ala	Thr	Gly	Ala	Lys	Arg	Arg	Leu	Ser	Ser	Thr
			20					25					30		

Ile	Ala	Ser	Ile	Glu	Arg	Ser	Pro	Gly	Ile	Ile	Ala	Leu	Asp	Gly	Pro
			35				40					45			

Phe	Thr	His	Asp	His	Val	Ser	Val	Arg	Gly	Ile	Arg	Leu	His	Leu	Ala
	50					55					60				

Glu	Ala	Gly	Ser	Pro	Thr	Lys	Pro	Leu	Val	Leu	Leu	Ile	His	Gly	Ala
	65				70					75					80

Phe	Gly	Gly	Trp	Tyr	Asp	Tyr	Arg	Glu	Val	Ile	Gly	Pro	Leu	Ala	Asp
				85					90					95	

Ala	Gly	Phe	His	Val	Ala	Ala	Ile	Asp	Leu	Arg	Gly	Tyr	Gly	Met	Ser
			100					105					110		

Asp Lys Pro Pro Thr Gly Tyr Asp Leu Arg His Ala Ala Gly Glu Leu
 115 120 125
 Ser Ser Val Ile Ala Ala Leu Gly His Asp Asp Ala Leu Leu Val Gly
 130 135 140
 Ser Asp Thr Gly Ala Ser Ile Ala Trp Ala Ile Ala Ser Met Tyr Pro
 145 150 155 160
 Glu Arg Val Arg Gly Leu Ile Ser Leu Gly Ala Ile His Pro Leu Asp
 165 170 175
 Met Arg Arg Ala Ile Arg Arg Lys Pro His Leu His Val Ser Asp Leu
 180 185 190
 Ser Arg Leu Ala Pro Phe Arg Leu Pro Ser Phe Leu His Asn Leu Phe
 195 200 205
 His Phe Gly Ile Thr Ser Glu Ala Arg Arg Glu Ile Val Asn Asn Thr
 210 215 220
 Ser Ser Ser Tyr Gln Arg Ser Asn Ala Phe Thr Glu Thr Val Leu Leu
 225 230 235 240
 Arg Lys Lys Ala Leu Ser Ile Asp His Thr Ile Thr Pro Ile Ile Arg
 245 250 255
 Thr Asn Arg Tyr Leu Val Gly Ser Ile Pro Ser Lys Thr Val Ser Ala
 260 265 270
 Pro Val Trp Leu Leu Arg Thr Asn Thr Arg Arg Trp Glu His Leu Ala
 275 280 285
 Asn Thr Ala Arg Thr Arg Thr Thr Gly Pro Phe Thr Thr Ile Ala Ile
 290 295 300
 Pro Gly Gly Tyr Glu Leu Pro Tyr Leu Glu Asn Pro Ser Glu Phe Ala
 305 310 315 320
 Ala Thr Ile Ala Glu Phe Ala Arg Thr Thr Phe
 325 330

<210> 227
 <211> 1020
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(997)
 <223> RXA01932

<400> 227
 tttctaacct gcatccaagc ctaggtggaa ttgagatgac gcgtcgtaga gatcgaaaac 60
 tcaaccaa at ttcttgcc ta aggcttctag gattgtcg tt atg ctc ctt cac cca 115
 Met Leu Leu His Pro
 1 5

gat gcg cag ttt tat atc gat acc ttg ccc act ctc agc gcg gag gag	163
Asp Ala Gln Phe Tyr Ile Asp Thr Leu Pro Thr Leu Ser Ala Glu Glu	
10 15 20	
cag gtg agt ttt ggt aaa gac gct cct gtt tca gag gct gat gca acc	211
Gln Val Ser Phe Gly Lys Asp Ala Pro Val Ser Glu Ala Asp Ala Thr	
25 30 35	
cat gtg gcg aca gat caa gat att gct ggg gtg ccg gtg agg gtt tat	259
His Val Ala Thr Asp Gln Asp Ile Ala Gly Val Pro Val Arg Val Tyr	
40 45 50	
acg cct tta tct ggg gct ggg gat ttg ccg tgt ttg gtg tac ttc cac	307
Thr Pro Leu Ser Gly Ala Gly Asp Leu Pro Cys Leu Val Tyr Phe His	
55 60 65	
ggc ggt ggc tgg tcc ggc ggc acc ctc aac atg atc gat gcc acg gtt	355
Gly Gly Gly Trp Ser Gly Gly Thr Leu Asn Met Ile Asp Ala Thr Val	
70 75 80 85	
cac tct cta gtg gtt ggc ctg ccg atc atc gcc atc agc gtg gac tac	403
His Ser Leu Val Val Gly Leu Pro Ile Ile Ala Ile Ser Val Asp Tyr	
90 95 100	
cga ctt gca ccc gca cac cca ttt cca gcg gct atc gac gac gcg ttt	451
Arg Leu Ala Pro Ala His Pro Phe Pro Ala Ala Ile Asp Asp Ala Phe	
105 110 115	
gca gtg gtc agt gcc gta ttg gat ggg gtg tct ggg ctg agt att gat	499
Ala Val Val Ser Ala Val Leu Asp Gly Val Ser Gly Leu Ser Ile Asp	
120 125 130	
act tcc cga gtg gca att ggc ggt gac agt gcc ggt gga aat att gcc	547
Thr Ser Arg Val Ala Ile Gly Gly Asp Ser Ala Gly Gly Asn Ile Ala	
135 140 145	
gcg gtt act gca caa cag ctg cgt gaa cgg gct gtg ggt tct act cct	595
Ala Val Thr Ala Gln Gln Leu Arg Glu Arg Ala Val Gly Ser Thr Pro	
150 155 160 165	
gta ttg gct cac cag gtg ctt att ttt ccg gta act gat gtt tcc act	643
Val Leu Ala His Gln Val Leu Ile Phe Pro Val Thr Asp Val Ser Thr	
170 175 180	
aca tct acg ccg agc tat ctc aca ttt ggc aaa gat tgc tac ctg aca	691
Thr Ser Thr Pro Ser Tyr Leu Thr Phe Gly Lys Asp Cys Tyr Leu Thr	
185 190 195	
aag gac gcg atg gaa cgc tac atc gaa caa tat gcc gat ggg cac gac	739
Lys Asp Ala Met Glu Arg Tyr Ile Glu Gln Tyr Ala Asp Gly His Asp	
200 205 210	
cgc acc gac cct cga ctc tca ccg cta ctg gca tct gat ttg agc gac	787
Arg Thr Asp Pro Arg Leu Ser Pro Leu Leu Ala Ser Asp Leu Ser Asp	
215 220 225	
ctc cca ccc acc acc att gtg tac ggc gaa tgc gac gtg tta gcc cat	835
Leu Pro Pro Thr Thr Ile Val Tyr Gly Glu Cys Asp Val Leu Ala His	
230 235 240 245	
gaa gtg cga gcc tat gga caa gct cta cta gag gct gga aat tcc gtg	883

Glu Val Arg Ala Tyr Gly Gln Ala Leu Leu Glu Ala Gly Asn Ser Val
 250 255 260

acg atg act gaa ttc aaa gga cag atc cac gcc ttt att aac cta ggg 931
 Thr Met Thr Glu Phe Lys Gly Gln Ile His Ala Phe Ile Asn Leu Gly
 265 270 275

gga atc agt tcc gat gcg cgg gct gct cga cga ctc atc cgc gcc gaa 979
 Gly Ile Ser Ser Asp Ala Arg Ala Ala Arg Arg Leu Ile Arg Ala Glu
 280 285 290

ttg gaa gca gca ctt tgt taaagggttga gatttaacat tcg 1020
 Leu Glu Ala Ala Leu Cys
 295

<210> 228
 <211> 299
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 228
 Met Leu Leu His Pro Asp Ala Gln Phe Tyr Ile Asp Thr Leu Pro Thr
 1 5 10 15

Leu Ser Ala Glu Glu Gln Val Ser Phe Gly Lys Asp Ala Pro Val Ser
 20 25 30

Glu Ala Asp Ala Thr His Val Ala Thr Asp Gln Asp Ile Ala Gly Val
 35 40 45

Pro Val Arg Val Tyr Thr Pro Leu Ser Gly Ala Gly Asp Leu Pro Cys
 50 55 60

Leu Val Tyr Phe His Gly Gly Gly Trp Ser Gly Gly Thr Leu Asn Met
 65 70 75 80

Ile Asp Ala Thr Val His Ser Leu Val Val Gly Leu Pro Ile Ile Ala
 85 90 95

Ile Ser Val Asp Tyr Arg Leu Ala Pro Ala His Pro Phe Pro Ala Ala
 100 105 110

Ile Asp Asp Ala Phe Ala Val Val Ser Ala Val Leu Asp Gly Val Ser
 115 120 125

Gly Leu Ser Ile Asp Thr Ser Arg Val Ala Ile Gly Gly Asp Ser Ala
 130 135 140

Gly Gly Asn Ile Ala Ala Val Thr Ala Gln Gln Leu Arg Glu Arg Ala
 145 150 155 160

Val Gly Ser Thr Pro Val Leu Ala His Gln Val Leu Ile Phe Pro Val
 165 170 175

Thr Asp Val Ser Thr Thr Ser Thr Pro Ser Tyr Leu Thr Phe Gly Lys
 180 185 190

Asp Cys Tyr Leu Thr Lys Asp Ala Met Glu Arg Tyr Ile Glu Gln Tyr
 195 200 205

Ala Asp Gly His Asp Arg Thr Asp Pro Arg Leu Ser Pro Leu Leu Ala
 210 215 220

Ser Asp Leu Ser Asp Leu Pro Pro Thr Thr Ile Val Tyr Gly Glu Cys
 225 230 235 240

Asp Val Leu Ala His Glu Val Arg Ala Tyr Gly Gln Ala Leu Leu Glu
 245 250 255

Ala Gly Asn Ser Val Thr Met Thr Glu Phe Lys Gly Gln Ile His Ala
 260 265 270

Phe Ile Asn Leu Gly Gly Ile Ser Ser Asp Ala Arg Ala Ala Arg Arg
 275 280 285

Leu Ile Arg Ala Glu Leu Glu Ala Ala Leu Cys
 290 295

<210> 229
 <211> 1131
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1108)
 <223> RXA02574

<400> 229
 tgtgtctcctt gcgggctgcg cagaagagcc ggaacagcaa aaagcaataa gccgcttattc 60

gacgtccccc tccaccctc ccgcaccgac cgcgaggagat ttg gcg cgc gcg caa 115
 Leu Ala Arg Ala Gln
 1 5

atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
 10 15 20

gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
 25 30 35

ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
 40 45 50

ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
 55 60 65

gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
 70 75 80 85

ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
 90 95 100

gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451

Glu	Gln	Val	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gly	Thr	Gly	Leu	Ala	Ala		
			105					110					115				
cat	ggg	gtg	aca	gtt	aac	ttt	gca	cct	gtt	gta	gat	gta	gat	gct	tgg	499	
His	Gly	Val	Thr	Val	Asn	Phe	Ala	Pro	Val	Val	Asp	Val	Asp	Ala	Trp		
			120					125					130				
ggg	ctc	ccc	gtc	gtt	ggc	gat	cgt	tcc	ttt	tcc	aac	gac	cca	gcc	gta	547	
Gly	Leu	Pro	Val	Val	Gly	Asp	Arg	Ser	Phe	Ser	Asn	Asp	Pro	Ala	Val		
			135					140				145					
gca	gct	act	tat	gcc	aca	gct	ttt	gca	aag	ggc	tta	agc	aaa	gta	gga	595	
Ala	Ala	Thr	Tyr	Ala	Thr	Ala	Phe	Ala	Lys	Gly	Leu	Ser	Lys	Val	Gly		
											160				165		
att	acc	cca	gta	ttc	aaa	cat	ttc	cca	ggg	cac	ggg	cgt	gca	agt	ggc	643	
Ile	Thr	Pro	Val	Phe	Lys	His	Phe	Pro	Gly	His	Gly	Arg	Ala	Ser	Gly		
															180		
gat	tcg	cac	acc	caa	gat	gtg	gtg	acc	ccc	gca	ctt	gat	gag	ctt	aaa	691	
Asp	Ser	His	Thr	Gln	Asp	Val	Val	Thr	Pro	Ala	Leu	Asp	Glu	Leu	Lys		
															195		
act	tac	gac	ctc	atc	cct	tat	ggg	caa	gca	ctt	tct	gaa	act	gac	gga	739	
Thr	Tyr	Asp	Leu	Ile	Pro	Tyr	Gly	Gln	Ala	Leu	Ser	Glu	Thr	Asp	Gly		
															210		
gcc	gtc	atg	gtg	ggc	cac	atg	att	gtt	cca	ggg	ctt	ggc	acc	gac	gga	787	
Ala	Val	Met	Val	Gly	His	Met	Ile	Val	Pro	Gly	Leu	Gly	Thr	Asp	Gly		
															225		
gtt	cca	tcc	tct	atc	gac	ccc	gcc	acc	tat	caa	ctg	ctc	cgc	agt	ggc	835	
Val	Pro	Ser	Ser	Ile	Asp	Pro	Ala	Thr	Tyr	Gln	Leu	Leu	Arg	Ser	Gly		
															245		
gat	tac	cca	ggg	ggc	gtg	cct	ttc	gat	ggc	gtg	atc	tac	acc	gac	gat	883	
Asp	Tyr	Pro	Gly	Gly	Val	Pro	Phe	Asp	Gly	Val	Ile	Tyr	Thr	Asp	Asp		
															260		
ctc	tct	gga	atg	agt	gcc	att	tcc	gcc	acc	cat	tca	ccc	gca	gaa	gca	931	
Leu	Ser	Gly	Met	Ser	Ala	Ile	Ser	Ala	Thr	His	Ser	Pro	Ala	Glu	Ala		
															275		
gtg	ctt	gcc	tcc	ctc	aaa	gca	ggc	gca	gac	caa	gca	cta	tgg	atc	gac	979	
Val	Leu	Ala	Ser	Leu	Lys	Ala	Gly	Ala	Asp	Gln	Ala	Leu	Trp	Ile	Asp		
															290		
tat	ggg	tcg	ttg	ggc	tcc	gcg	att	gat	cgc	gtt	gat	gct	gcc	gtt	agc	1027	
Tyr	Gly	Ser	Leu	Gly	Ser	Ala	Ile	Asp	Arg	Val	Asp	Ala	Ala	Val	Ser		
															305		
agc	ggg	gaa	tac	cct	caa	gaa	caa	atg	ctg	gca	tct	gcg	tta	aga	gtc	1075	
Ser	Gly	Glu	Tyr	Pro	Gln	Glu	Gln	Met	Leu	Ala	Ser	Ala	Leu	Arg	Val		
															325		
caa	ttg	ctc	tac	atc	aca	cgt	ctc	gaa	caa	aag	tgaagttacc	agtcgtaac	1128				
Gln	Leu	Leu	Tyr	Ile	Thr	Arg	Leu	Glu	Gln	Lys							
															335		
ccc																1131	

<210> 230

<211> 336

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 230

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser
 1 5 10 15
 Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu
 20 25 30
 Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn
 35 40 45
 Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
 50 55 60
 Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65 70 75 80
 Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
 85 90 95
 Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
 100 105 110
 Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
 115 120 125
 Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
 130 135 140
 Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
 145 150 155 160
 Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
 165 170 175
 Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
 180 185 190
 Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
 195 200 205
 Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
 210 215 220
 Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
 225 230 235 240
 Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
 245 250 255
 Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
 260 265 270
 Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
 275 280 285

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val
 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala
 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
 325 330 335

<210> 231
 <211> 1599
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1576)
 <223> RXN00983

<400> 231
 gtgagaaaac agtggctcaa atatcgacat cttctactca cagttcaacc tgctgtggct 60

ggaggccggc tgcattgggtg tcgacgccga tgaaacgtcc gtg act gca ggt gaa 115
 Val Thr Ala Gly Glu
 1 5

acc acc act atg aat gtc acg ttg acc aat cct ttc gac aac gca att 163
 Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro Phe Asp Asn Ala Ile
 10 15 20

ttt gac cga gca gtc tcc ctt gaa cgt ccc gaa gga tgg caa gct gag 211
 Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu Gly Trp Gln Ala Glu
 25 30 35

gat gtt cgt gtg tgc atc cca tct gga gaa tct gtc aca atc cca gtc 259
 Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser Val Thr Ile Pro Val
 40 45 50

cag gtc aca gca ccg ctg gta gcc gac aac ggt gaa ctt cca gtg gag 307
 Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly Glu Leu Pro Val Glu
 55 60 65

gtg tcc att ctt gat gga gca gac cgc tac acg ggt cgt ctc aat ctc 355
 Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr Gly Arg Leu Asn Leu
 70 75 80 85

act gtt cag ggt ggg caa gaa cct gca cca act tca gtg aag gtg agc 403
 Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr Ser Val Lys Val Ser
 90 95 100

att cca aat ctc aag gac act tat gta gca ggg gag aag atc agc att 451
 Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly Glu Lys Ile Ser Ile
 105 110 115

aac ttt gcg gtc aac aac ccg ttt gac gtt acg gtt aat tcg gtg cca 499
 Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr Val Asn Ser Val Pro
 120 125 130

agc	ctg	ggg	gaa	ggc	gag	aac	tgg	atg	cct	gca	aac	cta	cgc	gga	ttt	547
Ser	Leu	Gly	Glu	Gly	Glu	Asn	Trp	Met	Pro	Ala	Asn	Leu	Arg	Gly	Phe	
	135					140					145					
gat	cca	gag	cag	ggt	act	ccc	aac	tgt	cgt	tac	aag	aat	tta	ggc	gcg	595
Asp	Pro	Glu	Gln	Gly	Thr	Pro	Asn	Cys	Arg	Tyr	Lys	Asn	Leu	Gly	Ala	
	150				155					160					165	
aat	aag	agc	tat	gac	tgc	acc	aca	act	acc	tat	gaa	gtc	agc	gat	ttg	643
Asn	Lys	Ser	Tyr	Asp	Cys	Thr	Thr	Thr	Thr	Tyr	Glu	Val	Ser	Asp	Leu	
				170					175						180	
gat	gta	gaa	cgc	gga	tac	gtg	gat	att	cca	acg	gta	tgg	acg	ttt	act	691
Asp	Val	Glu	Arg	Gly	Tyr	Val	Asp	Ile	Pro	Thr	Val	Trp	Thr	Phe	Thr	
			185					190					195			
aac	tcc	gca	ggc	gaa	acg	gta	tgg	tcc	aaa	aac	gtt	gat	gtg	cct	cga	739
Asn	Ser	Ala	Gly	Glu	Thr	Val	Trp	Ser	Lys	Asn	Val	Asp	Val	Pro	Arg	
		200					205					210				
gtt	gaa	ctc	aat	gga	aca	cag	gat	gct	gtc	act	gat	gca	atc	gta	acg	787
Val	Glu	Leu	Asn	Gly	Thr	Gln	Asp	Ala	Val	Thr	Asp	Ala	Ile	Val	Thr	
	215					220					225					
gtt	gat	ccc	atc	aac	cca	gtt	cat	tcc	aac	ggc	cag	agc	caa	act	gtt	835
Val	Asp	Pro	Ile	Asn	Pro	Val	His	Ser	Asn	Gly	Gln	Ser	Gln	Thr	Val	
	230				235					240					245	
gag	gtc	cag	gct	aat	gtc	acc	tca	gag	gga	gat	ctg	cca	gct	gga	tct	883
Glu	Val	Gln	Ala	Asn	Val	Thr	Ser	Glu	Gly	Asp	Leu	Pro	Ala	Gly	Ser	
				250					255					260		
aag	gtg	gcc	ttt	tat	cta	gat	tca	tcg	ccc	att	gat	acc	gca	gct	gtt	931
Lys	Val	Ala	Phe	Tyr	Leu	Asp	Ser	Ser	Pro	Ile	Asp	Thr	Ala	Ala	Val	
			265					270					275			
gat	gcg	gaa	ggg	cat	gcc	agc	atc	tcg	att	gat	gtg	gac	aac	atc	gca	979
Asp	Ala	Glu	Gly	His	Ala	Ser	Ile	Ser	Ile	Asp	Val	Asp	Asn	Ile	Ala	
		280					285					290				
agc	gag	cag	cct	gaa	cgc	aca	ttt	gag	gtt	cgc	gcc	cga	ctc	gtc	gtt	1027
Ser	Glu	Gln	Pro	Glu	Arg	Thr	Phe	Glu	Val	Arg	Ala	Arg	Leu	Val	Val	
	295					300					305					
cca	gaa	gat	gca	cca	cga	tca	atc	gcg	cgt	gat	gcc	ttg	gca	cgt	ttt	1075
Pro	Glu	Asp	Ala	Pro	Arg	Ser	Ile	Ala	Arg	Asp	Ala	Leu	Ala	Arg	Phe	
	310				315					320					325	
aca	gtc	ctg	tct	gaa	caa	gtg	cag	cag	aac	tcc	ttg	gtg	atc	atg	aat	1123
Thr	Val	Leu	Ser	Glu	Gln	Val	Gln	Gln	Asn	Ser	Leu	Val	Ile	Met	Asn	
				330					335					340		
cat	cca	gat	gtg	ttt	tct	gat	gga	caa	aca	aag	act	att	gtc	atc	gca	1171
His	Pro	Asp	Val	Phe	Ser	Asp	Gly	Gln	Thr	Lys	Thr	Ile	Val	Ile	Ala	
			345					350					355			
gcg	aag	gcg	aca	gca	cac	gat	gga	tcg	ccg	gtg	gct	atc	ggg	act	ctc	1219
Ala	Lys	Ala	Thr	Ala	His	Asp	Gly	Ser	Pro	Val	Ala	Ile	Gly	Thr	Leu	
		360					365					370				

att gca ttt cgc gtc aac ggt att gag cgg gac gtg gtt cca act aac 1267
 Ile Ala Phe Arg Val Asn Gly Ile Glu Arg Asp Val Val Pro Thr Asn
 375 380 385

 gcg caa gga aca gca aag ctt cag cta gac ctc aag cca gta aat act 1315
 Ala Gln Gly Thr Ala Lys Leu Gln Leu Asp Leu Lys Pro Val Asn Thr
 390 395 400 405

 gaa gac gag gaa tat gaa gta aca gtt gaa gcc gag ctg gat gaa ttg 1363
 Glu Asp Glu Glu Tyr Glu Val Thr Val Glu Ala Glu Leu Asp Glu Leu
 410 415 420

 act gct cag acc acg ttc aaa gta ctt gct ggt gag gaa gag gaa ccc 1411
 Thr Ala Gln Thr Thr Phe Lys Val Leu Ala Gly Glu Glu Glu Glu Pro
 425 430 435

 acc agc acc gaa gaa caa ccg tca gaa act gag cag cct tct gaa cct 1459
 Thr Ser Thr Glu Glu Gln Pro Ser Glu Thr Glu Gln Pro Ser Glu Pro
 440 445 450

 gaa gag gaa tcg act ggt gtt gct gga agc tct aac ggt ggc agt ttt 1507
 Glu Glu Glu Ser Thr Gly Val Ala Gly Ser Ser Asn Gly Gly Ser Phe
 455 460 465

 gtc gcg ctt tta gcg ctg ctg gca gcg ctt ggt ggc atc gtc ggt gca 1555
 Val Ala Leu Leu Ala Leu Leu Ala Ala Leu Gly Gly Ile Val Gly Ala
 470 475 480 485

 gtc ctc gga ttg ctt aag ttg taggtggctg ggggcgtcga aaa 1599
 Val Leu Gly Leu Leu Lys Leu
 490

<210> 232

<211> 492

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Val Thr Ala Gly Glu Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro
 1 5 10 15

 Phe Asp Asn Ala Ile Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu
 20 25 30

 Gly Trp Gln Ala Glu Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser
 35 40 45

 Val Thr Ile Pro Val Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly
 50 55 60

 Glu Leu Pro Val Glu Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr
 65 70 75 80

 Gly Arg Leu Asn Leu Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr
 85 90 95

 Ser Val Lys Val Ser Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly
 100 105 110

 Glu Lys Ile Ser Ile Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr

115					120					125					
Val	Asn	Ser	Val	Pro	Ser	Leu	Gly	Glu	Gly	Glu	Asn	Trp	Met	Pro	Ala
130						135					140				
Asn	Leu	Arg	Gly	Phe	Asp	Pro	Glu	Gln	Gly	Thr	Pro	Asn	Cys	Arg	Tyr
145					150					155					160
Lys	Asn	Leu	Gly	Ala	Asn	Lys	Ser	Tyr	Asp	Cys	Thr	Thr	Thr	Thr	Tyr
				165					170						175
Glu	Val	Ser	Asp	Leu	Asp	Val	Glu	Arg	Gly	Tyr	Val	Asp	Ile	Pro	Thr
			180					185					190		
Val	Trp	Thr	Phe	Thr	Asn	Ser	Ala	Gly	Glu	Thr	Val	Trp	Ser	Lys	Asn
			195				200					205			
Val	Asp	Val	Pro	Arg	Val	Glu	Leu	Asn	Gly	Thr	Gln	Asp	Ala	Val	Thr
	210					215					220				
Asp	Ala	Ile	Val	Thr	Val	Asp	Pro	Ile	Asn	Pro	Val	His	Ser	Asn	Gly
225						230					235				240
Gln	Ser	Gln	Thr	Val	Glu	Val	Gln	Ala	Asn	Val	Thr	Ser	Glu	Gly	Asp
				245					250					255	
Leu	Pro	Ala	Gly	Ser	Lys	Val	Ala	Phe	Tyr	Leu	Asp	Ser	Ser	Pro	Ile
			260					265					270		
Asp	Thr	Ala	Ala	Val	Asp	Ala	Glu	Gly	His	Ala	Ser	Ile	Ser	Ile	Asp
			275				280					285			
Val	Asp	Asn	Ile	Ala	Ser	Glu	Gln	Pro	Glu	Arg	Thr	Phe	Glu	Val	Arg
	290					295					300				
Ala	Arg	Leu	Val	Val	Pro	Glu	Asp	Ala	Pro	Arg	Ser	Ile	Ala	Arg	Asp
305						310					315				320
Ala	Leu	Ala	Arg	Phe	Thr	Val	Leu	Ser	Glu	Gln	Val	Gln	Gln	Asn	Ser
				325					330					335	
Leu	Val	Ile	Met	Asn	His	Pro	Asp	Val	Phe	Ser	Asp	Gly	Gln	Thr	Lys
			340					345					350		
Thr	Ile	Val	Ile	Ala	Ala	Lys	Ala	Thr	Ala	His	Asp	Gly	Ser	Pro	Val
			355				360					365			
Ala	Ile	Gly	Thr	Leu	Ile	Ala	Phe	Arg	Val	Asn	Gly	Ile	Glu	Arg	Asp
	370					375					380				
Val	Val	Pro	Thr	Asn	Ala	Gln	Gly	Thr	Ala	Lys	Leu	Gln	Leu	Asp	Leu
385						390					395				400
Lys	Pro	Val	Asn	Thr	Glu	Asp	Glu	Glu	Tyr	Glu	Val	Thr	Val	Glu	Ala
				405					410					415	
Glu	Leu	Asp	Glu	Leu	Thr	Ala	Gln	Thr	Thr	Phe	Lys	Val	Leu	Ala	Gly
			420					425					430		
Glu	Glu	Glu	Glu	Pro	Thr	Ser	Thr	Glu	Glu	Gln	Pro	Ser	Glu	Thr	Glu
			435				440					445			

Gln Pro Ser Glu Pro Glu Glu Glu Ser Thr Gly Val Ala Gly Ser Ser
450 455 460

Asn Gly Gly Ser Phe Val Ala Leu Leu Ala Leu Leu Ala Ala Leu Gly
465 470 475 480

Gly Ile Val Gly Ala Val Leu Gly Leu Leu Lys Leu
485 490

<210> 233

<211> 1297

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1297)

<223> FRXA00983

<400> 233

gtgagaaaac agtgggtcaa atatcgacat cttctactca cagttcaacc tgtcgtggct 60

ggaggccggc tgcattggtg tcgacgccga tgaaacgtcc gtg act gca ggt gaa 115
Val Thr Ala Gly Glu
1 5

acc acc act atg aat gtc acg ttg acc aat cct ttc gac aac gca att 163
Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro Phe Asp Asn Ala Ile
10 15 20

ttt gac cga gca gtc tcc ctt gaa cgt ccc gaa gga tgg caa gct gag 211
Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu Gly Trp Gln Ala Glu
25 30 35

gat gtt cgt gtg tcg atc cca tct gga gaa tct gtc aca atc cca gtc 259
Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser Val Thr Ile Pro Val
40 45 50

cag gtc aca gca ccg ctg gta gcc gac aac ggt gaa ctt cca gtg gag 307
Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly Glu Leu Pro Val Glu
55 60 65

gtg tcc att ctt gat gga gca gac cgc tac acg ggt cgt ctc aat ctc 355
Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr Gly Arg Leu Asn Leu
70 75 80 85

act gtt cag ggt ggg caa gaa cct gca cca act tca gtg aag gtg agc 403
Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr Ser Val Lys Val Ser
90 95 100

att cca aat ctc aag gac act tat gta gca ggg gag aag atc agc att 451
Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly Glu Lys Ile Ser Ile
105 110 115

aac ttt gcg gtc aac aac ccg ttt gac gtt acg gtt aat tcg gtg cca 499
Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr Val Asn Ser Val Pro
120 125 130

agc ctg ggg gaa ggc gag aac tgg atg cct gca aac cta cgc gga ttt 547

Ser	Leu	Gly	Glu	Gly	Glu	Asn	Trp	Met	Pro	Ala	Asn	Leu	Arg	Gly	Phe	
135						140					145					
gat	cca	gag	cag	ggt	act	ccc	aac	tgt	cgt	tac	aag	aat	tta	ggc	gcg	595
Asp	Pro	Glu	Gln	Gly	Thr	Pro	Asn	Cys	Arg	Tyr	Lys	Asn	Leu	Gly	Ala	
150					155					160					165	
aat	aag	agc	tat	gac	tgc	acc	aca	act	acc	tat	gaa	gtc	agc	gat	ttg	643
Asn	Lys	Ser	Tyr	Asp	Cys	Thr	Thr	Thr	Thr	Tyr	Glu	Val	Ser	Asp	Leu	
				170					175					180		
gat	gta	gaa	cgc	gga	tac	gtg	gat	att	cca	acg	gta	tgg	acg	ttt	act	691
Asp	Val	Glu	Arg	Gly	Tyr	Val	Asp	Ile	Pro	Thr	Val	Trp	Thr	Phe	Thr	
			185					190					195			
aac	tcc	gca	ggc	gaa	acg	gta	tgg	tcc	aaa	aac	gtt	gat	gtg	cct	cga	739
Asn	Ser	Ala	Gly	Glu	Thr	Val	Trp	Ser	Lys	Asn	Val	Asp	Val	Pro	Arg	
		200					205				210					
gtt	gaa	ctc	aat	gga	aca	cag	gat	gct	gtc	act	gat	gca	atc	gta	acg	787
Val	Glu	Leu	Asn	Gly	Thr	Gln	Asp	Ala	Val	Thr	Asp	Ala	Ile	Val	Thr	
	215					220					225					
gtt	gat	ccc	atc	aac	cca	gtt	cat	tcc	aac	ggc	cag	agc	caa	act	gtt	835
Val	Asp	Pro	Ile	Asn	Pro	Val	His	Ser	Asn	Gly	Gln	Ser	Gln	Thr	Val	
230					235					240					245	
gag	gtc	cag	gct	aat	gtc	acc	tca	gag	gga	gat	ctg	cca	gct	gga	tct	883
Glu	Val	Gln	Ala	Asn	Val	Thr	Ser	Glu	Gly	Asp	Leu	Pro	Ala	Gly	Ser	
				250					255					260		
aag	gtg	gcc	ttt	tat	cta	gat	tca	tcg	ccc	att	gat	acc	gca	gct	gtt	931
Lys	Val	Ala	Phe	Tyr	Leu	Asp	Ser	Ser	Pro	Ile	Asp	Thr	Ala	Ala	Val	
			265					270					275			
gat	gcg	gaa	ggg	cat	gcc	agc	atc	tcg	att	gat	gtg	gac	aac	atc	gca	979
Asp	Ala	Glu	Gly	His	Ala	Ser	Ile	Ser	Ile	Asp	Val	Asp	Asn	Ile	Ala	
		280					285					290				
agc	gag	cag	cct	gaa	cgc	aca	ttt	gag	gtt	cgc	gcc	cga	ctc	gtc	gtt	1027
Ser	Glu	Gln	Pro	Glu	Arg	Thr	Phe	Glu	Val	Arg	Ala	Arg	Leu	Val	Val	
	295					300					305					
cca	gaa	gat	gca	cca	cga	tca	atc	gcg	cgt	gat	gcc	ttg	gca	cgt	ttt	1075
Pro	Glu	Asp	Ala	Pro	Arg	Ser	Ile	Ala	Arg	Asp	Ala	Leu	Ala	Arg	Phe	
310					315					320					325	
aca	gtc	ctg	tct	gaa	caa	gtg	cag	cag	aac	tcc	ttg	gtg	atc	atg	aat	1123
Thr	Val	Leu	Ser	Glu	Gln	Val	Gln	Gln	Asn	Ser	Leu	Val	Ile	Met	Asn	
				330					335					340		
cat	cca	gat	gtg	ttt	tct	gat	gga	caa	aca	aag	act	att	gtc	atc	gca	1171
His	Pro	Asp	Val	Phe	Ser	Asp	Gly	Gln	Thr	Lys	Thr	Ile	Val	Ile	Ala	
			345					350					355			
gcg	aag	gcg	aca	gca	cac	gat	gga	tcg	ccg	gcg	gct	atc	ggg	act	ctc	1219
Ala	Lys	Ala	Thr	Ala	His	Asp	Gly	Ser	Pro	Ala	Ala	Ile	Gly	Thr	Leu	
		360					365					370				
att	gca	ttt	cgc	gtc	aac	ggg	att	gag	cgg	gac	gtg	gtt	cca	act	aac	1267
Ile	Ala	Phe	Arg	Val	Asn	Gly	Ile	Glu	Arg	Asp	Val	Val	Pro	Thr	Asn	

375

380

385

gcg caa gga aca gca aag ctt cag cta gac
 Ala Gln Gly Thr Ala Lys Leu Gln Leu Asp
 390 395

1297

<210> 234

<211> 399

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

Val Thr Ala Gly Glu Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro
 1 5 10 15
 Phe Asp Asn Ala Ile Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu
 20 25 30
 Gly Trp Gln Ala Glu Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser
 35 40 45
 Val Thr Ile Pro Val Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly
 50 55 60
 Glu Leu Pro Val Glu Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr
 65 70 75 80
 Gly Arg Leu Asn Leu Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr
 85 90 95
 Ser Val Lys Val Ser Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly
 100 105 110
 Glu Lys Ile Ser Ile Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr
 115 120 125
 Val Asn Ser Val Pro Ser Leu Gly Glu Gly Glu Asn Trp Met Pro Ala
 130 135 140
 Asn Leu Arg Gly Phe Asp Pro Glu Gln Gly Thr Pro Asn Cys Arg Tyr
 145 150 155 160
 Lys Asn Leu Gly Ala Asn Lys Ser Tyr Asp Cys Thr Thr Thr Thr Tyr
 165 170 175
 Glu Val Ser Asp Leu Asp Val Glu Arg Gly Tyr Val Asp Ile Pro Thr
 180 185 190
 Val Trp Thr Phe Thr Asn Ser Ala Gly Glu Thr Val Trp Ser Lys Asn
 195 200 205
 Val Asp Val Pro Arg Val Glu Leu Asn Gly Thr Gln Asp Ala Val Thr
 210 215 220
 Asp Ala Ile Val Thr Val Asp Pro Ile Asn Pro Val His Ser Asn Gly
 225 230 235 240
 Gln Ser Gln Thr Val Glu Val Gln Ala Asn Val Thr Ser Glu Gly Asp
 245 250 255

Leu Pro Ala Gly Ser Lys Val Ala Phe Tyr Leu Asp Ser Ser Pro Ile
 260 265 270
 Asp Thr Ala Ala Val Asp Ala Glu Gly His Ala Ser Ile Ser Ile Asp
 275 280 285
 Val Asp Asn Ile Ala Ser Glu Gln Pro Glu Arg Thr Phe Glu Val Arg
 290 295 300
 Ala Arg Leu Val Val Pro Glu Asp Ala Pro Arg Ser Ile Ala Arg Asp
 305 310 315 320
 Ala Leu Ala Arg Phe Thr Val Leu Ser Glu Gln Val Gln Gln Asn Ser
 325 330 335
 Leu Val Ile Met Asn His Pro Asp Val Phe Ser Asp Gly Gln Thr Lys
 340 345 350
 Thr Ile Val Ile Ala Ala Lys Ala Thr Ala His Asp Gly Ser Pro Ala
 355 360 365
 Ala Ile Gly Thr Leu Ile Ala Phe Arg Val Asn Gly Ile Glu Arg Asp
 370 375 380
 Val Val Pro Thr Asn Ala Gln Gly Thr Ala Lys Leu Gln Leu Asp
 385 390 395

<210> 235
 <211> 440
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (1)..(417)
 <223> RXA00984

<400> 235
 caa cgt ggt acc cca gtg ctc ctt ggg gaa act cca tgg atg aaa aca 48
 Gln Arg Gly Thr Pro Val Leu Leu Gly Glu Thr Pro Trp Met Lys Thr
 1 5 10 15
 aaa atc gtg gaa ctc agc gat gga acc ctg atg aac aac agt cgt tca 96
 Lys Ile Val Glu Leu Ser Asp Gly Thr Leu Met Asn Asn Ser Arg Ser
 20 25 30
 tca gga gcc gat act tac cgc aag gtg tct tat tcc acc gac ggc ggc 144
 Ser Gly Ala Asp Thr Tyr Arg Lys Val Ser Tyr Ser Thr Asp Gly Gly
 35 40 45
 gtc act tgg acc gag cca act ctt gat acc cag ctg ccg gat cct cgc 192
 Val Thr Trp Thr Glu Pro Thr Leu Asp Thr Gln Leu Pro Asp Pro Arg
 50 55 60
 aac aat gct tcc ctg att cga gta ttc ccg aca gca cct gag gga agt 240
 Asn Asn Ala Ser Leu Ile Arg Val Phe Pro Thr Ala Pro Glu Gly Ser
 65 70 75 80
 gcg cag gca aag gtt ctg ctg ttc tcc aac act gcc acc acg agt ggc 288
 Ala Gln Ala Lys Val Leu Leu Phe Ser Asn Thr Ala Thr Thr Ser Gly

85										90					95					
cgc	acc	aat	ggc	acc	gtc	cgc	atg	tcg	tgt	gat	gat	ggt	cag	acc	tgg	336				
Arg	Thr	Asn	Gly	Thr	Val	Arg	Met	Ser	Cys	Asp	Asp	Gly	Gln	Thr	Trp					
			100					105					110							
ccg	gtg	tct	aag	gtg	ttt	gaa	cca	gga	gca	atc	caa	tat	acc	tcg	atg	384				
Pro	Val	Ser	Lys	Val	Phe	Glu	Pro	Gly	Ala	Ile	Gln	Tyr	Thr	Ser	Met					
			115					120					125							
gca	acg	ctt	ccc	aac	ggt	gac	atc	ggc	atg	ctg	tgagaaaaca	gtggctcaaa	437							
Ala	Thr	Leu	Pro	Asn	Gly	Asp	Ile	Gly	Met	Leu										
			130					135												
tat																440				

<210> 236
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 236
 Gln Arg Gly Thr Pro Val Leu Leu Gly Glu Thr Pro Trp Met Lys Thr
 1 5 10 15
 Lys Ile Val Glu Leu Ser Asp Gly Thr Leu Met Asn Asn Ser Arg Ser
 20 25 30
 Ser Gly Ala Asp Thr Tyr Arg Lys Val Ser Tyr Ser Thr Asp Gly Gly
 35 40 45
 Val Thr Trp Thr Glu Pro Thr Leu Asp Thr Gln Leu Pro Asp Pro Arg
 50 55 60
 Asn Asn Ala Ser Leu Ile Arg Val Phe Pro Thr Ala Pro Glu Gly Ser
 65 70 75 80
 Ala Gln Ala Lys Val Leu Leu Phe Ser Asn Thr Ala Thr Thr Ser Gly
 85 90 95
 Arg Thr Asn Gly Thr Val Arg Met Ser Cys Asp Asp Gly Gln Thr Trp
 100 105 110
 Pro Val Ser Lys Val Phe Glu Pro Gly Ala Ile Gln Tyr Thr Ser Met
 115 120 125
 Ala Thr Leu Pro Asn Gly Asp Ile Gly Met Leu
 130 135

<210> 237
 <211> 832
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(832)
 <223> RXN02513

<400> 237

acagcaccgt tttgtaggat aagaaaatcc cgcacacaac ccgtcctggt ggggtgaagtg 60

ggggaggcat gtctatgccc ccaattagac atctgacatc atg ctt cca atc tgg 115
Met Leu Pro Ile Trp
1 5

atg ggt ctt cca ttc aag aaa gca ggt gct ttg tct cgg cgt aaa gca 163
Met Gly Leu Pro Phe Lys Lys Ala Gly Ala Leu Ser Arg Arg Lys Ala
10 15 20

gta ttc tca gcg ctt ggt gca gcc gca ctc atg ggc gca gca cta ccc 211
Val Phe Ser Ala Leu Gly Ala Ala Ala Leu Met Gly Ala Ala Leu Pro
25 30 35

acc atc cca acg gcc caa gct caa aca ccc acg ggc tac gga ttc gat 259
Thr Ile Pro Thr Ala Gln Ala Gln Thr Pro Thr Gly Tyr Gly Phe Asp
40 45 50

gca aca gca agc atc agc gaa gaa cca gag ttt tca aca caa caa ctc 307
Ala Thr Ala Ser Ile Ser Glu Glu Pro Glu Phe Ser Thr Gln Gln Leu
55 60 65

gct gac ggc gga act ctc gga ttt gat tgc tac cgc atc cca tcg ctt 355
Ala Asp Gly Gly Thr Leu Gly Phe Asp Cys Tyr Arg Ile Pro Ser Leu
70 75 80 85

ggc gtc gca ccc aac ggc aac gtc ctc gca tcg tgg gat ggt cgc cca 403
Gly Val Ala Pro Asn Gly Asn Val Leu Ala Ser Trp Asp Gly Arg Pro
90 95 100

aac aac tgt tca gat gct cca caa ccc aac tcc atc gtg ggc aag gta 451
Asn Asn Cys Ser Asp Ala Pro Gln Pro Asn Ser Ile Val Gly Lys Val
105 110 115

tcg acc gac aac gga gca acc tgg ggc gaa cag cac gac att tcc gca 499
Ser Thr Asp Asn Gly Ala Thr Trp Gly Glu Gln His Asp Ile Ser Ala
120 125 130

ggt atc acc gcc gaa ccc aaa act ggc tat tcc gat ccc agc atc gtt 547
Gly Ile Thr Ala Glu Pro Lys Thr Gly Tyr Ser Asp Pro Ser Ile Val
135 140 145

gtg gac tgg gag agg ggc gat gtc ttt aac ttc cac gtg aag tca ttc 595
Val Asp Trp Glu Arg Gly Asp Val Phe Asn Phe His Val Lys Ser Phe
150 155 160 165

gat gca gga tac ttc acc tcc caa cca ggc acg gac ccg gat gat cgc 643
Asp Ala Gly Tyr Phe Thr Ser Gln Pro Gly Thr Asp Pro Asp Asp Arg
170 175 180

aac gtt gcc cat gtt gcc tac gcc aaa tca tca gat aac ggc tca acc 691
Asn Val Ala His Val Ala Tyr Ala Lys Ser Ser Asp Asn Gly Ser Thr
185 190 195

tgg gtt gca gac acc gtc att act gat caa gtg gtt gct cat gac acc 739
Trp Val Ala Asp Thr Val Ile Thr Asp Gln Val Val Ala His Asp Thr
200 205 210

tgg gac agc cga ttt gcc aca tcc gga aac ggc atc caa ctg caa tac 787
Trp Asp Ser Arg Phe Ala Thr Ser Gly Asn Gly Ile Gln Leu Gln Tyr

215

220

225

ggc gcg tac aag gga cga ttg gtc cag cca tcg gta act cgc atg 832
 Gly Ala Tyr Lys Gly Arg Leu Val Gln Pro Ser Val Thr Arg Met
 230 235 240

<210> 238

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Met Leu Pro Ile Trp Met Gly Leu Pro Phe Lys Lys Ala Gly Ala Leu
 1 5 10 15
 Ser Arg Arg Lys Ala Val Phe Ser Ala Leu Gly Ala Ala Ala Leu Met
 20 25 30
 Gly Ala Ala Leu Pro Thr Ile Pro Thr Ala Gln Ala Gln Thr Pro Thr
 35 40 45
 Gly Tyr Gly Phe Asp Ala Thr Ala Ser Ile Ser Glu Glu Pro Glu Phe
 50 55 60
 Ser Thr Gln Gln Leu Ala Asp Gly Gly Thr Leu Gly Phe Asp Cys Tyr
 65 70 75 80
 Arg Ile Pro Ser Leu Gly Val Ala Pro Asn Gly Asn Val Leu Ala Ser
 85 90 95
 Trp Asp Gly Arg Pro Asn Asn Cys Ser Asp Ala Pro Gln Pro Asn Ser
 100 105 110
 Ile Val Gly Lys Val Ser Thr Asp Asn Gly Ala Thr Trp Gly Glu Gln
 115 120 125
 His Asp Ile Ser Ala Gly Ile Thr Ala Glu Pro Lys Thr Gly Tyr Ser
 130 135 140
 Asp Pro Ser Ile Val Val Asp Trp Glu Arg Gly Asp Val Phe Asn Phe
 145 150 155 160
 His Val Lys Ser Phe Asp Ala Gly Tyr Phe Thr Ser Gln Pro Gly Thr
 165 170 175
 Asp Pro Asp Asp Arg Asn Val Ala His Val Ala Tyr Ala Lys Ser Ser
 180 185 190
 Asp Asn Gly Ser Thr Trp Val Ala Asp Thr Val Ile Thr Asp Gln Val
 195 200 205
 Val Ala His Asp Thr Trp Asp Ser Arg Phe Ala Thr Ser Gly Asn Gly
 210 215 220
 Ile Gln Leu Gln Tyr Gly Ala Tyr Lys Gly Arg Leu Val Gln Pro Ser
 225 230 235 240
 Val Thr Arg Met

```
<210> 239
<211> 824
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (93) .. (824)
<223> FRXA02513
```

<400> 239

gtcatgtagg ataagaaaat cccgcacaca acccgtcctg gtggggtaag tgagggagqc 60

atgtctatgc ccccaattag acatctgaca tcatg ctt cca atc tgg atg ggt 113
Met Leu Pro Ile Trp Met Gly
1 5

ctt cca ttc aag aaa gca ggg gct ttg tct cgg cgt aaa gca gta ttc 161
 Leu Pro Phe Lys Lys Ala Gly Ala Leu Ser Arg Arg Lys Ala Val Phe
 10 15 20

tca gcg ctt ggt gca gac gca ctc atg ggc gca gca cta ccc acc atc 209
Ser Ala Leu Gly Ala Asp Ala Leu Met Gly Ala Ala Leu Pro Thr Ile
25 30 35

cca acg gcc caa gct caa aca ccc acg ggc tac gga ttc gat gca aca 257
Pro Thr Ala Gln Ala Gln Thr Pro Thr Gly Tyr Gly Phe Asp Ala Thr
40 45 50 55

gca agc atc agc gaa gaa cca gag ttt tca aca caa caa ctc gct gac 305
Ala Ser Ile Ser Glu Glu Pro Glu Phe Ser Thr Gln Gln Leu Ala Asp
60 65 70

ggc gga act ctc gga ttt gat tgc tac cgc atc cca tcg ctt ggc gtc 353
Gly Gly Thr Leu Gly Phe Asp Cys Tyr Arg Ile Pro Ser Leu Gly Val
75 80 85

gca ccc aac ggc aac gtc ctc gca tcg tgg gat ggt cgc cca aac aac 401
Ala Pro Asn Gly Asn Val Leu Ala Ser Trp Asp Gly Arg Pro Asn Asn
90 95 100

tgt tca gat gct cca caa ccc aac tcc atc gtg ggc aag gta tcg acc 449
Cys Ser Asp Ala Pro Gln Pro Asn Ser Ile Val Gly Lys Val Ser Thr
105 110 115

gac aac gga gca acc tgg ggc gaa cag cac gac att tcc gca ggt atc 497
Asp Asn Gly Ala Thr Trp Gly Glu Gln His Asp Ile Ser Ala Gly Ile
120 125 130 135

acc gcc gaa ccc aaa act ggc tat tcc gat ccc agc atc gtt gtg gac 545
Thr Ala Glu Pro Lys Thr Gly Tyr Ser Asp Pro Ser Ile Val Val Asp
140 145 150

tgg	gag	agg	ggc	gat	gtc	ttt	aac	ttc	cac	gtg	aag	tca	ttc	gat	gca	593
Trp	Glu	Arg	Gly	Asp	Val	Phe	Asn	Phe	His	Val	Lys	Ser	Phe	Asp	Ala	
			155					160					165			

gga tac ttc acc tcc caa cca ggc acg gac ccg gat gat cgc aac gtt 641
Gly Tyr Phe Thr Ser Gln Pro Gly Thr Asp Pro Asp Asp Arg Asn Val
170 175 180

gcc cat gtt gcc tac gcc aaa tca tca gat aac ggc tca acc tgg gtt 689
 Ala His Val Ala Tyr Ala Lys Ser Ser Asp Asn Gly Ser Thr Trp Val
 185 190 195

gca gac acc gtc att act gat caa gtg gtt gct cat gac acc tgg gac 737
 Ala Asp Thr Val Ile Thr Asp Gln Val Val Ala His Asp Thr Trp Asp
 200 205 210 215

agc cga ttt gcc aca tcc gga aac ggc atc caa ctg caa tac ggc gcg 785
 Ser Arg Phe Ala Thr Ser Gly Asn Gly Ile Gln Leu Gln Tyr Gly Ala
 220 225 230

tac aag gga cga ttg gtc cag cca tcg gta act cgc atg 824
 Tyr Lys Gly Arg Leu Val Gln Pro Ser Val Thr Arg Met
 235 240

<210> 240

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Leu Pro Ile Trp Met Gly Leu Pro Phe Lys Lys Ala Gly Ala Leu
 1 5 10 15

Ser Arg Arg Lys Ala Val Phe Ser Ala Leu Gly Ala Asp Ala Leu Met
 20 25 30

Gly Ala Ala Leu Pro Thr Ile Pro Thr Ala Gln Ala Gln Thr Pro Thr
 35 40 45

Gly Tyr Gly Phe Asp Ala Thr Ala Ser Ile Ser Glu Glu Pro Glu Phe
 50 55 60

Ser Thr Gln Gln Leu Ala Asp Gly Gly Thr Leu Gly Phe Asp Cys Tyr
 65 70 75 80

Arg Ile Pro Ser Leu Gly Val Ala Pro Asn Gly Asn Val Leu Ala Ser
 85 90 95

Trp Asp Gly Arg Pro Asn Asn Cys Ser Asp Ala Pro Gln Pro Asn Ser
 100 105 110

Ile Val Gly Lys Val Ser Thr Asp Asn Gly Ala Thr Trp Gly Glu Gln
 115 120 125

His Asp Ile Ser Ala Gly Ile Thr Ala Glu Pro Lys Thr Gly Tyr Ser
 130 135 140

Asp Pro Ser Ile Val Val Asp Trp Glu Arg Gly Asp Val Phe Asn Phe
 145 150 155 160

His Val Lys Ser Phe Asp Ala Gly Tyr Phe Thr Ser Gln Pro Gly Thr
 165 170 175

Asp Pro Asp Asp Arg Asn Val Ala His Val Ala Tyr Ala Lys Ser Ser
 180 185 190

Asp Asn Gly Ser Thr Trp Val Ala Asp Thr Val Ile Thr Asp Gln Val

195 200 205

Val Ala His Asp Thr Trp Asp Ser Arg Phe Ala Thr Ser Gly Asn Gly
210 215 220

Ile Gln Leu Gln Tyr Gly Ala Tyr Lys Gly Arg Leu Val Gln Pro Ser
225 230 235 240

Val Thr Arg Met

<210> 241
<211> 733
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA00903

<400> 241
gcactcgga tgcgtcgtcct agaaaagaaa gacgcctaaa atgccctcta aaatatcgcg 60
gccctattac caagtagatg tattcagctc cgagccgttc atg gga aac ccg ctt 115
Met Gly Asn Pro Leu
1 5
gct gtc atc gcc gat gct gat gac tta agt gcc gaa caa atg gcc cga 163
Ala Val Ile Ala Asp Ala Asp Asp Leu Ser Ala Glu Gln Met Ala Arg
10 15 20
atc gct agg tgg aca aac ctc tca gaa acc aca ttt ctt tta aag cca 211
Ile Ala Arg Trp Thr Asn Leu Ser Glu Thr Thr Phe Leu Leu Lys Pro
25 30 35
acc caa gaa ggt gct gac tac cgg gta cgc att ttc acc cca acc ggt 259
Thr Gln Glu Gly Ala Asp Tyr Arg Val Arg Ile Phe Thr Pro Thr Gly
40 45 50
gag ctc ccc ttc gct gga cac cca aca ctc gga acc gcc cac gtg ttt 307
Glu Leu Pro Phe Ala Gly His Pro Thr Leu Gly Thr Ala His Val Phe
55 60 65
agg gaa ctg cac ggt gaa cag gga acc cag ttg gtt cag gaa tgt gtc 355
Arg Glu Leu His Gly Glu Gln Gly Thr Gln Leu Val Gln Glu Cys Val
70 75 80 85
gcc ggt tta gtt gct gtg cgc gct att gac ggg cca gca agt gga ttg 403
Ala Gly Leu Val Ala Val Arg Ala Ile Asp Gly Pro Ala Ser Gly Leu
90 95 100
gct ttt cag gct cca ccc aca ctc aaa gac ggg cca ttg gat gct tcc 451
Ala Phe Gln Ala Pro Pro Thr Leu Lys Asp Gly Pro Leu Asp Ala Ser
105 110 115
gac cta gac gca gct tgt gag gct tta gga atc agc ccc gac ttc att 499
Asp Leu Asp Ala Ala Cys Glu Ala Leu Gly Ile Ser Pro Asp Phe Ile
120 125 130

cga gcc cac caa tgg gta gac aac ggc ccc ggc tgg gca gta gtg gag 547
 Arg Ala His Gln Trp Val Asp Asn Gly Pro Gly Trp Ala Val Val Glu
 135 140 145
 cta ccg agc gcc caa cac gta ttg gat ctg gaa ccc gat ttc agt gca 595
 Leu Pro Ser Ala Gln His Val Leu Asp Leu Glu Pro Asp Phe Ser Ala
 150 155 160 165
 cat cca aca ttg aaa ctc gga gtg att ggg gcc tat ccc gaa ggg gct 643
 His Pro Thr Leu Lys Leu Gly Val Ile Gly Ala Tyr Pro Glu Gly Ala
 170 175 180
 ccc cac gcc ttt gaa gta cgg gca ttc gct caa gga atc ggt gaa gac 691
 Pro His Ala Phe Glu Val Arg Ala Phe Ala Gln Gly Ile Gly Glu Asp
 185 190 195
 cca gtt aca gga agc ctc aat gca ttc att gcg cag tgg cta 733
 Pro Val Thr Gly Ser Leu Asn Ala Phe Ile Ala Gln Trp Leu
 200 205 210

<210> 242

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Gly Asn Pro Leu Ala Val Ile Ala Asp Ala Asp Asp Leu Ser Ala
 1 5 10 15
 Glu Gln Met Ala Arg Ile Ala Arg Trp Thr Asn Leu Ser Glu Thr Thr
 20 25 30
 Phe Leu Leu Lys Pro Thr Gln Glu Gly Ala Asp Tyr Arg Val Arg Ile
 35 40 45
 Phe Thr Pro Thr Gly Glu Leu Pro Phe Ala Gly His Pro Thr Leu Gly
 50 55 60
 Thr Ala His Val Phe Arg Glu Leu His Gly Glu Gln Gly Thr Gln Leu
 65 70 75 80
 Val Gln Glu Cys Val Ala Gly Leu Val Ala Val Arg Ala Ile Asp Gly
 85 90 95
 Pro Ala Ser Gly Leu Ala Phe Gln Ala Pro Pro Thr Leu Lys Asp Gly
 100 105 110
 Pro Leu Asp Ala Ser Asp Leu Asp Ala Ala Cys Glu Ala Leu Gly Ile
 115 120 125
 Ser Pro Asp Phe Ile Arg Ala His Gln Trp Val Asp Asn Gly Pro Gly
 130 135 140
 Trp Ala Val Val Glu Leu Pro Ser Ala Gln His Val Leu Asp Leu Glu
 145 150 155 160
 Pro Asp Phe Ser Ala His Pro Thr Leu Lys Leu Gly Val Ile Gly Ala
 165 170 175
 Tyr Pro Glu Gly Ala Pro His Ala Phe Glu Val Arg Ala Phe Ala Gln

180 185 190

Gly Ile Gly Glu Asp Pro Val Thr Gly Ser Leu Asn Ala Phe Ile Ala
195 200 205

Gln Trp Leu
210

<210> 243
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXA01224

<400> 243
ttggcggcgg gaagttcagg cttgggggca aacagtgcctt ggatttttaga caaaaaactc 60

acggaagtca tcctatggca ggcgcgccta ggatggtgcc atg agc atc ctt gac 115
Met Ser Ile Leu Asp
1 5

acg ttg aaa act ccc gtg att gtc gcc ccg atg gct ggc ggc ccg tcc 163
Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met Ala Gly Gly Pro Ser
10 15 20

act ccc gcg ttg gtc aat gca gca gca gag gca ggt tcc ctc ggg ttc 211
Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala Gly Ser Leu Gly Phe
25 30 35

ttg gct ggt ggc gtc atg cct ctt gag cag ctg aaa cag gaa ttg tca 259
Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu Lys Gln Glu Leu Ser
40 45 50

gag gta aaa ggc gtc ttt ggc gtc aac ctg ttt cgc ccg cag acg gat 307
Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe Arg Pro Gln Thr Asp
55 60 65

gcg cct aag cct tca gac att gat gag ctg gcg gga ttg ttg tcc tcg 355
Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala Gly Leu Leu Ser Ser
70 75 80 85

gcg ttt cgg caa ttt ggc ctc gat gag ccg acg gtg cct acg ccg gat 403
Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr Val Pro Thr Pro Asp
90 95 100

ttg agc aat ggg tgg gag gct aaa ttt gag gcc gtt ctt gcc gct aag 451
Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala Val Leu Ala Ala Lys
105 110 115

ccc gcc gtt ttt tcc tgc acc ttt ggt att ttt agc gct gaa gaa ttc 499
Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe Ser Ala Glu Glu Phe
120 125 130

gcc cgg atc aaa gcc acc gga att gag gcg tgg gtg acg gtg acc aat 547
Ala Arg Ile Lys Ala Thr Gly Ile Glu Ala Trp Val Thr Val Thr Asn
135 140 145

ccg gag gac gcg ctg gct gcg cag aaa gct ggc gcc aac gcg ctt gtc	595
Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly Ala Asn Ala Leu Val	
150 155 160 165	
gtg caa ggc ccc gag gcg ggt ggg cac cgc tct acc tgg tcc att gaa	643
Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser Thr Trp Ser Ile Glu	
170 175 180	
gtg gag ccg gac gag cgc gac ctg aaa acc ctc ctc gca gct gtc aaa	691
Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu Leu Ala Ala Val Lys	
185 190 195	
caa gcg ggc gtt tac ctc ccg ctc atc gca gcc ggc ggc ctt tca acc	739
Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala Gly Gly Leu Ser Thr	
200 205 210	
tcc gca gac gtg gca gca att tta gaa gcc ggc gcc agc gct gcc tcc	787
Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly Ala Ser Ala Ala Ser	
215 220 225	
tgt ggt tcc gcc ttt ttg ctt agc gac gaa gcc ggc acc agc tca ctt	835
Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala Gly Thr Ser Ser Leu	
230 235 240 245	
aac cgc gag atc ttg gac gcc gcc cca gca ctt ggt ttg gaa tcg gtg	883
Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu Gly Leu Glu Ser Val	
250 255 260	
tca tct cgc gca ttt tcg ggc cgt tat gcc agg gga gtg gaa acc agg	931
Ser Ser Arg Ala Phe Ser Gly Arg Tyr Ala Arg Gly Val Glu Thr Arg	
265 270 275	
ttc acc cgt tcg aac gag ggg tta ccc ccg ttg tac cca tac ctc aac	979
Phe Thr Arg Ser Asn Glu Gly Leu Pro Pro Leu Tyr Pro Tyr Leu Asn	
280 285 290	
cca atg atc aca tct tta cgt aag gtg gcg gga agt gca ggg aac tgg	1027
Pro Met Ile Thr Ser Leu Arg Lys Val Ala Gly Ser Ala Gly Asn Trp	
295 300 305	
gat tac gcc tac tgc ctg gta gga gtc ggc ctg gaa tcg att gcg aag	1075
Asp Tyr Ala Tyr Cys Leu Val Gly Val Gly Leu Glu Ser Ile Ala Lys	
310 315 320 325	
ggt agt gca aag cag ata ctg gaa tca tta aca cct tcc gct ttg ggc	1123
Gly Ser Ala Lys Gln Ile Leu Glu Ser Leu Thr Pro Ser Ala Leu Gly	
330 335 340	
taatgttggg gggagtgcctt tca	1146
<210> 244	
<211> 341	
<212> PRT	
<213> Corynebacterium glutamicum	
<400> 244	
Met Ser Ile Leu Asp Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met	
1 5 10 15	

Ala Gly Gly Pro Ser Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala
 20 25 30
 Gly Ser Leu Gly Phe Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu
 35 40 45
 Lys Gln Glu Leu Ser Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe
 50 55 60
 Arg Pro Gln Thr Asp Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala
 65 70 75 80
 Gly Leu Leu Ser Ser Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr
 85 90 95
 Val Pro Thr Pro Asp Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala
 100 105 110
 Val Leu Ala Ala Lys Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe
 115 120 125
 Ser Ala Glu Glu Phe Ala Arg Ile Lys Ala Thr Gly Ile Glu Ala Trp
 130 135 140
 Val Thr Val Thr Asn Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly
 145 150 155 160
 Ala Asn Ala Leu Val Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser
 165 170 175
 Thr Trp Ser Ile Glu Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu
 180 185 190
 Leu Ala Ala Val Lys Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala
 195 200 205
 Gly Gly Leu Ser Thr Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly
 210 215 220
 Ala Ser Ala Ala Ser Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala
 225 230 235 240
 Gly Thr Ser Ser Leu Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu
 245 250 255
 Gly Leu Glu Ser Val Ser Ser Arg Ala Phe Ser Gly Arg Tyr Ala Arg
 260 265 270
 Gly Val Glu Thr Arg Phe Thr Arg Ser Asn Glu Gly Leu Pro Pro Leu
 275 280 285
 Tyr Pro Tyr Leu Asn Pro Met Ile Thr Ser Leu Arg Lys Val Ala Gly
 290 295 300
 Ser Ala Gly Asn Trp Asp Tyr Ala Tyr Cys Leu Val Gly Val Gly Leu
 305 310 315 320
 Glu Ser Ile Ala Lys Gly Ser Ala Lys Gln Ile Leu Glu Ser Leu Thr
 325 330 335
 Pro Ser Ala Leu Gly

```
<210> 245
<211> 723
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(700)  
<223> RXA01571
```

336

Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val
 170 175 180

atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc 691
 Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser
 185 190 195

caa ggg tgc tgaggttacc gttctgtccc gtt 723
 Gln Gly Cys
 200

<210> 246
 <211> 200
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 246
 Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro
 1 5 10 15

Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val
 20 25 30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
 35 40 45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
 50 55 60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
 65 70 75 80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
 85 90 95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
 100 105 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
 115 120 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys
 195 200

<210> 247
 <211> 1338
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1315)

<223> RXN02478

<400> 247

```

gacatcgctcg aagcgcctctc cagcggcaac atcgacgatt atcgcagcgc cgtgctcgct 60
cactacgcgc cgtttcgccg catgatttcc aacatgctcg atg cgc act agc ctc 115
                                         Met Arg Thr Ser Leu
                                         1           5

att gcg cgc ggg ttg tac cgc att ccc gcg ctg gtc tgg gat cag ggt 163
Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu Val Trp Asp Gln Gly
              10              15              20

ctt tta acg ctt ttc gac gcc cgc ctc agt gtt gac gac ctc ccc gca 211
Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val Asp Asp Leu Pro Ala
              25              30              35

ccc atc gac gtg gtg tca gcg cga tcc tca gac ggc atc acc tgg acc 259
Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp Gly Ile Thr Trp Thr
              40              45              50

acc cca gaa cca gca atc gtc gaa act gaa cac cgc ggt gtg ggc gat 307
Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His Arg Gly Val Gly Asp
              55              60              65

gtc tgc ctt gtc acg ggc gat ctg tgc ttc cac gga ttg tcc aac ctc 355
Val Cys Leu Val Thr Gly Asp Leu Cys Phe His Gly Leu Ser Asn Leu
              70              75              80              85

gca gga ttt ttt gag gat ccc acc gac ctt gaa ccc cgg ctg gcg cgc 403
Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu Pro Arg Leu Ala Arg
              90              95              100

cgg gat gtg agt ggg tgg acg tcg ata agc atg gcc cac tat ttt gcg 451
Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met Ala His Tyr Phe Ala
              105              110              115

gat gtt gat gcc gcg ttc gcc tcg tcg ggg acg gga ctt gtc ctg gcg 499
Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr Gly Leu Val Leu Ala
              120              125              130

gat ggg cgg tgg att cag agt ttt gtg gtg cgg cgc ggg cgc gag att 547
Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg Arg Gly Arg Glu Ile
              135              140              145

tcg ctt cgg att ctg cgc agc gat ggc cac atc acc gat att gcc ggc 595
Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile Thr Asp Ile Ala Gly
              150              155              160              165

ggt aac gaa tcc gcg atg acg cag ctg ccg agc ggt cgg att gtg ctg 643
Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser Gly Arg Ile Val Leu
              170              175              180

cat tcc agg ggg gtg gga cac cgt ctg agc agt gtg tcc gat gat ttc 691
His Ser Arg Gly Val Gly His Arg Leu Ser Ser Val Ser Asp Asp Phe
              185              190              195

```

```

ggg gag aca ttc act ccg ctg gag cct gtg cct gaa cta atc gac ccc 739
Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro Glu Leu Ile Asp Pro
      200                      205                      210

ggc tgc aac ggc cac gtg ttc tac tgg aaa gcg gct gga atg ctc gcc 787
Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala Ala Gly Met Leu Ala
      215                      220                      225

gca acg cac ctg gcg gac cct gat ctg cga cgc cac ttg gtg gtt gat 835
Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg His Leu Val Val Asp
      230                      235                      240                      245

tta tcc agc gac gaa gga gcg acc tgg gcg cat cgc atc acc atc gag 883
Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His Arg Ile Thr Ile Glu
      250                      255                      260

cgc gaa gaa gcc gcc tat tca acc gct gcg gaa atg ccc aac gga gat 931
Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu Met Pro Asn Gly Asp
      265                      270                      275

gtt gcc gtg gtg tgg gaa gca gag gga acg cgc gcg ata aaa tgc acg 979
Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg Ala Ile Lys Cys Thr
      280                      285                      290

gtg atc agc gta aat gat att tcg ctg cgg atc gat gag ccc att tcc 1027
Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile Asp Glu Pro Ile Ser
      295                      300                      305

gat gcc ata tcc ctc cgc cat gtg gtg atc aac gat gac cat gac ggc 1075
Asp Ala Ile Ser Leu Arg His Val Val Ile Asn Asp Asp His Asp Gly
      310                      315                      320                      325

atc gaa gtc gca ctg cct gac gca tcg caa tgg ggt gaa ggt gta ttc 1123
Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp Gly Glu Gly Val Phe
      330                      335                      340

aaa att gtg tcc aat cca gac gcg agc acc caa aaa atc cgc act cga 1171
Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln Lys Ile Arg Thr Arg
      345                      350                      355

ggc aag ccc gcg cga cag acc ctg gaa att ggg gat gaa ttg gtt ttt 1219
Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly Asp Glu Leu Val Phe
      360                      365                      370

gat atc cgc aag ggt gga gaa gtg gct tac ggc gtc acg gtt cct tat 1267
Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly Val Thr Val Pro Tyr
      375                      380                      385

gat ggt cgc tcg ttg ggg gaa gtt aaa cag gat ttt gga gtg ggg ctg 1315
Asp Gly Arg Ser Leu Gly Glu Val Lys Gln Asp Phe Gly Val Gly Leu
      390                      395                      400                      405

tagaggccga tttgcggtcc ttt 1338

```

<210> 248

<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Met Arg Thr Ser Leu Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu
1 5 10 15

Val Trp Asp Gln Gly Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val
20 25 30

Asp Asp Leu Pro Ala Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp
35 40 45

Gly Ile Thr Trp Thr Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His
50 55 60

Arg Gly Val Gly Asp Val Cys Leu Val Thr Gly Asp Leu Cys Phe His
65 70 75 80

Gly Leu Ser Asn Leu Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu
85 90 95

Pro Arg Leu Ala Arg Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met
100 105 110

Ala His Tyr Phe Ala Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr
115 120 125

Gly Leu Val Leu Ala Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg
130 135 140

Arg Gly Arg Glu Ile Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile
145 150 155 160

Thr Asp Ile Ala Gly Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser
165 170 175

Gly Arg Ile Val Leu His Ser Arg Gly Val Gly His Arg Leu Ser Ser
180 185 190

Val Ser Asp Asp Phe Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro
195 200 205

Glu Leu Ile Asp Pro Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala
210 215 220

Ala Gly Met Leu Ala Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg
225 230 235 240

His Leu Val Val Asp Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His
245 250 255

Arg Ile Thr Ile Glu Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu
260 265 270

Met Pro Asn Gly Asp Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg
275 280 285

Ala Ile Lys Cys Thr Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile
290 295 300

Asp Glu Pro Ile Ser Asp Ala Ile Ser Leu Arg His Val Val Ile Asn
305 310 315 320

<400> 249															60
ttcggtagaa tgggtaggtt gtcgtgcttg aggtgtgggtg gataaccacc tctacaacac															
cacccaagct ctggttagaaa aaattgagga agcagtcctaa atg aaa cac caa tat															115
											Met Lys His Gln Tyr	5			
											1				
gat gtc atc gtt gtc ggt tcc ggc gct ggc gga tta tca gct gca gtc	163														
Asp Val Ile Val Val Gly Ser Gly Ala Gly Gly Leu Ser Ala Ala Val															
										10	15	20			
agt gca gct tac ggc ggt aag aaa gtc gct gta att gaa aag gcc tca															211
Ser Ala Ala Tyr Gly Gly Lys Lys Val Ala Val Ile Glu Lys Ala Ser															
										25	30	35			
gta ctc ggt gga gcc acc acc tgg tcc ggc ggt tgg gct tgg act cct															259
Val Leu Gly Gly Ala Thr Thr Trp Ser Gly Gly Trp Ala Trp Thr Pro															
										40	45	50			
gga acc agc ctt gcg cgc aaa gac gga gta gtg gaa tcc aaa gaa gaa															307
Gly Thr Ser Leu Ala Arg Lys Asp Gly Val Val Glu Ser Lys Glu Glu															
										55	60	65			
ttc caa acc tac ctg caa gcg gta gtg ggg gag tac tac caa gaa gac															355
Phe Gln Thr Tyr Leu Gln Ala Val Val Gly Glu Tyr Tyr Gln Glu Asp															
										70	75	80	85		
aac atc tcc gcc ttc ttg gac gca gcc cct gaa atg gtc gat ttc ttt															403
Asn Ile Ser Ala Phe Leu Asp Ala Ala Pro Glu Met Val Asp Phe Phe															
										90	95	100			
gaa aaa aac acc gac ctg cag tgg acc ccc ggc gcg aaa atc aac gac															451

Glu	Lys	Asn	Thr	Asp	Leu	Gln	Trp	Thr	Pro	Gly	Ala	Lys	Ile	Asn	Asp	
			105					110					115			
atc	tac	ggc	aac	ctc	ccc	ggg	gct	ggc	act	gga	cac	cgc	tcc	gtt	ggg	499
Ile	Tyr	Gly	Asn	Leu	Pro	Gly	Ala	Gly	Thr	Gly	His	Arg	Ser	Val	Gly	
		120					125					130				
cca	aaa	cca	ttc	aac	gga	cgc	aaa	gta	ccc	aag	agt	gtt	ctt	cca	aaa	547
Pro	Lys	Pro	Phe	Asn	Gly	Arg	Lys	Val	Pro	Lys	Ser	Val	Leu	Pro	Lys	
		135				140					145					
ctg	cgc	cac	cag	ctg	tat	gaa	acc	tcc	ttc	ctg	gga	atg	ggc	atc	atg	595
Leu	Arg	His	Gln	Leu	Tyr	Glu	Thr	Ser	Phe	Leu	Gly	Met	Gly	Ile	Met	
150					155					160					165	
gct	ggg	cct	gac	ctg	acg	aaa	ttc	ctc	tct	gct	tca	cag	ttc	gat	cca	643
Ala	Gly	Pro	Asp	Leu	Thr	Lys	Phe	Leu	Ser	Ala	Ser	Gln	Phe	Asp	Pro	
				170					175					180		
cgt	ggg	tgg	gta	cat	gcc	gcc	agg	cgc	gtc	atc	gtg	cac	atg	tgg	gac	691
Arg	Gly	Trp	Val	His	Ala	Ala	Arg	Arg	Val	Ile	Val	His	Met	Trp	Asp	
			185					190					195			
atg	gtc	gtg	cac	aaa	cgc	aat	atg	cag	atg	gtc	aac	ggg	gca	gca	ctc	739
Met	Val	Val	His	Lys	Arg	Asn	Met	Gln	Met	Val	Asn	Gly	Ala	Ala	Leu	
		200					205					210				
acc	gct	cga	ctg	gct	acc	tct	gca	gac	aag	ctg	ggc	gtt	gat	ctc	ctg	787
Thr	Ala	Arg	Leu	Ala	Thr	Ser	Ala	Asp	Lys	Leu	Gly	Val	Asp	Leu	Leu	
		215				220					225					
gtc	aat	cac	tcc	gca	gtg	tgc	ttg	aat	tac	aaa	aac	gac	cgc	gtt	acc	835
Val	Asn	His	Ser	Ala	Val	Ser	Leu	Asn	Tyr	Lys	Asn	Asp	Arg	Val	Thr	
230					235				240						245	
ggc	gtg	aaa	gta	caa	acc	cca	cag	ggc	ttg	gta	gat	ttc	gaa	gcc	act	883
Gly	Val	Lys	Val	Gln	Thr	Pro	Gln	Gly	Leu	Val	Asp	Phe	Glu	Ala	Thr	
			250					255					260			
gcc	ggc	gtc	gtg	ctc	gcc	act	ggg	gga	ttc	ccc	aac	aac	gtt	gac	ctg	931
Ala	Gly	Val	Val	Leu	Ala	Thr	Gly	Gly	Phe	Pro	Asn	Asn	Val	Asp	Leu	
			265				270						275			
cgc	aag	gaa	ctc	ttc	cca	cgc	acc	cca	tca	ggg	caa	gaa	cac	tgg	acc	979
Arg	Lys	Glu	Leu	Phe	Pro	Arg	Thr	Pro	Ser	Gly	Gln	Glu	His	Trp	Thr	
		280					285					290				
ctc	gcg	cca	gca	gaa	acc	acc	ggc	gac	gga	cta	tcc	atg	gct	cgg	gaa	1027
Leu	Ala	Pro	Ala	Glu	Thr	Thr	Gly	Asp	Gly	Leu	Ser	Met	Ala	Arg	Glu	
		295				300					305					
atc	ggg	gca	ggg	ttt	gtc	aac	gac	ctg	aaa	tcc	cca	gca	gca	tgg	tgc	1075
Ile	Gly	Ala	Gly	Phe	Val	Asn	Asp	Leu	Lys	Ser	Pro	Ala	Ala	Trp	Cys	
310					315					320					325	
cct	gtt	tca	ttg	gtc	cca	tac	ttc	aac	gga	aaa	gtc	ggc	acc	ttc	ccc	1123
Pro	Val	Ser	Leu	Val	Pro	Tyr	Phe	Asn	Gly	Lys	Val	Gly	Thr	Phe	Pro	
				330					335					340		
cac	atc	atg	gac	cgc	gca	aaa	cca	ggc	tcc	atc	ggg	gtt	gtc	tcc	aca	1171
His	Ile	Met	Asp	Arg	Ala	Lys	Pro	Gly	Ser	Ile	Gly	Val	Val	Ser	Thr	

345							350				355				
ggt	aag	cga	ttc	gtc	aat	gaa	gcc	aac	ggc	tac	tac	gac	tac		
Gly	Lys	Arg	Phe	Val	Asn	Glu	Ala	Asn	Gly	Tyr	Tyr	Asp	Tyr	1213	
		360					365					370			

<400> 251																	
ctggttttgt gccgaggatc agccagcaag ttaatgatcc ttacatggcg ctgttgttgg																	60
cgcggtagtc aatcatgggg gagtatccca ccgtatccgc																	115
										gtg	aac	aag	ggc	gtg			
										Val	Asn	Lys	Gly	Val			
										1				5			
gtg ctg gta gca ggt gga ttc tcc cag aat cca gaa ctg cgc atg aag																	163
Val	Leu	Val	Ala	Gly	Gly	Phe	Ser	Gln	Asn	Pro	Glu	Leu	Arg	Met	Lys		
				10					15					20			
tac atg cca gaa ccc acc cca cag ttc tcc cgc acc aac gaa agc gcc																	211
Tyr	Met	Pro	Glu	Pro	Thr	Pro	Gln	Phe	Ser	Arg	Thr	Asn	Glu	Ser	Ala		
			25					30					35				
acc ggc gac acc atg gcc ctt gct gcg aaa gtg gga gca cgc cta ggc																	259
Thr	Gly	Asp	Thr	Met	Ala	Leu	Ala	Ala	Lys	Val	Gly	Ala	Arg	Leu	Gly		
		40					45					50					
gac gac aac ggt gaa aac gca ctg tgg ttc cca tcg tcc atc ggc acc																	307
Asp	Asp	Asn	Gly	Glu	Asn	Ala	Leu	Trp	Phe	Pro	Ser	Ser	Ile	Gly	Thr		
	55					60					65						
cgc gcc gac gga tcc acc gcg gtg tac cca cac att tgg gac cgt ggc																	355
Arg	Ala	Asp	Gly	Ser	Thr	Ala	Val	Tyr	Pro	His	Ile	Trp	Asp	Arg	Gly		
70					75					80					85		

cgc ctc gga gtc atc gca gtc aac gca gca ggc gag cgt ttc gtc gat	403
Arg Leu Gly Val Ile Ala Val Asn Ala Ala Gly Glu Arg Phe Val Asp	
90 95 100	
gaa tcc gtc tcc tac cac cgc ttc gtg cgc gcc atg tac gaa tcc aac	451
Glu Ser Val Ser Tyr His Arg Phe Val Arg Ala Met Tyr Glu Ser Asn	
105 110 115	
aaa acc acc ccg act gtt tca gcc tgg ctc att gtt gat tcc cac acc	499
Lys Thr Thr Pro Thr Val Ser Ala Trp Leu Ile Val Asp Ser His Thr	
120 125 130	
ctg gca aaa tac ggc ctc ggc atg atc acc atg cca cac ctg cct aaa	547
Leu Ala Lys Tyr Gly Leu Gly Met Ile Thr Met Pro His Leu Pro Lys	
135 140 145	
ctc gct ctg caa aaa tac atc gac tcc gga tac ctg cac gca gga tca	595
Leu Ala Leu Gln Lys Tyr Ile Asp Ser Gly Tyr Leu His Ala Gly Ser	
150 155 160 165	
tcc ttg gat gaa ttg gca cgc agc att ggt gtg gac gct cgc ggc ctg	643
Ser Leu Asp Glu Leu Ala Arg Ser Ile Gly Val Asp Ala Arg Gly Leu	
170 175 180	
gaa caa acc gtc aaa cgc tac aat acc ttc gct aaa acg ggt atc gac	691
Glu Gln Thr Val Lys Arg Tyr Asn Thr Phe Ala Lys Thr Gly Ile Asp	
185 190 195	
gaa gac ttc cac aag ggc gaa ctc ctc ttc ggt caa gcc gcc ggc gat	739
Glu Asp Phe His Lys Gly Glu Leu Leu Phe Gly Gln Ala Ala Gly Asp	
200 205 210	
cca gac aac aag cca aac ccc aac gtc gga cca atc aag aag gga ccg	787
Pro Asp Asn Lys Pro Asn Pro Asn Val Gly Pro Ile Lys Lys Gly Pro	
215 220 225	
ttc tac gca atc gct gta gtc cca acc cct ctg gcc act gcc ttt ggc	835
Phe Tyr Ala Ile Ala Val Val Pro Thr Pro Leu Ala Thr Ala Phe Gly	
230 235 240 245	
atc agc atc aac ccc aac gga cag gtt gtt agt gaa gat ggg gag ccc	883
Ile Ser Ile Asn Pro Asn Gly Gln Val Val Ser Glu Asp Gly Glu Pro	
250 255 260	
atc att gga ctg tac tcc gca gga aat gat gcc caa tct gtc atg gct	931
Ile Ile Gly Leu Tyr Ser Ala Gly Asn Asp Ala Gln Ser Val Met Ala	
265 270 275	
tct gaa tat cct ggt gct ggt tca cag gtt ggt tcc gga atg acc ttt	979
Ser Glu Tyr Pro Gly Ala Gly Ser Gln Val Gly Ser Gly Met Thr Phe	
280 285 290	
ggt tgg atc gca gca cag cac gcg gtg ggg aaa gcg gga aaa tcc gga	1027
Gly Trp Ile Ala Ala Gln His Ala Val Gly Lys Ala Gly Lys Ser Gly	
295 300 305	
gga gct aag gca gga tat gcc gcg tct tct aag taattgcttg gtgggttgct	1080
Gly Ala Lys Ala Gly Tyr Ala Ala Ser Ser Lys	
310 315 320	

tac

1083

<210> 252

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val 1	Asn	Lys	Gly	Val 5	Val	Leu	Val	Ala	Gly 10	Gly	Phe	Ser	Gln	Asn 15	Pro
Glu	Leu	Arg	Met 20	Lys	Tyr	Met	Pro	Glu 25	Pro	Thr	Pro	Gln	Phe 30	Ser	Arg
Thr	Asn	Glu 35	Ser	Ala	Thr	Gly	Asp 40	Thr	Met	Ala	Leu	Ala 45	Ala	Lys	Val
Gly	Ala 50	Arg	Leu	Gly	Asp	Asp 55	Asn	Gly	Glu	Asn	Ala 60	Leu	Trp	Phe	Pro
Ser 65	Ser	Ile	Gly	Thr	Arg 70	Ala	Asp	Gly	Ser	Thr 75	Ala	Val	Tyr	Pro	His 80
Ile	Trp	Asp	Arg	Gly 85	Arg	Leu	Gly	Val	Ile 90	Ala	Val	Asn	Ala 95	Ala	Gly
Glu	Arg	Phe	Val 100	Asp	Glu	Ser	Val	Ser 105	Tyr	His	Arg	Phe	Val 110	Arg	Ala
Met	Tyr	Glu 115	Ser	Asn	Lys	Thr	Thr 120	Pro	Thr	Val	Ser	Ala 125	Trp	Leu	Ile
Val 130	Asp	Ser	His	Thr	Leu	Ala 135	Lys	Tyr	Gly	Leu	Gly 140	Met	Ile	Thr	Met
Pro 145	His	Leu	Pro	Lys	Leu 150	Ala	Leu	Gln	Lys	Tyr 155	Ile	Asp	Ser	Gly	Tyr 160
Leu	His	Ala	Gly	Ser 165	Ser	Leu	Asp	Glu	Leu 170	Ala	Arg	Ser	Ile	Gly 175	Val
Asp	Ala	Arg	Gly 180	Leu	Glu	Gln	Thr	Val 185	Lys	Arg	Tyr	Asn	Thr 190	Phe	Ala
Lys	Thr	Gly 195	Ile	Asp	Glu	Asp	Phe 200	His	Lys	Gly	Glu	Leu 205	Leu	Phe	Gly
Gln	Ala 210	Ala	Gly	Asp	Pro	Asp 215	Asn	Lys	Pro	Asn	Pro 220	Asn	Val	Gly	Pro
Ile 225	Lys	Lys	Gly	Pro	Phe 230	Tyr	Ala	Ile	Ala	Val 235	Val	Pro	Thr	Pro	Leu 240
Ala	Thr	Ala	Phe 245	Gly	Ile	Ser	Ile	Asn	Pro 250	Asn	Gly	Gln	Val 255	Val	Ser
Glu	Asp	Gly	Glu 260	Pro	Ile	Ile	Gly	Leu 265	Tyr	Ser	Ala	Gly	Asn 270	Asp	Ala
Gln	Ser	Val	Met	Ala	Ser	Glu	Tyr	Pro	Gly	Ala	Gly	Ser	Gln	Val	Gly

275					280					285					
Ser	Gly	Met	Thr	Phe	Gly	Trp	Ile	Ala	Ala	Gln	His	Ala	Val	Gly	Lys
	290					295					300				
Ala	Gly	Lys	Ser	Gly	Gly	Ala	Lys	Ala	Gly	Tyr	Ala	Ala	Ser	Ser	Lys
305					310					315					320

```
<210> 253
<211> 1428
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1405)
<223> RXN01166
```

Genetic Code Table																	Position
<div><400> 253</div> <div>accgtaccca cagacacacc agaattaaca gaaacagact gaaaaacaac atcgtctcgac</div>																	60
<div>atgcgcgtaa tcctaaccgcg cgcacactaa tgtggccgat</div> <div>Met Gly Tyr Thr Asn</div> <div>1 5</div>																	115
<div>ctc aac gac aca cgg gtc ttg cgc gcc ggg tca tgt gat gcc tgg tgg</div> <div>Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser Cys Asp Ala Trp Trp</div> <div>10 15 20</div>																	163
<div>cgc acg atg tct ccg cta gtg cag cag gga agt gag gca gtc ttt cgg</div> <div>Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser Glu Ala Val Phe Arg</div> <div>25 30 35</div>																	211
<div>cgc atc atg ggt ctc tcg cgg cgt cct gat cgg aaa cct ggc ttt gac</div> <div>Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg Lys Pro Gly Phe Asp</div> <div>40 45 50</div>																	259
<div>gat gtc cca cat ttc ggc gca gct gtt cga gtt ccc ggt cta aaa cac</div> <div>Asp Val Pro His Phe Gly Ala Ala Val Arg Val Pro Gly Leu Lys His</div> <div>55 60 65</div>																	307
<div>ggc acg ttg gtc aat gct gca ccc ttg aaa gtt ttg ggc gca cgg ggc</div> <div>Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val Leu Gly Ala Arg Gly</div> <div>70 75 80 85</div>																	355
<div>gag ccc aac ccc gcg agt tcg tac cgt ttt gaa tac atc acc ggt gat</div> <div>Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu Tyr Ile Thr Gly Asp</div> <div>90 95 100</div>																	403
<div>tcc gca ggt cga gcc atc act gcg acc ggc gct gtc ctc ttt tcc aca</div> <div>Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala Val Leu Phe Ser Thr</div> <div>105 110 115</div>																	451
<div>cgc ccc tgg aca acc ggc ccg cgt ccc gcg atc gcc atg gct cca tcc</div> <div>Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile Ala Met Ala Pro Ser</div> <div>120 125 130</div>																	499

acc	caa	ggc	gtc	gca	cag	cac	tgc	gat	ccc	tcc	cac	acc	tgc	gcc	atc	547
Thr	Gln	Gly	Val	Ala	Gln	His	Cys	Asp	Pro	Ser	His	Thr	Cys	Ala	Ile	
135						140					145					
gga	ctc	aac	gca	ttc	tat	gac	aaa	ccc	ttc	gac	gca	atc	att	gct	tac	595
Gly	Leu	Asn	Ala	Phe	Tyr	Asp	Lys	Pro	Phe	Asp	Ala	Ile	Ile	Ala	Tyr	
150					155					160					165	
gaa	ctc	ccc	gtc	atc	ctc	tgg	ttt	cta	gct	cac	gga	ctt	gac	gtt	gtg	643
Glu	Leu	Pro	Val	Ile	Leu	Trp	Phe	Leu	Ala	His	Gly	Leu	Asp	Val	Val	
				170					175					180		
ttc	atc	gat	tac	ccc	cgc	gac	ccc	gca	acc	ggc	gtc	caa	tac	tat	tgc	691
Phe	Ile	Asp	Tyr	Pro	Arg	Asp	Pro	Ala	Thr	Gly	Val	Gln	Tyr	Tyr	Cys	
			185					190					195			
gat	tcc	atc	gct	gca	gct	aaa	tcg	ctt	ctc	gac	gcc	gtc	ctc	gcc	tcc	739
Asp	Ser	Ile	Ala	Ala	Ala	Lys	Ser	Leu	Leu	Asp	Ala	Val	Leu	Ala	Ser	
		200					205					210				
aga	caa	ctc	ggc	ctt	tca	ccg	gaa	gca	ccg	ctt	ggc	ctg	tgg	gga	ttc	787
Arg	Gln	Leu	Gly	Leu	Ser	Pro	Glu	Ala	Pro	Leu	Gly	Leu	Trp	Gly	Phe	
	215					220					225					
tcc	caa	gga	ggc	ggc	gcc	act	ggc	tgg	gct	gca	caa	ttg	cag	gat	tac	835
Ser	Gln	Gly	Gly	Gly	Ala	Thr	Gly	Trp	Ala	Ala	Gln	Leu	Gln	Asp	Tyr	
230					235					240					245	
gca	cct	gat	gtc	cgc	cca	aag	gca	gcg	gtc	gtg	ggc	gct	cca	cca	gtg	883
Ala	Pro	Asp	Val	Arg	Pro	Lys	Ala	Ala	Val	Val	Gly	Ala	Pro	Pro	Val	
				250					255					260		
gat	ctc	ttc	cgc	gtc	ttg	gac	act	gtc	gac	ggc	gga	ttg	ctc	acc	gga	931
Asp	Leu	Phe	Arg	Val	Leu	Asp	Thr	Val	Asp	Gly	Gly	Leu	Leu	Thr	Gly	
			265					270					275			
gtg	att	gcc	tac	gcc	atc	gcg	gga	ctt	gca	gtg	aac	tct	tca	gag	atg	979
Val	Ile	Ala	Tyr	Ala	Ile	Ala	Gly	Leu	Ala	Val	Asn	Ser	Ser	Glu	Met	
		280					285					290				
ttt	gag	gaa	atc	atg	tcg	gtg	tta	aat	gaa	cgc	gga	gtc	agt	gat	gtg	1027
Phe	Glu	Glu	Ile	Met	Ser	Val	Leu	Asn	Glu	Arg	Gly	Val	Ser	Asp	Val	
	295					300					305					
ctg	aaa	aat	atc	acc	agc	tgc	gcg	gga	ggc	tcc	ttg	ttg	gcc	agt	ggc	1075
Leu	Lys	Asn	Ile	Thr	Ser	Cys	Ala	Gly	Gly	Ser	Leu	Leu	Ala	Ser	Gly	
310						315				320					325	
tac	tcg	tct	tcc	cgc	ggg	tgg	aca	cat	cag	ggc	acg	ccg	ctg	gca	gac	1123
Tyr	Ser	Ser	Ser	Arg	Gly	Trp	Thr	His	Gln	Gly	Thr	Pro	Leu	Ala	Asp	
				330					335					340		
att	ctg	gac	gat	ctg	cca	ctt	gtt	gtc	gct	gag	ttt	ggg	aag	caa	aag	1171
Ile	Leu	Asp	Asp	Leu	Pro	Leu	Val	Val	Ala	Glu	Phe	Gly	Lys	Gln	Lys	
			345					350					355			
ctg	ggc	cgt	gtg	gcg	cca	gaa	atc	cca	gtg	ctg	ttg	tgg	ggc	tct	aaa	1219
Leu	Gly	Arg	Val	Ala	Pro	Glu	Ile	Pro	Val	Leu	Leu	Trp	Gly	Ser	Lys	
		360					365					370				
aat	gat	gat	gtc	att	ccc	att	gat	ccc	att	agg	gaa	ttg	cgt	gat	agc	1267

Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu Arg Asp Ser
 375 380 385
 tgg gcg gac aag ggt acg cca ttg acc tgg cat gaa tcc caa gcg ccg 1315
 Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser Gln Ala Pro
 390 395 400 405
 cgt gtg cca gga cgc aca ggt ctc aac cat ttc ggg ccc tat ttt aga 1363
 Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro Tyr Phe Arg
 410 415 420
 aac ctg gaa aag tac tcg gga tgg ctc ata gat cat ctt gtc 1405
 Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu Val
 425 430 435
 tgagtgccgt tttaaaggct cgg 1428

<210> 254

<211> 435

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Gly Tyr Thr Asn Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser
 1 5 10 15
 Cys Asp Ala Trp Trp Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser
 20 25 30
 Glu Ala Val Phe Arg Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg
 35 40 45
 Lys Pro Gly Phe Asp Asp Val Pro His Phe Gly Ala Ala Val Arg Val
 50 55 60
 Pro Gly Leu Lys His Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val
 65 70 75 80
 Leu Gly Ala Arg Gly Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu
 85 90 95
 Tyr Ile Thr Gly Asp Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala
 100 105 110
 Val Leu Phe Ser Thr Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile
 115 120 125
 Ala Met Ala Pro Ser Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser
 130 135 140
 His Thr Cys Ala Ile Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp
 145 150 155 160
 Ala Ile Ile Ala Tyr Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His
 165 170 175
 Gly Leu Asp Val Val Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly
 180 185 190
 Val Gln Tyr Tyr Cys Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp

195	200	205
Ala Val Leu Ala Ser Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu 210 215 220		
Gly Leu Trp Gly Phe Ser Gln Gly Gly Gly Ala Thr Gly Trp Ala Ala 225 230 235 240		
Gln Leu Gln Asp Tyr Ala Pro Asp Val Arg Pro Lys Ala Ala Val Val 245 250 255		
Gly Ala Pro Pro Val Asp Leu Phe Arg Val Leu Asp Thr Val Asp Gly 260 265 270		
Gly Leu Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val 275 280 285		
Asn Ser Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg 290 295 300		
Gly Val Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser 305 310 315 320		
Leu Leu Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly 325 330 335		
Thr Pro Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu 340 345 350		
Phe Gly Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu 355 360 365		
Leu Trp Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg 370 375 380		
Glu Leu Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His 385 390 395 400		
Glu Ser Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe 405 410 415		
Gly Pro Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp 420 425 430		
His Leu Val 435		

<210> 255

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXN02001

<400> 255

gcgggtttcgt catggataag gactgtgttc gggaccattg cgatactcgt gtcaaaaggc 60

gatagtcacag	catagaccgt	gctttatcga	aggtgaaccc	atg	ccc	gtt	atc	aat	115
				Met	Pro	Val	Ile	Asn	
				1				5	
agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg	163								
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu									
10 15 20									
cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc	211								
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe									
25 30 35									
gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc	259								
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly									
40 45 50									
atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc	307								
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly									
55 60 65									
ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag	355								
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu									
70 75 80 85									
att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc	403								
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala									
90 95 100									
tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat	451								
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr									
105 110 115									
ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag	499								
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln									
120 125 130									
cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc	547								
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly									
135 140 145									
gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag	595								
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln									
150 155 160 165									
ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg	643								
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met									
170 175 180									
gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac	691								
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His									
185 190 195									
ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga	739								
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly									
200 205 210									
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc	787								
Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val									
215 220 225									
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat	835								

Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp
 230 235 240 245
 aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc 883
 Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe
 250 255 260
 aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc 931
 Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val
 265 270 275
 gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac 979
 Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn
 280 285 290
 cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027
 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala
 295 300 305
 gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075
 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser
 310 315 320 325
 cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123
 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro
 330 335 340
 ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171
 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn
 345 350 355
 ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc 1219
 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe
 360 365 370
 ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg 1268
 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly
 375 380 385
 cgctcgaaga tgc 1281
 <210> 256
 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 256
 Met Pro Val Ile Asn Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg
 1 5 10 15
 Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
 20 25 30
 Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
 35 40 45
 Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
 50 55 60
 Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala

65						70						75						80
Leu	Pro	Leu	Thr	Glu	Ile	Thr	Gly	Val	Asp	Tyr	Ala	Ser	Thr	Thr	Pro			
				85					90					95				
Gly	Lys	Met	His	Ala	Cys	Gly	His	Asp	Gly	His	Thr	Thr	Met	Leu	Leu			
			100					105					110					
Gly	Ala	Ala	Lys	Tyr	Leu	Ala	Glu	Thr	Arg	Asn	Phe	Ala	Gly	Thr	Val			
		115					120					125						
Ala	Leu	Ile	Phe	Gln	Pro	Ala	Glu	Glu	Asn	Gly	Gly	Gly	Ala	Gly	Val			
	130					135					140							
Met	Val	Asp	Glu	Gly	Val	Leu	Asp	Arg	Phe	Ala	Ile	Ala	Glu	Val	Tyr			
145					150				155						160			
Ala	Leu	His	Asn	Gln	Pro	Gly	Leu	Pro	Leu	Gly	His	Phe	Met	Thr	Thr			
			165						170					175				
Ala	Gly	Pro	Ile	Met	Ala	Ala	Val	Asp	Thr	Phe	Asp	Ile	Asn	Ile	Thr			
			180					185					190					
Gly	Arg	Gly	Gly	His	Gly	Ala	Lys	Pro	His	Gln	Thr	Arg	Asp	Pro	Ile			
		195					200					205						
Val	Ala	Ala	Val	Gly	Ile	Val	Gln	Ala	Phe	Gln	Thr	Ile	Val	Ser	Arg			
	210					215					220							
Asn	His	Asn	Pro	Val	Glu	Asp	Leu	Val	Val	Ser	Val	Thr	Gln	Ile	His			
225					230					235					240			
Thr	Gly	Ser	Ala	Asp	Asn	Ile	Ile	Pro	Glu	Thr	Ala	Tyr	Ile	Asn	Gly			
			245						250					255				
Thr	Val	Arg	Thr	Phe	Asn	Lys	Asp	Val	Gln	Ala	Met	Val	Ile	Thr	Arg			
			260					265					270					
Met	Glu	Glu	Ile	Val	Ala	Gly	Gln	Ala	Ala	Ala	Tyr	Gly	Val	Glu	Ala			
		275					280					285						
Thr	Leu	Thr	Tyr	Asn	Arg	Asn	Tyr	Pro	Ala	Thr	Ile	Asn	Asp	Ala	Ala			
	290					295					300							
Lys	Ala	Ala	Ile	Ala	Ala	Glu	Val	Ala	Gly	Glu	Val	Gly	Leu	Gly	Val			
305					310					315					320			
Asn	Pro	Asn	Gly	Ser	Arg	Gly	Met	Gly	Ala	Glu	Asp	Phe	Ser	Tyr	Phe			
			325						330					335				
Leu	Glu	Lys	Arg	Pro	Gly	Ala	Tyr	Leu	Phe	Val	Gly	Asn	Gly	Asp	Ser			
			340					345					350					
Ala	Gly	Leu	His	Asn	Pro	Ala	Tyr	Asn	Phe	Asn	Asp	Glu	Ala	Ala	Pro			
		355					360					365						
Tyr	Gly	Ala	Ser	Phe	Leu	Ala	Arg	Met	Ala	Glu	Arg	Pro	Leu	Pro	Leu			
	370					375					380							
Lys	Gly																	
385																		

<210> 257
 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(547)
 <223> RXN03145

<400> 257

```

agaggtggtt aaattccgc ctctgccccca gatttaaaac tatgatgagg gatagcttct 60

caattttcca ggttttccaa aatgaaagag gttcacgcac atg cct act tat act 115
                                         Met Pro Thr Tyr Thr
                                         1      5

tgt tgg tcg caa aga att cgc att tct agg gaa gcc aag caa cgc atc 163
Cys Trp Ser Gln Arg Ile Arg Ile Ser Arg Glu Ala Lys Gln Arg Ile
                        10      15      20

gct gag gca atc acc gat gcc cac cat gaa tta gcg cat gct ccc aag 211
Ala Glu Ala Ile Thr Asp Ala His His Glu Leu Ala His Ala Pro Lys
                        25      30      35

tat ttg gtg cag gtg att ttc aat gag gtg gag cct gat tct tat ttc 259
Tyr Leu Val Gln Val Ile Phe Asn Glu Val Glu Pro Asp Ser Tyr Phe
                        40      45      50

att gcg gcg cag tcg gcg tcg gaa aac cac att tgg gtc caa gca acg 307
Ile Ala Ala Gln Ser Ala Ser Glu Asn His Ile Trp Val Gln Ala Thr
                        55      60      65

att cgt tcg ggg cgt aca gag aag caa aaa gag gaa ctt ctg ctt cgg 355
Ile Arg Ser Gly Arg Thr Glu Lys Gln Lys Glu Glu Leu Leu Leu Arg
                        70      75      80      85

ctg aca caa gag atc gcg ctg att ctt ggg atc ccc aat gaa gaa gta 403
Leu Thr Gln Glu Ile Ala Leu Ile Leu Gly Ile Pro Asn Glu Glu Val
                        90      95      100

tgg gta tat ata ccg gag att cct ggt tcc aat atg acg gaa tat ggc 451
Trp Val Tyr Ile Pro Glu Ile Pro Gly Ser Asn Met Thr Glu Tyr Gly
                        105      110      115

cgt ctc ctc atg gaa cct ggc gaa gag gag aag tgg ttt aat tcg ctt 499
Arg Leu Leu Met Glu Pro Gly Glu Glu Glu Lys Trp Phe Asn Ser Leu
                        120      125      130

ccc gaa ggc ctg cgg gaa agg ttg acc gag cta gaa gga tcg tca gaa 547
Pro Glu Gly Leu Arg Glu Arg Leu Thr Glu Leu Glu Gly Ser Ser Glu
                        135      140      145

tagctctcga ataggccatt tct 570

```

<210> 258
 <211> 149
 <212> PRT

<213> Corynebacterium glutamicum

<400> 258

```

Met Pro Thr Tyr Thr Cys Trp Ser Gln Arg Ile Arg Ile Ser Arg Glu
 1           5           10           15

Ala Lys Gln Arg Ile Ala Glu Ala Ile Thr Asp Ala His His Glu Leu
          20           25           30

Ala His Ala Pro Lys Tyr Leu Val Gln Val Ile Phe Asn Glu Val Glu
          35           40           45

Pro Asp Ser Tyr Phe Ile Ala Ala Gln Ser Ala Ser Glu Asn His Ile
          50           55           60

Trp Val Gln Ala Thr Ile Arg Ser Gly Arg Thr Glu Lys Gln Lys Glu
          65           70           75           80

Glu Leu Leu Leu Arg Leu Thr Gln Glu Ile Ala Leu Ile Leu Gly Ile
          85           90           95

Pro Asn Glu Glu Val Trp Val Tyr Ile Pro Glu Ile Pro Gly Ser Asn
          100          105          110

Met Thr Glu Tyr Gly Arg Leu Leu Met Glu Pro Gly Glu Glu Glu Lys
          115          120          125

Trp Phe Asn Ser Leu Pro Glu Gly Leu Arg Glu Arg Leu Thr Glu Leu
          130          135          140

Glu Gly Ser Ser Glu
145

```

<210> 259

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXN01466

<400> 259

```

aatccatgat cccaaactac ctcaaagcgc ttgtaggcta agacttatgg atacacaacg 60

cggctcattg cggggaaaaag ctcataaagc aaggctaaag atg acg cca aat ggt 115
                               Met Thr Pro Asn Gly
                               1           5

cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt 163
Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg
          10           15           20

acc ccg ggt cta aaa cac gtc gac cgc cac acc atc gtg gac tcc gac 211
Thr Pro Gly Leu Lys His Val Asp Arg His Thr Ile Val Asp Ser Asp
          25           30           35

ggc ctc agc atc cac acg tac atg gtt ggc cat gcc gaa aat gcc acg 259
Gly Leu Ser Ile His Thr Tyr Met Val Gly His Ala Glu Asn Ala Thr

```

40	45	50	
gca acg gtc gtg ttc atc cac ggc ttc acc ctc gcc gcc gaa gtg tat Ala Thr Val Val Phe Ile His Gly Phe Thr Leu Ala Ala Glu Val Tyr 55 60 65			307
tac atg cag gtc gac tac cta caa acc ttt tac cca aat att aaa agc Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr Pro Asn Ile Lys Ser 70 75 80 85			355
gtg ctt atc gac gcc cgc ggc cac ggc gcc acc ggc cag atc cgc cca Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr Gly Gln Ile Arg Pro 90 95 100			403
gag ctc tgc acc atc gaa gga aca gcg aac gat gtt ctc gca gcc atc Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp Val Leu Ala Ala Ile 105 110 115			451
cac gaa cac gca ccg acc ggc ccg ctc att ttg gtt ggg cat tcc ctc His Glu His Ala Pro Thr Gly Pro Leu Ile Leu Val Gly His Ser Leu 120 125 130			499
ggc gga ctc acg gca ctt aac ctg gtt aaa cgg gca gat cac tca ctt Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg Ala Asp His Ser Leu 135 140 145			547
cgg aag agg atc gtc ggc atg gtt cta gtc gcc aca tcg atc gaa tca Arg Lys Arg Ile Val Gly Met Val Leu Val Ala Thr Ser Ile Glu Ser 150 155 160 165			595
tta tcc acc caa ggt cta cca caa gtc ctg gca tca ccc ctt gcc gac Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala Ser Pro Leu Ala Asp 170 175 180			643
aac atc aaa aac gcc gtc gaa gca gcc ccc aac gat gcc caa aaa ttc Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn Asp Ala Gln Lys Phe 185 190 195			691
cgc caa tac gcc acc aca ttt cta gcc ccc acc ctg gcc acc gca gtc Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr Leu Ala Thr Ala Val 200 205 210			739
ttc caa cga gac aca aac gat gaa gtc atc gat ttc cac gcc gcc atg Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp Phe His Ala Ala Met 215 220 225			787
atc cac gaa acc ccc ttg gat acc ttc gtc ggt ttc ttc gac gac ctc Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly Phe Phe Asp Asp Leu 230 235 240 245			835
caa gaa cac gac gaa ctc gat gcc gca cca gca ttg gaa ggc ctc aaa Gln Glu His Asp Glu Leu Asp Ala Ala Pro Ala Leu Glu Gly Leu Lys 250 255 260			883
ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca att agc caa Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro Ile Ser Gln 265 270 275			931
gcc gac cgc atc tgc gaa gtc tgg ccc ggc gca cgc ctt caa atc gca Ala Asp Arg Ile Cys Glu Val Trp Pro Gly Ala Arg Leu Gln Ile Ala 280 285 290			979

gaa gga gca ggt cat atg ctt ccg ctt gaa gcg cca gga atc ctc aat 1027
 Glu Gly Ala Gly His Met Leu Pro Leu Glu Ala Pro Gly Ile Leu Asn
 295 300 305

aat gcg atc ggc aac att ttg gac ggg ctg ggc tgaggaacct ggttcgggacg 1080
 Asn Ala Ile Gly Asn Ile Leu Asp Gly Leu Gly
 310 315 320

tgg 1083

<210> 260

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Thr Pro Asn Gly Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala
 1 5 10 15

Phe Ser Lys Asn Arg Thr Pro Gly Leu Lys His Val Asp Arg His Thr
 20 25 30

Ile Val Asp Ser Asp Gly Leu Ser Ile His Thr Tyr Met Val Gly His
 35 40 45

Ala Glu Asn Ala Thr Ala Thr Val Val Phe Ile His Gly Phe Thr Leu
 50 55 60

Ala Ala Glu Val Tyr Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr
 65 70 75 80

Pro Asn Ile Lys Ser Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr
 85 90 95

Gly Gln Ile Arg Pro Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp
 100 105 110

Val Leu Ala Ala Ile His Glu His Ala Pro Thr Gly Pro Leu Ile Leu
 115 120 125

Val Gly His Ser Leu Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg
 130 135 140

Ala Asp His Ser Leu Arg Lys Arg Ile Val Gly Met Val Leu Val Ala
 145 150 155 160

Thr Ser Ile Glu Ser Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala
 165 170 175

Ser Pro Leu Ala Asp Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn
 180 185 190

Asp Ala Gln Lys Phe Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr
 195 200 205

Leu Ala Thr Ala Val Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp
 210 215 220

Phe His Ala Ala Met Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly

225		230		235		240									
Phe	Phe	Asp	Asp	Leu	Gln	Glu	His	Asp	Glu	Leu	Asp	Ala	Ala	Pro	Ala
				245					250					255	
Leu	Glu	Gly	Leu	Lys	Gly	Tyr	Val	Leu	Ala	Gly	Glu	Leu	Asp	Asp	Val
			260					265					270		
Thr	Pro	Ile	Ser	Gln	Ala	Asp	Arg	Ile	Cys	Glu	Val	Trp	Pro	Gly	Ala
		275					280					285			
Arg	Leu	Gln	Ile	Ala	Glu	Gly	Ala	Gly	His	Met	Leu	Pro	Leu	Glu	Ala
	290					295					300				
Pro	Gly	Ile	Leu	Asn	Asn	Ala	Ile	Gly	Asn	Ile	Leu	Asp	Gly	Leu	Gly
305				310						315				320	

<210> 261
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXN01145

<400> 261
 taatgtagtt gtctgcccaa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaatttttac gaaaggcgag atttttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307
 Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	
gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc	1027
Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser	
295 300 305	
tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc	1075
Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu	
310 315 320 325	
atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagttttcac	1124
Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala	
330 335	

ccctttgacg gct

1137

<210> 262

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
 145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
 165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
 180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205

Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220

Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240

Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270

Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe

275	280	285
Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu		
290	295	300
Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala		
305	310	315
Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu		
325	330	335
Thr Ala		

<210> 263
 <211> 487
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(487)
 <223> RXN03088

<400> 263
 tcatggcacc gggacctggc atcgtagcta aggtttcttt tgatgatttc tccgacgtca 60
 ccggcggcga tgaactcctc gaattggagg caaagaacta atg ggt caa acc cgc 115
 Met Gly Gln Thr Arg
 1 5
 atc att tcc ggc gac gca cgc ggc cgc aag atc gaa gta cca cca gca 163
 Ile Ile Ser Gly Asp Ala Arg Gly Arg Lys Ile Glu Val Pro Pro Ala
 10 15 20
 ggt acc cgc ccc acc tct gac cgc gca cgc gaa ggt ctc ttc tcc tca 211
 Gly Thr Arg Pro Thr Ser Asp Arg Ala Arg Glu Gly Leu Phe Ser Ser
 25 30 35
 ctg cag gtc cgt ttc gga ttt gag ggc cag cgc gtc ctc gac att ttt 259
 Leu Gln Val Arg Phe Gly Phe Glu Gly Gln Arg Val Leu Asp Ile Phe
 40 45 50
 gcc ggc tcc ggc gca ctc gga ttg gaa gct gcc tcc agg ggt gcc gat 307
 Ala Gly Ser Gly Ala Leu Gly Leu Glu Ala Ala Ser Arg Gly Ala Asp
 55 60 65
 gag gta gtt ctg gtc gag tcg aat cct aag gcc gta gag gta att cga 355
 Glu Val Val Leu Val Glu Ser Asn Pro Lys Ala Val Glu Val Ile Arg
 70 75 80 85
 cgg aat gtg gac gtc gta aag cat cct cgc gta acc gtc gca gag atg 403
 Arg Asn Val Asp Val Val Lys His Pro Arg Val Thr Val Ala Glu Met
 90 95 100
 aaa gca tcc acc tac ctt gcg tcc gca ccc gat aag ttt ttc acg atg 451
 Lys Ala Ser Thr Tyr Leu Ala Ser Ala Pro Asp Lys Phe Phe Thr Met
 105 110 115
 gtg ctc gcc gac ccg ccc tat gag ctt gcg acg acg 487

Val Leu Ala Asp Pro Pro Tyr Glu Leu Ala Thr Thr
120 125

<210> 264

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Gly Gln Thr Arg Ile Ile Ser Gly Asp Ala Arg Gly Arg Lys Ile
1 5 10 15

Glu Val Pro Pro Ala Gly Thr Arg Pro Thr Ser Asp Arg Ala Arg Glu
20 25 30

Gly Leu Phe Ser Ser Leu Gln Val Arg Phe Gly Phe Glu Gly Gln Arg
35 40 45

Val Leu Asp Ile Phe Ala Gly Ser Gly Ala Leu Gly Leu Glu Ala Ala
50 55 60

Ser Arg Gly Ala Asp Glu Val Val Leu Val Glu Ser Asn Pro Lys Ala
65 70 75 80

Val Glu Val Ile Arg Arg Asn Val Asp Val Val Lys His Pro Arg Val
85 90 95

Thr Val Ala Glu Met Lys Ala Ser Thr Tyr Leu Ala Ser Ala Pro Asp
100 105 110

Lys Phe Phe Thr Met Val Leu Ala Asp Pro Pro Tyr Glu Leu Ala Thr
115 120 125

Thr

<210> 265

<211> 639

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(616)

<223> RXN02952

<400> 265

tccaaaccgc tgtttctgct cgtggcgaat cctggatatt gaagtaattg aaatccgaga 60

cctgatcttt gatctcgcta cctcattcac aagcgccggc atg agc tcc cca gca 115
Met Ser Ser Pro Ala
1 5

ctt gac gct gca aaa cag cgc ctt gct gaa tcc gat ggc ctg atc gct 163
Leu Asp Ala Ala Lys Gln Arg Leu Ala Glu Ser Asp Gly Leu Ile Ala
10 15 20

gtt acc cca gta ttt acc gcg agc tac tcc ggc atc ttc aag atg ttc 211
Val Thr Pro Val Phe Thr Ala Ser Tyr Ser Gly Ile Phe Lys Met Phe

25										30					35					
ttt gat gtc ctg gac ccc aag acc att gtg ggt ctg ccc acc atc att	259																			
Phe Asp Val Leu Asp Pro Lys Thr Ile Val Gly Leu Pro Thr Ile Ile																				
40 45 50																				
gcg gca tct gct gga acg gca cgc cac tca ttg gtt ctc gac cac gcc	307																			
Ala Ala Ser Ala Gly Thr Ala Arg His Ser Leu Val Leu Asp His Ala																				
55 60 65																				
atc cga cca ctg ttt acc tac ttg cga gca gtt gtc gta ccc acc ggc	355																			
Ile Arg Pro Leu Phe Thr Tyr Leu Arg Ala Val Val Val Pro Thr Gly																				
70 75 80 85																				
gtg ttc gca gcc acg gaa gat ttc ggc act gaa gct ggc gca gac att	403																			
Val Phe Ala Ala Thr Glu Asp Phe Gly Thr Glu Ala Gly Ala Asp Ile																				
90 95 100																				
gaa cgt cgc gtg aac cgc gca gct ggc gaa tta gcg aca ctc atg ttg	451																			
Glu Arg Arg Val Asn Arg Ala Ala Gly Glu Leu Ala Thr Leu Met Leu																				
105 110 115																				
cag gat tac tcc agt gtg caa ggc ctt ggg ggc gca acc gcg aac caa	499																			
Gln Asp Tyr Ser Ser Val Gln Gly Leu Gly Gly Ala Thr Ala Asn Gln																				
120 125 130																				
gac gct gac ctt tcc ttc cgt cgc acc act ggc gtg acc ccg gga gag	547																			
Asp Ala Asp Leu Ser Phe Arg Arg Thr Thr Gly Val Thr Pro Gly Glu																				
135 140 145																				
aac ttc agc agc ttt gcc gat ctt tct caa agg aca cga cgg aaa cgg	595																			
Asn Phe Ser Ser Phe Ala Asp Leu Ser Gln Arg Thr Arg Arg Lys Arg																				
150 155 160 165																				
cta aat tcg cgg atc tcc gtt taaggcattg aagcatttgg agg	639																			
Leu Asn Ser Arg Ile Ser Val																				
170																				

<210> 266

<211> 172

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Met Ser Ser Pro Ala Leu Asp Ala Ala Lys Gln Arg Leu Ala Glu Ser	1 5 10 15
Asp Gly Leu Ile Ala Val Thr Pro Val Phe Thr Ala Ser Tyr Ser Gly	20 25 30
Ile Phe Lys Met Phe Phe Asp Val Leu Asp Pro Lys Thr Ile Val Gly	35 40 45
Leu Pro Thr Ile Ile Ala Ala Ser Ala Gly Thr Ala Arg His Ser Leu	50 55 60
Val Leu Asp His Ala Ile Arg Pro Leu Phe Thr Tyr Leu Arg Ala Val	65 70 75 80
Val Val Pro Thr Gly Val Phe Ala Ala Thr Glu Asp Phe Gly Thr Glu	

85										90					95															
Ala	Gly	Ala	Asp	Ile	Glu	Arg	Arg	Val	Asn	Arg	Ala	Ala	Gly	Glu	Leu															
			100					105					110																	
Ala	Thr	Leu	Met	Leu	Gln	Asp	Tyr	Ser	Ser	Val	Gln	Gly	Leu	Gly	Gly															
		115					120					125																		
Ala	Thr	Ala	Asn	Gln	Asp	Ala	Asp	Leu	Ser	Phe	Arg	Arg	Thr	Thr	Gly															
		130				135					140																			
Val	Thr	Pro	Gly	Glu	Asn	Phe	Ser	Ser	Phe	Ala	Asp	Leu	Ser	Gln	Arg															
		145			150					155					160															
Thr	Arg	Arg	Lys	Arg	Leu	Asn	Ser	Arg	Ile	Ser	Val																			
				165					170																					

<210> 267
 <211> 1044
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1021)
 <223> RXN00513

<400> 267
 cacagcgtac gcacgagctt gaggatcttt cagaactcaa cattgaattg gatgccgata 60

ttttggccaa ggctcctgtg attccggaag gactgttctg atg gcg ggt ttg ttt 115
 Met Ala Gly Leu Phe
 1 5

tcc tct gct gtt gca cca acg gag cgt cga aaa gca tta cgc gcg gca 163
 Ser Ser Ala Val Ala Pro Thr Glu Arg Arg Lys Ala Leu Arg Ala Ala
 10 15 20

ctg gct gcg cct gaa att gcc cgc atg cct ggt gca ttc tcc ccg ctg 211
 Leu Ala Ala Pro Glu Ile Ala Arg Met Pro Gly Ala Phe Ser Pro Leu
 25 30 35

gcg gcg cgc gca atc cag gaa gcc gga ttt gaa ggc gtg tac gtc tcg 259
 Ala Ala Arg Ala Ile Gln Glu Ala Gly Phe Glu Gly Val Tyr Val Ser
 40 45 50

ggc gcc gtc gtg gcg gct gac ctt gca ttg ccg gat atc ggc ttg acc 307
 Gly Ala Val Val Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr
 55 60 65

aca ttg acc gaa gtg gcg cac cgc tcc cgg cag atc gca cgc gtg aca 355
 Thr Leu Thr Glu Val Ala His Arg Ser Arg Gln Ile Ala Arg Val Thr
 70 75 80 85

gac ttg ccc gtg ctg gtc gac gcc gac acc ggc ttc ggc gaa ccc atg 403
 Asp Leu Pro Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met
 90 95 100

tcc gca gcg cgc acc gtc tcc gaa ctc gaa gat gca ggt gtc gcg ggc 451
 Ser Ala Ala Arg Thr Val Ser Glu Leu Glu Asp Ala Gly Val Ala Gly

105	110	115	
tgc cac ctg gaa gat caa gtc aac ccc aaa cgc tgt ggg cac ctg gac			499
Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys Gly His Leu Asp			
120	125	130	
gga aaa gaa gta gtg ggc acg gac atc atg gtt cgt cgc atc gcc gca			547
Gly Lys Glu Val Val Gly Thr Asp Ile Met Val Arg Arg Ile Ala Ala			
135	140	145	
gct gtc aac gag cgt cgc gat gag caa ttc gtc atc tgc gct cgc acc			595
Ala Val Asn Glu Arg Arg Asp Glu Gln Phe Val Ile Cys Ala Arg Thr			
150	155	160	165
gac gcc gcg gga gtg gaa ggc atc gac tcc gcg atc gag cgc gcc aaa			643
Asp Ala Ala Gly Val Glu Gly Ile Asp Ser Ala Ile Glu Arg Ala Lys			
	170	175	180
gct tac gcg gat gcc ggc gcc gac atg atc ttc acc gaa gcg ctg tac			691
Ala Tyr Ala Asp Ala Gly Ala Asp Met Ile Phe Thr Glu Ala Leu Tyr			
	185	190	195
agc cct gca gat ttt gaa aaa ttc cgc gcg gcc gtc gac att ccg ctg			739
Ser Pro Ala Asp Phe Glu Lys Phe Arg Ala Ala Val Asp Ile Pro Leu			
	200	205	210
ctg gcc aac atg acg gaa ttt ggc aaa acc gaa ctt ctg ccc gcg cag			787
Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Glu Leu Leu Pro Ala Gln			
	215	220	225
ctt ctg gaa gac atc gga tac aac gca gtg atc tac cca gtg acc ctg			835
Leu Leu Glu Asp Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Leu			
230	235	240	245
ctg cgc att gcg atg gga cag gtc gaa caa gct ctc ggc gac att gca			883
Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Gly Asp Ile Ala			
	250	255	260
aac acc gga atc caa acc gac tgg gtc gac cgg atg caa cac cga tcc			931
Asn Thr Gly Ile Gln Thr Asp Trp Val Asp Arg Met Gln His Arg Ser			
	265	270	275
agg ctg tat gag ctg ctg cgc tac aac gag tac aac gct ttc gac cag			979
Arg Leu Tyr Glu Leu Leu Arg Tyr Asn Glu Tyr Asn Ala Phe Asp Gln			
	280	285	290
caa gta ttc acc tat tcc gct gac agc tac aag ccc atc ttc			1021
Gln Val Phe Thr Tyr Ser Ala Asp Ser Tyr Lys Pro Ile Phe			
	295	300	305
taacccgcct atatataagg agt			1044

<210> 268

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met	Ala	Gly	Leu	Phe	Ser	Ser	Ala	Val	Ala	Pro	Thr	Glu	Arg	Arg	Lys
1					5				10						15

Ala Leu Arg Ala Ala Leu Ala Ala Pro Glu Ile Ala Arg Met Pro Gly
 20 25 30
 Ala Phe Ser Pro Leu Ala Ala Arg Ala Ile Gln Glu Ala Gly Phe Glu
 35 40 45
 Gly Val Tyr Val Ser Gly Ala Val Val Ala Ala Asp Leu Ala Leu Pro
 50 55 60
 Asp Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ser Arg Gln
 65 70 75 80
 Ile Ala Arg Val Thr Asp Leu Pro Val Leu Val Asp Ala Asp Thr Gly
 85 90 95
 Phe Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ser Glu Leu Glu Asp
 100 105 110
 Ala Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg
 115 120 125
 Cys Gly His Leu Asp Gly Lys Glu Val Val Gly Thr Asp Ile Met Val
 130 135 140
 Arg Arg Ile Ala Ala Ala Val Asn Glu Arg Arg Asp Glu Gln Phe Val
 145 150 155 160
 Ile Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ser Ala
 165 170 175
 Ile Glu Arg Ala Lys Ala Tyr Ala Asp Ala Gly Ala Asp Met Ile Phe
 180 185 190
 Thr Glu Ala Leu Tyr Ser Pro Ala Asp Phe Glu Lys Phe Arg Ala Ala
 195 200 205
 Val Asp Ile Pro Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Glu
 210 215 220
 Leu Leu Pro Ala Gln Leu Leu Glu Asp Ile Gly Tyr Asn Ala Val Ile
 225 230 235 240
 Tyr Pro Val Thr Leu Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala
 245 250 255
 Leu Gly Asp Ile Ala Asn Thr Gly Ile Gln Thr Asp Trp Val Asp Arg
 260 265 270
 Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Asn Glu Tyr
 275 280 285
 Asn Ala Phe Asp Gln Gln Val Phe Thr Tyr Ser Ala Asp Ser Tyr Lys
 290 295 300
 Pro Ile Phe
 305

<210> 269

<211> 957

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(934)

<223> RXN01152

<400> 269

```

agtgaaggat ctgatgtggt ttgaacaagc cctggaagcc tatctggtaa attaacgccg 60

agttcaatca agacaagcac acagaagaaa gtgagggctc atg ccc tac tca ggt 115
                               Met Pro Tyr Ser Gly
                               1           5

ccg ttc caa gca ggc gac cgc gtt cag ctc acc gac gct aaa cgc cgc 163
Pro Phe Gln Ala Gly Asp Arg Val Gln Leu Thr Asp Ala Lys Arg Arg
                               10           15           20

cat ttc acc atc att ttg gaa cca gga acc acc tac cac acc cac cgt 211
His Phe Thr Ile Ile Leu Glu Pro Gly Thr Thr Tyr His Thr His Arg
                               25           30           35

gga caa atc gca cac gat gac atc atc ggc gcc gat gag ggc act gtt 259
Gly Gln Ile Ala His Asp Asp Ile Ile Gly Ala Asp Glu Gly Thr Val
                               40           45           50

gtc cac tcc acc atg ggc tct gat tac ttg tgc ttc cgt cac ctc atg 307
Val His Ser Thr Met Gly Ser Asp Tyr Leu Cys Phe Arg His Leu Met
                               55           60           65

gtt gat cac gtg ctg agc atg cct cgt ggc gct gca gtt att tat cca 355
Val Asp His Val Leu Ser Met Pro Arg Gly Ala Ala Val Ile Tyr Pro
                               70           75           80           85

aag gac tct gca cag att ctg gtc gag ggc gat att ttc cct ggc gcc 403
Lys Asp Ser Ala Gln Ile Leu Val Glu Gly Asp Ile Phe Pro Gly Ala
                               90           95           100

cga gtt ctg gaa gct ggc gct ggt tcc ggt gca ctg tcc atg gcg ctg 451
Arg Val Leu Glu Ala Gly Ala Gly Ser Gly Ala Leu Ser Met Ala Leu
                               105           110           115

ctt cgt gca gtg ggt gaa aag ggc aat gtc atc tcc tac gaa atc cgt 499
Leu Arg Ala Val Gly Glu Lys Gly Asn Val Ile Ser Tyr Glu Ile Arg
                               120           125           130

gag gat cac ctg gag tac gca gtc tcc aac gtg gag gag tac ttc ggt 547
Glu Asp His Leu Glu Tyr Ala Val Ser Asn Val Glu Glu Tyr Phe Gly
                               135           140           145

gag cgt cca gca acc tgg gat cca cgt ctt ggt gac ctg aaa gaa gtc 595
Glu Arg Pro Ala Thr Trp Asp Pro Arg Leu Gly Asp Leu Lys Glu Val
                               150           155           160           165

acc gtt gag gat ctc ggc gga cct gtt gac cgc atc atc ttg gat atg 643
Thr Val Glu Asp Leu Gly Gly Pro Val Asp Arg Ile Ile Leu Asp Met
                               170           175           180

ctt gag ccg tgg gaa atg ctg gag acc tgc aag gat ctt ctc atc cct 691
Leu Glu Pro Trp Glu Met Leu Glu Thr Cys Lys Asp Leu Leu Ile Pro

```

185					190					195						
ggt	ggt	gtg	ttt	atg	acg	tat	gtg	gcg	acc	gtg	cca	cag	ctg	atg	aag	739
Gly	Gly	Val	Phe	Met	Thr	Tyr	Val	Ala	Thr	Val	Pro	Gln	Leu	Met	Lys	
200					205					210						
gtc	atg	gaa	ggc	atc	cgc	gag	caa	aaa	tgc	ttc	acg	gag	cca	cgc	gcg	787
Val	Met	Glu	Gly	Ile	Arg	Glu	Gln	Lys	Cys	Phe	Thr	Glu	Pro	Arg	Ala	
215					220					225						
tgg	gaa	tct	ttg	gtt	cgt	gat	tgg	aag	gtg	gag	ggc	ttg	gca	aca	cgc	835
Trp	Glu	Ser	Leu	Val	Arg	Asp	Trp	Lys	Val	Glu	Gly	Leu	Ala	Thr	Arg	
230					235					240					245	
cct	gag	cac	cgc	atg	aat	gcc	cac	acc	gcg	ttc	ttg	gtg	ttg	acc	agg	883
Pro	Glu	His	Arg	Met	Asn	Ala	His	Thr	Ala	Phe	Leu	Val	Leu	Thr	Arg	
250					255					260						
cgt	ttg	gct	gat	ggc	gtg	gag	cct	cct	cgt	ccg	cag	cgt	aag	gca	cgt	931
Arg	Leu	Ala	Asp	Gly	Val	Glu	Pro	Pro	Arg	Pro	Gln	Arg	Lys	Ala	Arg	
265					270					275						
cga	taaaaagacc tagttggagg gcg														957	
Arg																

<210> 270

<211> 278

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 270

Met	Pro	Tyr	Ser	Gly	Pro	Phe	Gln	Ala	Gly	Asp	Arg	Val	Gln	Leu	Thr
1				5					10					15	
Asp	Ala	Lys	Arg	Arg	His	Phe	Thr	Ile	Ile	Leu	Glu	Pro	Gly	Thr	Thr
			20					25					30		
Tyr	His	Thr	His	Arg	Gly	Gln	Ile	Ala	His	Asp	Asp	Ile	Ile	Gly	Ala
		35					40					45			
Asp	Glu	Gly	Thr	Val	Val	His	Ser	Thr	Met	Gly	Ser	Asp	Tyr	Leu	Cys
	50					55					60				
Phe	Arg	His	Leu	Met	Val	Asp	His	Val	Leu	Ser	Met	Pro	Arg	Gly	Ala
65					70					75					80
Ala	Val	Ile	Tyr	Pro	Lys	Asp	Ser	Ala	Gln	Ile	Leu	Val	Glu	Gly	Asp
				85					90					95	
Ile	Phe	Pro	Gly	Ala	Arg	Val	Leu	Glu	Ala	Gly	Ala	Gly	Ser	Gly	Ala
		100					105						110		
Leu	Ser	Met	Ala	Leu	Leu	Arg	Ala	Val	Gly	Glu	Lys	Gly	Asn	Val	Ile
		115					120					125			
Ser	Tyr	Glu	Ile	Arg	Glu	Asp	His	Leu	Glu	Tyr	Ala	Val	Ser	Asn	Val
	130					135					140				
Glu	Glu	Tyr	Phe	Gly	Glu	Arg	Pro	Ala	Thr	Trp	Asp	Pro	Arg	Leu	Gly

<400> 271																	
ccagcccgcc caataaataa tttctctctt ctaattgcgg agcctcatat attgagtacg															60		
gtattttgaa acaccttcag cccctttttt aggagccaca															gtg tct cag cct ctc	115	
															Val Ser Gln Pro Leu		
															1	5	
agc aag cgt ctc agc ata cga aaa gca ctc gcc agc gcc ttc ata gtt															163		
Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala Ser Ala Phe Ile Val																	
															10	15	20
gcg ctg gcg ttt tcg ctt tcc cca gta gcc aaa gcc caa gcc aat gaa															211		
Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys Ala Gln Ala Asn Glu																	
															25	30	35
act ccg acg atg atc gtg ttg gac aat tca ggc tcc atg aca gct caa															259		
Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly Ser Met Thr Ala Gln																	
															40	45	50
gat gcc ggc gga cag acc cgt atc gat gca gca aaa caa gcc tcc act															307		
Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala Lys Gln Ala Ser Thr																	
															55	60	65
cag tta att aat gac atc tcc gac cgc acc gac qta qqt ctg acc tac															355		

Gln	Leu	Ile	Asn	Asp	Ile	Ser	Asp	Arg	Thr	Asp	Val	Gly	Leu	Thr	Tyr	
70					75					80					85	
tac	ggc	gga	aac	acc	ggc	gaa	aca	gaa	gca	gac	gtt	gag	atg	gga	tgc	403
Tyr	Gly	Gly	Asn	Thr	Gly	Glu	Thr	Glu	Ala	Asp	Val	Glu	Met	Gly	Cys	
			90					95						100		
caa	gac	gtc	acc	atc	ctt	ggc	ggc	ccc	tcc	cga	gga	aat	gca	gac	acc	451
Gln	Asp	Val	Thr	Ile	Leu	Gly	Gly	Pro	Ser	Arg	Gly	Asn	Ala	Asp	Thr	
			105					110					115			
tta	att	gac	acg	atc	aac	agc	ctg	cag	cct	cga	ggc	ttc	acc	ccc	atc	499
Leu	Ile	Asp	Thr	Ile	Asn	Ser	Leu	Gln	Pro	Arg	Gly	Phe	Thr	Pro	Ile	
		120					125					130				
ggc	aaa	gca	ctc	acc	gat	acc	gcc	gcc	gag	ctc	ccc	gaa	ggc	gga	aac	547
Gly	Lys	Ala	Leu	Thr	Asp	Thr	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Gly	Asn	
	135					140					145					
att	gtg	ttg	gtc	tcc	gat	ggc	atc	gcc	aac	tgc	acc	cca	ccg	gat	gtc	595
Ile	Val	Leu	Val	Ser	Asp	Gly	Ile	Ala	Asn	Cys	Thr	Pro	Pro	Asp	Val	
150					155					160					165	
tgc	gaa	gta	gcc	caa	gaa	ctg	gct	caa	agt	gga	atc	aac	ctg	gtt	atc	643
Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly	Ile	Asn	Leu	Val	Ile	
				170					175					180		
aac	acc	atc	gga	cta	aat	gtt	gat	cca	gca	gcg	cgc	gaa	gaa	ctg	gag	691
Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala	Arg	Glu	Glu	Leu	Glu	
			185					190					195			
tgc	atc	gct	gga	gtc	ggc	ggc	ggc	act	tac	gcg	gat	gct	tcc	gac	gcg	739
Cys	Ile	Ala	Gly	Val	Gly	Gly	Gly	Thr	Tyr	Ala	Asp	Ala	Ser	Asp	Ala	
		200				205						210				
cag	agc	ctt	acc	gat	gcg	ctg	aca	cga	gcc	gcc	agt	agg	caa	tac	aac	787
Gln	Ser	Leu	Thr	Asp	Ala	Leu	Thr	Arg	Ala	Ala	Ser	Arg	Gln	Tyr	Asn	
		215				220					225					
tct	tac	acc	tcc	gat	gtg	aca	aaa	att	gat	ggg	gca	tcg	gaa	caa	agc	835
Ser	Tyr	Thr	Ser	Asp	Val	Thr	Lys	Ile	Asp	Gly	Ala	Ser	Glu	Gln	Ser	
230					235					240					245	
gca	gcc	gta	gaa	att	gat	gag	gat	aca	gaa	cta	ttc	ctc	acc	gac	ctg	883
Ala	Ala	Val	Glu	Ile	Asp	Glu	Asp	Thr	Glu	Leu	Phe	Leu	Thr	Asp	Leu	
				250					255					260		
cca	caa	gaa	tcc	cgc	ttt	tgg	aaa	atc	cct	gta	gag	cca	ggc	gaa	acc	931
Pro	Gln	Glu	Ser	Arg	Phe	Trp	Lys	Ile	Pro	Val	Glu	Pro	Gly	Glu	Thr	
			265					270					275			
atc	tca	gtt	tct	gcc	aac	aca	gtt	acc	gac	cca	aca	gta	ctc	acc	atg	979
Ile	Ser	Val	Ser	Ala	Asn	Thr	Val	Thr	Asp	Pro	Thr	Val	Leu	Thr	Met	
		280					285					290				
ggg	caa	ggc	gga	atc	aag	ctt	gaa	gcc	caa	ctc	cat	act	gaa	gag	gct	1027
Gly	Gln	Gly	Gly	Ile	Lys	Leu	Glu	Ala	Gln	Leu	His	Thr	Glu	Glu	Ala	
	295					300					305					
cca	caa	tac	ggc	ctg	cgt	ggc	cgg	tgc	act	cgg	gtc	tca	ttt	gat	aat	1075
Pro	Gln	Tyr	Gly	Leu	Arg	Gly	Arg	Cys	Thr	Arg	Val	Ser	Phe	Asp	Asn	

310	315	320	325	
ttc aag ccc ggc ctt ggt gta cgc gga atc caa aac gcg tcc gtt gca				1123
Phe Lys Pro Gly Leu Gly Val Arg Gly Ile Gln Asn Ala Ser Val Ala				
	330	335	340	
tca aaa gaa gtg ggc acc aac aac tgt gac acc gat gcc atc tac ctc				1171
Ser Lys Glu Val Gly Thr Asn Asn Cys Asp Thr Asp Ala Ile Tyr Leu				
	345	350	355	
gaa att tct aga agc gga gat tac ctc aac ggg cag gac att cca acg				1219
Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn Gly Gln Asp Ile Pro Thr				
	360	365	370	
gaa atc acc atc gag cgc ttc gga aaa gta gat gaa tca aca atc gga				1267
Glu Ile Thr Ile Glu Arg Phe Gly Lys Val Asp Glu Ser Thr Ile Gly				
	375	380	385	
aat gtc aca gag gaa cat agc tcc gtc gat ctt acc gag gct gca gca				1315
Asn Val Thr Glu Glu His Ser Ser Val Asp Leu Thr Glu Ala Ala Ala				
	390	395	400	405
tca gag gca cac cct gtc aca cct ggc cag tgg ttc aca tcg gcc gct				1363
Ser Glu Ala His Pro Val Thr Pro Gly Gln Trp Phe Thr Ser Ala Ala				
	410	415	420	
gat cta gat ccc gca ggt gag aaa gtc tcc tcc atc atc gtt cca gga				1411
Asp Leu Asp Pro Ala Gly Glu Lys Val Ser Ser Ile Ile Val Pro Gly				
	425	430	435	
gaa acc cac ttc tat gcg ctg cct gtc gac tac ggc caa gaa ctg cgc				1459
Glu Thr His Phe Tyr Ala Leu Pro Val Asp Tyr Gly Gln Glu Leu Arg				
	440	445	450	
gca gct gta gaa aca act ttt gac caa atc gac agt tcc gcg ctt ggc				1507
Ala Ala Val Glu Thr Thr Phe Asp Gln Ile Asp Ser Ser Ala Leu Gly				
	455	460	465	
acg cat ctt tat atc caa gcg ttc agc cca aac cgg gca gag ata gag				1555
Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn Arg Ala Glu Ile Glu				
	470	475	480	485
ctc acc aat aga gat acg tca tat gcg gac gac aac ggg ctc aaa act				1603
Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp Asn Gly Leu Lys Thr				
	490	495	500	
ttt gga ttc ttc acc cca gtg agt gca gca aat ttg ttc gag aaa agt				1651
Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn Leu Phe Glu Lys Ser				
	505	510	515	
tct caa ggc ata tcg cta agg agc cca tgg caa ggt ggc acc caa tac				1699
Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln Gly Gly Thr Gln Tyr				
	520	525	530	
ctc gca gtg aca tac cta cca agt ggt caa gat gaa gat gta tcc gca				1747
Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp Glu Asp Val Ser Ala				
	535	540	545	
act gat cag ctg ccc aca ttg gaa tat gaa ctc gtg gca gaa gcg ttt				1795
Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu Val Ala Glu Ala Phe				
	550	555	560	565

gga gac cct gtt gac cca ccg gtt ttc gct tca ttg acg gga gca acc 1843
Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser Leu Thr Gly Ala Thr
570 575 580

cca agc acc tcc acc ccc cca tca gat gtt gcg gaa gat gaa caa atc 1891
Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala Glu Asp Glu Gln Ile
585 590 595

tcc gag gca aca gaa gaa gac tca agc agt ttc ccc atc gtg tgg att 1939
Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe Pro Ile Val Trp Ile
600 605 610

ggg ctg ggt gtc att ggc tta ggc ata atc att ggt ttg atc ttt gcg 1987
Gly Leu Gly Val Ile Gly Leu Gly Ile Ile Ile Gly Leu Ile Phe Ala
615 620 625

ctg aga aga aag aat taagccctaa aagataaaga gtc 2025
Leu Arg Arg Lys Asn
630

<210> 272

<211> 634

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 272

Val Ser Gln Pro Leu Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala
1 5 10 15

Ser Ala Phe Ile Val Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys
20 25 30

Ala Gln Ala Asn Glu Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly
35 40 45

Ser Met Thr Ala Gln Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala
50 55 60

Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
65 70 75 80

Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
85 90 95

Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
100 105 110

Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg
115 120 125

Gly Phe Thr Pro Ile Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu
130 135 140

Pro Glu Gly Gly Asn Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys
145 . 150 155 . 160

Thr Pro Pro Asp Val Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly
165 170 175

Ile Asn Leu Val Ile Asn Thr Ile Gly Leu Asn Val Asp Pro Ala Ala
 180 185 190
 Arg Glu Glu Leu Glu Cys Ile Ala Gly Val Gly Gly Gly Thr Tyr Ala
 195 200 205
 Asp Ala Ser Asp Ala Gln Ser Leu Thr Asp Ala Leu Thr Arg Ala Ala
 210 215 220
 Ser Arg Gln Tyr Asn Ser Tyr Thr Ser Asp Val Thr Lys Ile Asp Gly
 225 230 235 240
 Ala Ser Glu Gln Ser Ala Ala Val Glu Ile Asp Glu Asp Thr Glu Leu
 245 250 255
 Phe Leu Thr Asp Leu Pro Gln Glu Ser Arg Phe Trp Lys Ile Pro Val
 260 265 270
 Glu Pro Gly Glu Thr Ile Ser Val Ser Ala Asn Thr Val Thr Asp Pro
 275 280 285
 Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln Leu
 290 295 300
 His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr Arg
 305 310 315 320
 Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile Gln
 325 330 335
 Asn Ala Ser Val Ala Ser Lys Glu Val Gly Thr Asn Asn Cys Asp Thr
 340 345 350
 Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn Gly
 355 360 365
 Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val Asp
 370 375 380
 Glu Ser Thr Ile Gly Asn Val Thr Glu Glu His Ser Ser Val Asp Leu
 385 390 395 400
 Thr Glu Ala Ala Ala Ser Glu Ala His Pro Val Thr Pro Gly Gln Trp
 405 410 415
 Phe Thr Ser Ala Ala Asp Leu Asp Pro Ala Gly Glu Lys Val Ser Ser
 420 425 430
 Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp Tyr
 435 440 445
 Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile Asp
 450 455 460
 Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn
 465 470 475 480
 Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp
 485 490 495
 Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn

500 505 510
 Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln
 515 520 525
 Gly Gly Thr Gln Tyr Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp
 530 535 540
 Glu Asp Val Ser Ala Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu
 545 550 555 560
 Val Ala Glu Ala Phe Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser
 565 570 575
 Leu Thr Gly Ala Thr Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala
 580 585 590
 Glu Asp Glu Gln Ile Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe
 595 600 605
 Pro Ile Val Trp Ile Gly Leu Gly Val Ile Gly Leu Gly Ile Ile Ile
 610 615 620
 Gly Leu Ile Phe Ala Leu Arg Arg Lys Asn
 625 630

<210> 273
 <211> 576
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(553)
 <223> RXN01302

<400> 273
 tggggctgcg tgggtgttctt catcatcgcc accgctttga cctggatcta ctacgcccgc 60
 ccgaacgctc cattcccggg ataaaccgaa aggccaatcc atg act aca act act 115
 Met Thr Thr Thr Thr
 1 5
 tct tct ggg aag tct tct gaa aag atc aac ccc ctc ttc aag ctc ggc 163
 Ser Ser Gly Lys Ser Ser Glu Lys Ile Asn Pro Leu Phe Lys Leu Gly
 10 15 20
 agt ttc cta aga aaa ggc acc gtc ggt tct gaa ggc cag cag att ttc 211
 Ser Phe Leu Arg Lys Gly Thr Val Gly Ser Glu Gly Gln Gln Ile Phe
 25 30 35
 ctt cag ggc gga cgc caa gcc gat gtg ttt tat cgc aac cga tgg gct 259
 Leu Gln Gly Gly Arg Gln Ala Asp Val Phe Tyr Arg Asn Arg Trp Ala
 40 45 50
 ttc gat aaa gtc gtg cgc tcc aca cat ggc gtg aac tgc acg ggc tcc 307
 Phe Asp Lys Val Val Arg Ser Thr His Gly Val Asn Cys Thr Gly Ser
 55 60 65
 tgc tcg tgg aaa gtg tat gta aaa gac ggt gtg atc acc tgg gaa tcc 355

Cys Ser Trp Lys Val Tyr Val Lys Asp Gly Val Ile Thr Trp Glu Ser
 70 75 80 85
 cag gca gtg gat tac cca act acc ggt gcg gat atg ccc gac aat gaa 403
 Gln Ala Val Asp Tyr Pro Thr Thr Gly Ala Asp Met Pro Asp Asn Glu
 90 95 100
 cca cgt ggc tgc cct cgt ggt gca tca ttt tcc tgg tac acc tac tcc 451
 Pro Arg Gly Cys Pro Arg Gly Ala Ser Phe Ser Trp Tyr Thr Tyr Ser
 105 110 115
 cca acc cgc atc cgc tac cca tac atc ggt ggc gtg cta gtt gat atg 499
 Pro Thr Arg Ile Arg Tyr Pro Tyr Ile Gly Gly Val Leu Val Asp Met
 120 125 130
 tcc gcg aag cca agg aac gcc tgg gcg atc cgg tgc tgg cgt ggc gcg 547
 Ser Ala Lys Pro Arg Asn Ala Trp Ala Ile Arg Cys Trp Arg Gly Ala
 135 140 145
 aca ttg tagaaacccc agaaaagcgc aaa 576
 Thr Leu
 150

<210> 274

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Thr Thr Thr Thr Ser Ser Gly Lys Ser Ser Glu Lys Ile Asn Pro
 1 5 10 15
 Leu Phe Lys Leu Gly Ser Phe Leu Arg Lys Gly Thr Val Gly Ser Glu
 20 25 30
 Gly Gln Gln Ile Phe Leu Gln Gly Gly Arg Gln Ala Asp Val Phe Tyr
 35 40 45
 Arg Asn Arg Trp Ala Phe Asp Lys Val Val Arg Ser Thr His Gly Val
 50 55 60
 Asn Cys Thr Gly Ser Cys Ser Trp Lys Val Tyr Val Lys Asp Gly Val
 65 70 75 80
 Ile Thr Trp Glu Ser Gln Ala Val Asp Tyr Pro Thr Thr Gly Ala Asp
 85 90 95
 Met Pro Asp Asn Glu Pro Arg Gly Cys Pro Arg Gly Ala Ser Phe Ser
 100 105 110
 Trp Tyr Thr Tyr Ser Pro Thr Arg Ile Arg Tyr Pro Tyr Ile Gly Gly
 115 120 125
 Val Leu Val Asp Met Ser Ala Lys Pro Arg Asn Ala Trp Ala Ile Arg
 130 135 140
 Cys Trp Arg Gly Ala Thr Leu
 145 150

```
<220>
<221> CDS
<222> (101)..(466)
<223> FRXA01302
```

```
<210> 276
<211> 122
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 276
Met Thr Thr Thr Thr Ser Ser Gly Lys Ser Ser Glu Lys Ile Asn Pro
  1             5             10             15
Leu Phe Lys Leu Gly Ser Phe Leu Arg Lys Gly Thr Val Gly Ser Glu
      20             25             30

```

tttctctggta	cacctactcc	ccaaccgcga	tccgctaccc	atacatcggt	ggcgtgctag	60										
ttgatatgtc	cgcgaagcca	aggaacgcct	gggcgatccg	gtg	ctg	gcg	tgg	cg		115						
				Val	Leu	Ala	Trp	Arg		5						
				1												
gac	att	gta	gaa	acc	cca	gaa	aag	cgc	aaa	gca	tat	gta	tcc	cag	cg	163
Asp	Ile	Val	Glu	Thr	Pro	Glu	Lys	Arg	Lys	Ala	Tyr	Val	Ser	Gln	Arg	
				10					15					20		
ggc	aaa	ggg	ggc	ctc	atc	cgc	gtt	cag	tat	gag	gaa	gcc	atg	gag	att	211
Gly	Lys	Gly	Gly	Leu	Ile	Arg	Val	Gln	Tyr	Glu	Glu	Ala	Met	Glu	Ile	
				25				30					35			
gct	gcg	gca	gcc	cat	gtg	tac	acc	atc	cgc	caa	tac	ggc	ccc	gac	cg	259
Ala	Ala	Ala	Ala	His	Val	Tyr	Thr	Ile	Arg	Gln	Tyr	Gly	Pro	Asp	Arg	
				40				45				50				
att	cat	gga	ttc	acc	gtt	att	ccc	gca	atg	tcg	cag	gtg	tct	tac	ggt	307
Ile	His	Gly	Phe	Thr	Val	Ile	Pro	Ala	Met	Ser	Gln	Val	Ser	Tyr	Gly	
	55					60					65					
gct	ggg	act	cgc	ttc	ttg	cag	atg	atc	ggc	gga	gtg	gcg	ctg	tcc	ttc	355
Ala	Gly	Thr	Arg	Phe	Leu	Gln	Met	Ile	Gly	Gly	Val	Ala	Leu	Ser	Phe	
	70				75					80					85	
tac	gat	tgg	tac	gcc	gac	ctc	cca	cca	gca	tca	cca	caa	act	ttc	ggc	403
Tyr	Asp	Trp	Tyr	Ala	Asp	Leu	Pro	Pro	Ala	Ser	Pro	Gln	Thr	Phe	Gly	
				90					95					100		

gat	caa	act	gac	gtt	ccg	gaa	tct	ggc	gac	tgg	tac	aac	tcc	agc	tac	451
Asp	Gln	Thr	Asp	Val	Pro	Glu	Ser	Gly	Asp	Trp	Tyr	Asn	Ser	Ser	Tyr	
			105					110					115			
ctc	atg	atg	tgg	ggg	tcc	aac	att	ccg	gtg	acc	cgc	acg	cct	gac	tcc	499
Leu	Met	Met	Trp	Gly	Ser	Asn	Ile	Pro	Val	Thr	Arg	Thr	Pro	Asp	Ser	
			120				125						130			
cac	ttc	atg	gtg	gaa	gcc	cgc	tac	aag	ggc	acc	aag	gtt	gtt	gtg	gtt	547
His	Phe	Met	Val	Glu	Ala	Arg	Tyr	Lys	Gly	Thr	Lys	Val	Val	Val	Val	
			135				140				145					
tcc	ccg	gat	ttc	gct	gac	tcc	acc	aaa	ttt	gct	gat	gaa	tgg	gca	cgc	595
Ser	Pro	Asp	Phe	Ala	Asp	Ser	Thr	Lys	Phe	Ala	Asp	Glu	Trp	Ala	Arg	
					155					160					165	
atc	cac	cct	ggg	act	gac	ggc	gca	ctc	gcc	ttt	gcc	atg	ggc	cat	gtg	643
Ile	His	Pro	Gly	Thr	Asp	Gly	Ala	Leu	Ala	Phe	Ala	Met	Gly	His	Val	
				170					175						180	
atc	ttg	aag	gaa	ttc	cat	gtt	gac	aag	aag	acg	ccg	tac	ttc	atg	gac	691
Ile	Leu	Lys	Glu	Phe	His	Val	Asp	Lys	Lys	Thr	Pro	Tyr	Phe	Met	Asp	
			185					190						195		
tac	atg	cgc	aaa	tac	acg	gac	tct	cct	ttc	ctc	gtg	gaa	tta	gat	gag	739
Tyr	Met	Arg	Lys	Tyr	Thr	Asp	Ser	Pro	Phe	Leu	Val	Glu	Leu	Asp	Glu	
			200				205					210				
cac	ggc	gat	ggc	acc	tac	acc	cca	ggg	aaa	ttc	ctc	act	gca	gac	cgc	787
His	Gly	Asp	Gly	Thr	Tyr	Thr	Pro	Gly	Lys	Phe	Leu	Thr	Ala	Asp	Arg	
			215				220				225					
gca	gct	gat	atc	tcc	cca	gcg	ctt	gcc	gcc	act	cca	aat	gcc	acc	cac	835
Ala	Ala	Asp	Ile	Ser	Pro	Ala	Leu	Ala	Ala	Thr	Pro	Asn	Ala	Thr	His	
					235					240					245	
cgt	ctc	ctt	gtg	ctg	caa	aaa	gat	ggc	tca	gtt	gta	gat	ccc	ggg	ggc	883
Arg	Leu	Leu	Val	Leu	Gln	Lys	Asp	Gly	Ser	Val	Val	Asp	Pro	Gly	Gly	
				250					255					260		
act	gtc	gcg	gac	cgt	tgg	ggg	gaa	gaa	ggc	atg	ggg	aag	tgg	aat	ctg	931
Thr	Val	Ala	Asp	Arg	Trp	Gly	Glu	Glu	Gly	Met	Gly	Lys	Trp	Asn	Leu	
			265				270						275			
cgc	tta	gac	ggc	gta	gat	cca	gtg	atg	act	att	gca	gat	gta	cag	act	979
Arg	Leu	Asp	Gly	Val	Asp	Pro	Val	Met	Thr	Ile	Ala	Asp	Val	Gln	Thr	
			280				285					290				
gac	acc	gaa	act	gcg	gaa	gtc	ctc	ttc	ccc	cgc	ttc	gat	ctc	cca	gca	1027
Asp	Thr	Glu	Thr	Ala	Glu	Val	Leu	Phe	Pro	Arg	Phe	Asp	Leu	Pro	Ala	
			295			300					305					
act	gcc	acc	caa	gaa	ggc	ccc	att	ggg	gct	ggc	acc	atc	agc	cgg	ggc	1075
Thr	Ala	Thr	Gln	Glu	Gly	Pro	Ile	Gly	Ala	Gly	Thr	Ile	Ser	Arg	Gly	
					315					320					325	
gtt	ccc	acc	atc	acg	ttg	aat	ggc	cga	aag	tac	acc	act	gtc	ttt	gat	1123
Val	Pro	Thr	Ile	Thr	Leu	Asn	Gly	Arg	Lys	Tyr	Thr	Thr	Val	Phe	Asp	
				330					335					340		
gtg	ttg	ctc	gca	cac	tac	ggg	gtg	aac	cgc	gaa	gag	ctc	aac	ctt	cct	1171

Val	Leu	Leu	Ala	His	Tyr	Gly	Val	Asn	Arg	Glu	Glu	Leu	Asn	Leu	Pro	
			345					350					355			
ggt	gag	tgg	cct	aag	gat	ttc	cag	gat	cca	gtc	atg	ggt	act	cct	gcg	1219
Gly	Glu	Trp	Pro	Lys	Asp	Phe	Gln	Asp	Pro	Val	Met	Gly	Thr	Pro	Ala	
		360					365					370				
tgg	cag	gaa	gag	ctc	acg	ggt	gtt	cct	gct	aat	cag	gcg	att	cgt	ttg	1267
Trp	Gln	Glu	Glu	Leu	Thr	Gly	Val	Pro	Ala	Asn	Gln	Ala	Ile	Arg	Leu	
		375				380					385					
ggt	cgg	gaa	ttt	gct	cag	aat	gct	gat	gat	tcc	aag	ggc	cgt	tcc	cag	1315
Gly	Arg	Glu	Phe	Ala	Gln	Asn	Ala	Asp	Asp	Ser	Lys	Gly	Arg	Ser	Gln	
390					395				400					405		
atc	atc	atg	ggt	gct	ggt	gtg	aac	cac	tac	ttc	cat	gcg	gat	tct	att	1363
Ile	Ile	Met	Gly	Ala	Gly	Val	Asn	His	Tyr	Phe	His	Ala	Asp	Ser	Ile	
				410				415						420		
tat	cgc	aca	ttc	ttg	gcg	ctg	acc	tct	atg	tgt	ggc	acc	caa	ggt	gtt	1411
Tyr	Arg	Thr	Phe	Leu	Ala	Leu	Thr	Ser	Met	Cys	Gly	Thr	Gln	Gly	Val	
			425					430					435			
aac	ggt	ggc	ggt	tgg	gct	cac	tac	gtt	ggt	cag	gag	aaa	ctc	cgt	cca	1459
Asn	Gly	Gly	Gly	Trp	Ala	His	Tyr	Val	Gly	Gln	Glu	Lys	Leu	Arg	Pro	
		440					445					450				
atg	aat	ggt	tgg	gca	cag	tat	gcc	ttt	gct	aca	gac	tgg	cag	cgt	cca	1507
Met	Asn	Gly	Trp	Ala	Gln	Tyr	Ala	Phe	Ala	Thr	Asp	Trp	Gln	Arg	Pro	
	455				460					465						
cca	cgt	cag	atg	atc	acc	act	ggt	ttc	tac	tac	ctc	acc	acg	gat	cag	1555
Pro	Arg	Gln	Met	Ile	Thr	Thr	Gly	Phe	Tyr	Tyr	Leu	Thr	Thr	Asp	Gln	
470					475				480						485	
tgg	agg	tat	gac	aac	act	cgt	gct	aat	cgt	ctg	gct	tcc	cca	ctg	gct	1603
Trp	Arg	Tyr	Asp	Asn	Thr	Arg	Ala	Asn	Arg	Leu	Ala	Ser	Pro	Leu	Ala	
				490					495					500		
aat	cgt	ggc	acc	gtg	ggt	gac	aaa	atg	acg	gcg	gat	acc	ttg	gtg	gaa	1651
Asn	Arg	Gly	Thr	Val	Gly	Asp	Lys	Met	Thr	Ala	Asp	Thr	Leu	Val	Glu	
			505					510					515			
tcc	atg	aaa	cgt	gga	tgg	atg	ccg	tca	ttc	ccg	caa	ttc	aac	cgc	aat	1699
Ser	Met	Lys	Arg	Gly	Trp	Met	Pro	Ser	Phe	Pro	Gln	Phe	Asn	Arg	Asn	
		520					525					530				
ccc	ctc	atc	ttg	agc	cag	gag	gcg	gaa	gaa	aag	ggc	gtg	tct	gtt	tct	1747
Pro	Leu	Ile	Leu	Ser	Gln	Glu	Ala	Glu	Glu	Lys	Gly	Val	Ser	Val	Ser	
		535				540					545					
gac	cat	att	gtt	cag	cag	ctc	acc	gat	ggt	gac	ttg	cag	ttc	gcc	tgc	1795
Asp	His	Ile	Val	Gln	Gln	Leu	Thr	Asp	Gly	Asp	Leu	Gln	Phe	Ala	Cys	
550					555				560					565		
gag	gat	ccg	gat	gca	ccg	gaa	aac	tgg	cca	gcg	att	ctg	ctt	aac	tgg	1843
Glu	Asp	Pro	Asp	Ala	Pro	Glu	Asn	Trp	Pro	Arg	Ile	Leu	Leu	Asn	Trp	
				570					575					580		
cgc	aca	aac	cta	atg	ggc	tct	tca	gct	aag	ggc	acg	gag	ttt	ttc	ttg	1891
Arg	Thr	Asn	Leu	Met	Gly	Ser	Ser	Ala	Lys	Gly	Thr	Glu	Phe	Phe	Leu	

585										590					595									
cgc	cat	atg	ttg	ggg	gtg	gat	tct	gat	gca	tct	gct	gaa	gaa	aac	gcg	1939								
Arg	His	Met	Leu	Gly	Val	Asp	Ser	Asp	Ala	Ser	Ala	Glu	Glu	Asn	Ala									
600										605					610									
ccg	gag	gat	cgt	cca	agt	tcc	att	gtg	tgg	agg	gat	gag	gct	ccg	gaa	1987								
Pro	Glu	Asp	Arg	Pro	Ser	Ser	Ile	Val	Trp	Arg	Asp	Glu	Ala	Pro	Glu									
615										620					625									
gga	aag	ctc	gat	ttg	atg	ctg	acc	acg	gat	ttc	cgc	aac	act	tcc	acc	2035								
Gly	Lys	Leu	Asp	Leu	Met	Leu	Thr	Thr	Asp	Phe	Arg	Asn	Thr	Ser	Thr									
630										635					640					645				
acc	ttg	gtc	tcg	gat	atc	gtg	ctg	ccg	gca	gcc	acc	tgg	tat	gag	aag	2083								
Thr	Leu	Val	Ser	Asp	Ile	Val	Leu	Pro	Ala	Ala	Thr	Trp	Tyr	Glu	Lys									
650										655					660									
cat	gat	ttg	tcc	acc	acg	gat	atg	cac	ccc	ttc	atc	cac	tcg	ttc	aat	2131								
His	Asp	Leu	Ser	Thr	Thr	Asp	Met	His	Pro	Phe	Ile	His	Ser	Phe	Asn									
665										670					675									
gct	gcg	atc	aac	cca	ccg	tgg	gag	acg	cgt	act	gac	tgg	gag	gtc	ttc	2179								
Ala	Ala	Ile	Asn	Pro	Pro	Trp	Glu	Thr	Arg	Thr	Asp	Trp	Glu	Val	Phe									
680										685					690									
cac	gat	ctc	acc	aaa	gaa	ttc	tcc	tca	cag	gca	gca	acc	tgg	ttg	ggc	2227								
His	Asp	Leu	Thr	Lys	Glu	Phe	Ser	Ser	Gln	Ala	Ala	Thr	Trp	Leu	Gly									
695										700					705									
acc	caa	acc	gat	gtg	atc	acc	gca	ccg	att	gcc	cat	gac	tcc	ccg	gat	2275								
Thr	Gln	Thr	Asp	Val	Ile	Thr	Ala	Pro	Ile	Ala	His	Asp	Ser	Pro	Asp									
710										715					720					725				
gag	ctc	aat	atg	cct	ggc	ggg	atc	gtg	cca	gat	att	gat	gag	gtc	ggg	2323								
Glu	Leu	Asn	Met	Pro	Gly	Gly	Ile	Val	Pro	Asp	Ile	Asp	Glu	Val	Gly									
730										735					740									
ctg	atc	cct	ggc	aag	acg	atg	gcc	aag	atc	atc	ccg	gtg	gaa	cgt	gat	2371								
Leu	Ile	Pro	Gly	Lys	Thr	Met	Ala	Lys	Ile	Ile	Pro	Val	Glu	Arg	Asp									
745										750					755									
tac	tcc	aag	gtg	tat	gaa	aag	tgg	aca	cac	ttg	gga	cca	ctc	acc	gcc	2419								
Tyr	Ser	Lys	Val	Tyr	Glu	Lys	Trp	Thr	His	Leu	Gly	Pro	Leu	Thr	Ala									
760										765					770									
aaa	gcg	ggg	acc	gga	acc	cac	ggc	act	gcg	ttt	aac	gtg	acc	aag	caa	2467								
Lys	Ala	Gly	Thr	Gly	Thr	His	Gly	Thr	Ala	Phe	Asn	Val	Thr	Lys	Gln									
775										780					785									
acc	gag	gag	ctg	gcg	ctg	atc	aac	ggc	acc	tcc	atc					2503								
Thr	Glu	Glu	Leu	Ala	Leu	Ile	Asn	Gly	Thr	Ser	Ile													
790										795					800									

<210> 278

<211> 801

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val Leu Ala Trp Arg Asp Ile Val Glu Thr Pro Glu Lys Arg Lys Ala
 1 5 10 15
 Tyr Val Ser Gln Arg Gly Lys Gly Gly Leu Ile Arg Val Gln Tyr Glu
 20 25 30
 Glu Ala Met Glu Ile Ala Ala Ala Ala His Val Tyr Thr Ile Arg Gln
 35 40 45
 Tyr Gly Pro Asp Arg Ile His Gly Phe Thr Val Ile Pro Ala Met Ser
 50 55 60
 Gln Val Ser Tyr Gly Ala Gly Thr Arg Phe Leu Gln Met Ile Gly Gly
 65 70 75 80
 Val Ala Leu Ser Phe Tyr Asp Trp Tyr Ala Asp Leu Pro Pro Ala Ser
 85 90 95
 Pro Gln Thr Phe Gly Asp Gln Thr Asp Val Pro Glu Ser Gly Asp Trp
 100 105 110
 Tyr Asn Ser Ser Tyr Leu Met Met Trp Gly Ser Asn Ile Pro Val Thr
 115 120 125
 Arg Thr Pro Asp Ser His Phe Met Val Glu Ala Arg Tyr Lys Gly Thr
 130 135 140
 Lys Val Val Val Val Ser Pro Asp Phe Ala Asp Ser Thr Lys Phe Ala
 145 150 155 160
 Asp Glu Trp Ala Arg Ile His Pro Gly Thr Asp Gly Ala Leu Ala Phe
 165 170 175
 Ala Met Gly His Val Ile Leu Lys Glu Phe His Val Asp Lys Lys Thr
 180 185 190
 Pro Tyr Phe Met Asp Tyr Met Arg Lys Tyr Thr Asp Ser Pro Phe Leu
 195 200 205
 Val Glu Leu Asp Glu His Gly Asp Gly Thr Tyr Thr Pro Gly Lys Phe
 210 215 220
 Leu Thr Ala Asp Arg Ala Ala Asp Ile Ser Pro Ala Leu Ala Ala Thr
 225 230 235 240
 Pro Asn Ala Thr His Arg Leu Leu Val Leu Gln Lys Asp Gly Ser Val
 245 250 255
 Val Asp Pro Gly Gly Thr Val Ala Asp Arg Trp Gly Glu Glu Gly Met
 260 265 270
 Gly Lys Trp Asn Leu Arg Leu Asp Gly Val Asp Pro Val Met Thr Ile
 275 280 285
 Ala Asp Val Gln Thr Asp Thr Glu Thr Ala Glu Val Leu Phe Pro Arg
 290 295 300
 Phe Asp Leu Pro Ala Thr Ala Thr Gln Glu Gly Pro Ile Gly Ala Gly
 305 310 315 320
 Thr Ile Ser Arg Gly Val Pro Thr Ile Thr Leu Asn Gly Arg Lys Tyr

382

Thr Trp Tyr Glu Lys His Asp Leu Ser Thr Thr Asp Met His Pro Phe
 660 665 670
 Ile His Ser Phe Asn Ala Ala Ile Asn Pro Pro Trp Glu Thr Arg Thr
 675 680 685
 Asp Trp Glu Val Phe His Asp Leu Thr Lys Glu Phe Ser Ser Gln Ala
 690 695 700
 Ala Thr Trp Leu Gly Thr Gln Thr Asp Val Ile Thr Ala Pro Ile Ala
 705 710 715 720
 His Asp Ser Pro Asp Glu Leu Asn Met Pro Gly Gly Ile Val Pro Asp
 725 730 735
 Ile Asp Glu Val Gly Leu Ile Pro Gly Lys Thr Met Ala Lys Ile Ile
 740 745 750
 Pro Val Glu Arg Asp Tyr Ser Lys Val Tyr Glu Lys Trp Thr His Leu
 755 760 765
 Gly Pro Leu Thr Ala Lys Ala Gly Thr Gly Thr His Gly Thr Ala Phe
 770 775 780
 Asn Val Thr Lys Gln Thr Glu Glu Leu Ala Leu Ile Asn Gly Thr Ser
 785 790 795 800
 Ile

<210> 279
 <211> 765
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (85)..(765)
 <223> FRXA01307

<400> 279
 ttccccaacc cgcacccgct acccatacat cgggtggcgtg ctagttagata tgtccgcgaa 60
 gccaaaggaac gcctgggcga tccgggtgctg gcg tgg cgc gac att gta gaa acc 114
 Val Leu Ala Trp Arg Asp Ile Val Glu Thr
 1 5 10
 cca gaa aag cgc aaa gca tat gta tcc cag cgg ggc aaa ggt ggc ctc 162
 Pro Glu Lys Arg Lys Ala Tyr Val Ser Gln Arg Gly Lys Gly Gly Leu
 15 20 25
 atc cgc gtt cag tat gag gaa gcc atg gag att gct gcg gca gcc cat 210
 Ile Arg Val Gln Tyr Glu Glu Ala Met Glu Ile Ala Ala Ala His
 30 35 40
 gtg tac acc atc cgc caa tac ggc ccc gac cgc att cat gga ttc acc 258
 Val Tyr Thr Ile Arg Gln Tyr Gly Pro Asp Arg Ile His Gly Phe Thr
 45 50 55

gtt att ccc gca atg tcg cag gtg tct tac ggt gct ggt act cgc ttc 306
 Val Ile Pro Ala Met Ser Gln Val Ser Tyr Gly Ala Gly Thr Arg Phe
 60 65 70

ttg cag atg atc ggc gga gtg gcg ctg tcc ttc tac gat tgg tac gcc 354
 Leu Gln Met Ile Gly Gly Val Ala Leu Ser Phe Tyr Asp Trp Tyr Ala
 75 80 85 90

gac ctc cca cca gca tca cca caa act ttc ggc gat caa act gac gtt 402
 Asp Leu Pro Pro Ala Ser Pro Gln Thr Phe Gly Asp Gln Thr Asp Val
 95 100 105

ccg gaa tct ggc gac tgg tac aac tcc agc tac ctc atg atg tgg ggt 450
 Pro Glu Ser Gly Asp Trp Tyr Asn Ser Ser Tyr Leu Met Met Trp Gly
 110 115 120

tcc aac att ccg gtg acc cgc acg cct gac tcc cac ttc atg gtg gaa 498
 Ser Asn Ile Pro Val Thr Arg Thr Pro Asp Ser His Phe Met Val Glu
 125 130 135

gcc cgc tac aag ggc acc aag gtt gtt gtg gtt tcc ccg gat ttc gct 546
 Ala Arg Tyr Lys Gly Thr Lys Val Val Val Val Ser Pro Asp Phe Ala
 140 145 150

gac tcc acc aaa ttt gct gat gaa tgg gca cgc atc cac cct ggt act 594
 Asp Ser Thr Lys Phe Ala Asp Glu Trp Ala Arg Ile His Pro Gly Thr
 155 160 165 170

gac ggc gca ctc gcc ttt gcc atg ggc cat gtg atc ttg aag gaa ttc 642
 Asp Gly Ala Leu Ala Phe Ala Met Gly His Val Ile Leu Lys Glu Phe
 175 180 185

cat gtt gac aag aag acg ccg tac ttc atg gac tac atg cgc aaa tac 690
 His Val Asp Lys Lys Thr Pro Tyr Phe Met Asp Tyr Met Arg Lys Tyr
 190 195 200

acg gac tct cct ttc ctc gtg gaa tta gat gag cac ggc gat ggc acc 738
 Thr Asp Ser Pro Phe Leu Val Glu Leu Asp Glu His Gly Asp Gly Thr
 205 210 215

tac acc cca ggt aaa ttc ctc act gca 765
 Tyr Thr Pro Gly Lys Phe Leu Thr Ala
 220 225

<210> 280
 <211> 227
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280
 Val Leu Ala Trp Arg Asp Ile Val Glu Thr Pro Glu Lys Arg Lys Ala
 1 5 10 15
 Tyr Val Ser Gln Arg Gly Lys Gly Gly Leu Ile Arg Val Gln Tyr Glu
 20 25 30
 Glu Ala Met Glu Ile Ala Ala Ala His Val Tyr Thr Ile Arg Gln
 35 40 45
 Tyr Gly Pro Asp Arg Ile His Gly Phe Thr Val Ile Pro Ala Met Ser

50 55 60

Gln Val Ser Tyr Gly Ala Gly Thr Arg Phe Leu Gln Met Ile Gly Gly
65 70 75 80

Val Ala Leu Ser Phe Tyr Asp Trp Tyr Ala Asp Leu Pro Pro Ala Ser
85 90 95

Pro Gln Thr Phe Gly Asp Gln Thr Asp Val Pro Glu Ser Gly Asp Trp
100 105 110

Tyr Asn Ser Ser Tyr Leu Met Met Trp Gly Ser Asn Ile Pro Val Thr
115 120 125

Arg Thr Pro Asp Ser His Phe Met Val Glu Ala Arg Tyr Lys Gly Thr
130 135 140

Lys Val Val Val Val Ser Pro Asp Phe Ala Asp Ser Thr Lys Phe Ala
145 150 155 160

Asp Glu Trp Ala Arg Ile His Pro Gly Thr Asp Gly Ala Leu Ala Phe
165 170 175

Ala Met Gly His Val Ile Leu Lys Glu Phe His Val Asp Lys Lys Thr
180 185 190

Pro Tyr Phe Met Asp Tyr Met Arg Lys Tyr Thr Asp Ser Pro Phe Leu
195 200 205

Val Glu Leu Asp Glu His Gly Asp Gly Thr Tyr Thr Pro Gly Lys Phe
210 215 220

Leu Thr Ala
225

<210> 281
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1206)
 <223> FRXA01308

<400> 281

gcc gcc act cca aat gcc acc cac cgt ctc ctt gtg ctg caa aaa gat	48
Ala Ala Thr Pro Asn Ala Thr His Arg Leu Leu Val Leu Gln Lys Asp	
1 5 10 15	
ggc tca gtt gta gat ccc ggt ggc act gtc gcg gac cgt tgg ggt gaa	96
Gly Ser Val Val Asp Pro Gly Gly Thr Val Ala Asp Arg Trp Gly Glu	
20 25 30	
gaa ggc atg ggt aag tgg aat ctg cgc tta gac ggc gta gat cca gtg	144
Glu Gly Met Gly Lys Trp Asn Leu Arg Leu Asp Gly Val Asp Pro Val	
35 40 45	
atg act att gca gat gta cag act gac acc gaa act gcg gaa gtc ctc	192
Met Thr Ile Ala Asp Val Gln Thr Asp Thr Glu Thr Ala Glu Val Leu	

50			55			60										
ttc Phe 65	ccc Pro	cgc Arg	ttc Phe	gat Asp	ctc Leu 70	cca Pro	gca Ala	act Thr	gcc Ala	acc Thr 75	caa Gln	gaa Glu	ggc Gly	ccc Pro	att Ile 80	240
ggt Gly	gct Ala	ggc Gly	acc Thr	atc Ile 85	agc Ser	cgg Arg	ggc Gly	gtt Val	ccc Pro 90	acc Thr	atc Ile	acg Thr	ttg Leu	aat Asn 95	ggc Gly	288
cga Arg	aag Lys	tac Tyr	acc Thr 100	act Thr	gtc Val	ttt Phe	gat Asp	gtg Val 105	ttg Leu	ctc Leu	gca Ala	cac His	tac Tyr 110	ggt Gly	gtg Val	336
aac Asn	cgc Arg	gaa Glu 115	gag Glu	ctc Leu	aac Asn	ctt Leu	cct Pro 120	ggt Gly	gag Glu	tgg Trp	cct Pro	aag Lys 125	gat Asp	ttc Phe	cag Gln	384
gat Asp	cca Pro 130	gtc Val	atg Met	ggg Gly	act Thr	cct Pro 135	gcg Ala	tgg Trp	cag Gln	gaa Glu	gag Glu 140	ctc Leu	acg Thr	ggt Gly	gtt Val	432
cct Pro 145	gct Ala	aat Asn	cag Gln	gcg Ala	att Ile 150	cgt Arg	ttg Leu	ggg Gly	cgg Arg	gaa Glu 155	ttt Phe	gct Ala	cag Gln	aat Asn	gct Ala 160	480
gat Asp	gat Asp	tcc Ser	aag Lys	ggc Gly 165	cgt Arg	tcc Ser	cag Gln	atc Ile	atc Ile 170	atg Met	ggg Gly	gct Ala	ggg Gly	gtg Val 175	aac Asn	528
cac His	tac Tyr	ttc Phe	cat His 180	gcg Ala	gat Asp	tct Ser	att Ile	tat Tyr 185	cgc Arg	aca Thr	ttc Phe	ttg Leu	gcg Ala 190	ctg Leu	acc Thr	576
tct Ser	atg Met	tgt Cys 195	ggc Gly	acc Thr	caa Gln	ggg Gly	gtt Val 200	aac Asn	ggg Gly	ggc Gly	ggg Gly	tgg Trp 205	gct Ala	cac His	tac Tyr	624
gtt Val	ggg Gly 210	cag Gln	gag Glu	aaa Lys	ctc Leu	cgt Arg 215	cca Pro	atg Met	aat Asn	ggg Gly 220	tgg Trp	gca Ala	cag Gln	tat Tyr	gcc Ala	672
ttt Phe 225	gct Ala	aca Thr	gac Asp	tgg Trp	cag Gln 230	cgt Arg	cca Pro	cca Pro	cgt Arg	cag Gln 235	atg Met	atc Ile	acc Thr	act Thr	ggg Gly 240	720
ttc Phe	tac Tyr	tac Tyr	ctc Leu	acc Thr 245	acg Thr	gat Asp	cag Gln	tgg Trp	agg Arg 250	tat Tyr	gac Asp	aac Asn	act Thr	cgt Arg 255	gct Ala	768
aat Asn	cgt Arg	ctg Leu	gct Ala 260	tcc Ser	cca Pro	ctg Leu	gct Ala	aat Asn 265	cgt Arg	ggc Gly	acc Thr	gtg Val	ggg Gly 270	gac Asp	aaa Lys	816
atg Met	acg Thr	gcg Ala	gat Asp	acc Thr	ttg Leu	gtg Val	gaa Glu 280	tcc Ser	atg Met	aaa Lys	cgt Arg	gga Gly 285	tgg Trp	atg Met	ccg Pro	864
tca Ser	ttc Phe 290	ccg Pro	caa Gln	ttc Phe	aac Asn	cgc Arg 295	aat Asn	ccc Pro	ctc Leu	atc Ile	ttg Leu 300	agc Ser	cag Gln	gag Glu	gcg Ala	912

gaa gaa aag ggc gtg tct gtt tct gac cat att gtt cag cag ctc acc 960
 Glu Glu Lys Gly Val Ser Val Ser Asp His Ile Val Gln Gln Leu Thr
 305 310 315 320
 gat ggt gac ttg cag ttc gcc tgc gag gat ccg gat gca ccg gaa aac 1008
 Asp Gly Asp Leu Gln Phe Ala Cys Glu Asp Pro Asp Ala Pro Glu Asn
 325 330 335
 tgg cca cgc att ctg ctt aac tgg cgc aca aac cta atg ggc tct tca 1056
 Trp Pro Arg Ile Leu Leu Asn Trp Arg Thr Asn Leu Met Gly Ser Ser
 340 345 350
 gct aag ggc acg gag ttt ttc ttg cgc cat atg ttg ggt gtg gat tct 1104
 Ala Lys Gly Thr Glu Phe Phe Leu Arg His Met Leu Gly Val Asp Ser
 355 360 365
 gat gca tct gct gaa aaa aac gcg ccg gag gat cgt cca agt tcc att 1152
 Asp Ala Ser Ala Glu Lys Asn Ala Pro Glu Asp Arg Pro Ser Ser Ile
 370 375 380
 gtg tgg agg gat gaa gct tcc gaa ggg aag ctc gat ttg atg ctg acc 1200
 Val Trp Arg Asp Glu Ala Ser Glu Gly Lys Leu Asp Leu Met Leu Thr
 385 390 395 400
 acg gat 1206
 Thr Asp

<210> 282
 <211> 402
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 282
 Ala Ala Thr Pro Asn Ala Thr His Arg Leu Leu Val Leu Gln Lys Asp
 1 5 10 15
 Gly Ser Val Val Asp Pro Gly Gly Thr Val Ala Asp Arg Trp Gly Glu
 20 25 30
 Glu Gly Met Gly Lys Trp Asn Leu Arg Leu Asp Gly Val Asp Pro Val
 35 40 45
 Met Thr Ile Ala Asp Val Gln Thr Asp Thr Glu Thr Ala Glu Val Leu
 50 55 60
 Phe Pro Arg Phe Asp Leu Pro Ala Thr Ala Thr Gln Glu Gly Pro Ile
 65 70 75 80
 Gly Ala Gly Thr Ile Ser Arg Gly Val Pro Thr Ile Thr Leu Asn Gly
 85 90 95
 Arg Lys Tyr Thr Thr Val Phe Asp Val Leu Leu Ala His Tyr Gly Val
 100 105 110
 Asn Arg Glu Glu Leu Asn Leu Pro Gly Glu Trp Pro Lys Asp Phe Gln
 115 120 125
 Asp Pro Val Met Gly Thr Pro Ala Trp Gln Glu Glu Leu Thr Gly Val

130	135	140
Pro Ala Asn Gln Ala Ile Arg Leu Gly Arg Glu Phe Ala Gln Asn Ala 145	150	155 160
Asp Asp Ser Lys Gly Arg Ser Gln Ile Ile Met Gly Ala Gly Val Asn 165	170	175
His Tyr Phe His Ala Asp Ser Ile Tyr Arg Thr Phe Leu Ala Leu Thr 180	185	190
Ser Met Cys Gly Thr Gln Gly Val Asn Gly Gly Gly Trp Ala His Tyr 195	200	205
Val Gly Gln Glu Lys Leu Arg Pro Met Asn Gly Trp Ala Gln Tyr Ala 210	215	220
Phe Ala Thr Asp Trp Gln Arg Pro Pro Arg Gln Met Ile Thr Thr Gly 225	230	235 240
Phe Tyr Tyr Leu Thr Thr Asp Gln Trp Arg Tyr Asp Asn Thr Arg Ala 245	250	255
Asn Arg Leu Ala Ser Pro Leu Ala Asn Arg Gly Thr Val Gly Asp Lys 260	265	270
Met Thr Ala Asp Thr Leu Val Glu Ser Met Lys Arg Gly Trp Met Pro 275	280	285
Ser Phe Pro Gln Phe Asn Arg Asn Pro Leu Ile Leu Ser Gln Glu Ala 290	295	300
Glu Glu Lys Gly Val Ser Val Ser Asp His Ile Val Gln Gln Leu Thr 305	310	315 320
Asp Gly Asp Leu Gln Phe Ala Cys Glu Asp Pro Asp Ala Pro Glu Asn 325	330	335
Trp Pro Arg Ile Leu Leu Asn Trp Arg Thr Asn Leu Met Gly Ser Ser 340	345	350
Ala Lys Gly Thr Glu Phe Phe Leu Arg His Met Leu Gly Val Asp Ser 355	360	365
Asp Ala Ser Ala Glu Lys Asn Ala Pro Glu Asp Arg Pro Ser Ser Ile 370	375	380
Val Trp Arg Asp Glu Ala Ser Glu Gly Lys Leu Asp Leu Met Leu Thr 385	390	395 400

Thr Asp

<210> 283

<211> 824

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(801)

<223> RXN01309

<400> 283

att gca gac cac gaa ggt acc cac atc aat tgg gac atg gtc aaa gaa	48
Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu	
1 5 10 15	
cgt tcc gcc gag gtg atc acc tca ccg gag tgg act ggt tcc aag aag	96
Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys	
20 25 30	
gac gga cgt cgc tac acc gcg ttt tcc atc aac att gaa tac gac aag	144
Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys	
35 40 45	
ccg tgg cac acc ctg tct ggt cgc atg cac tac tac ctc gac cac gat	192
Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp	
50 55 60	
tgg ttt att gat tac ggc gag cag ttg cca atc ttt agg cca ccg ttg	240
Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu	
65 70 75 80	
gac aag atc cac atc aat ggt gag gtc ggc cct ggc cag tcg gtc aca	288
Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr	
85 90 95	
ggc acc gac ggc gaa cca gaa gta acc gtg cgt tat ctg acc acc cac	336
Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His	
100 105 110	
aac aag tgg tcg att cac tcg cag tac tac gac aat ctg cat gtg ctt	384
Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu	
115 120 125	
tct att tct cgt ggc ggc cag gtg atc tgg atg tcc aac aag gat gca	432
Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala	
130 135 140	
gag aaa ctc ggt atc gct gac aac gat tgg atc gag gct tat aac cgc	480
Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg	
145 150 155 160	
aac ggc gtt gtt tct gct cgt gcg att gtc tcc cac cgc att cct gaa	528
Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu	
165 170 175	
ggc acc gtg ttt atg aac cac gcg cag gaa cgc acc gct ggc acc ccg	576
Gly Thr Val Phe Met Asn His Ala Gln Glu Arg Thr Ala Gly Thr Pro	
180 185 190	
ctg aac gag aag tct ggc agg cgc ggc gga act cac aac tct ctt act	624
Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr	
195 200 205	
cga atc atg att aag ccg gtc cat gtt gcc ggt ggc tac ggc cac tta	672
Arg Ile Met Ile Lys Pro Val His Val Ala Gly Gly Tyr Gly His Leu	
210 215 220	
acc tat ggc ttc aac tac atc ggc caa ccg gaa ata acc gcg atg agg	720

Thr Tyr Gly Phe Asn Tyr Ile Gly Gln Pro Glu Ile Thr Ala Met Arg
 225 230 235 240

tca cca gaa ttc gtc gcc gct ccc agg agg tgc agt act aat gaa ggt 768
 Ser Pro Glu Phe Val Ala Ala Pro Arg Arg Cys Ser Thr Asn Glu Gly
 245 250 255

cat ggc tca gat cgc aat gat cat gaa ctt gga taagtgcatt ggctgccaca 821
 His Gly Ser Asp Arg Asn Asp His Glu Leu Gly
 260 265

cgt 824

<210> 284
 <211> 267
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 284
 Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu
 1 5 10 15

Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys
 20 25 30

Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys
 35 40 45

Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp
 50 55 60

Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu
 65 70 75 80

Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr
 85 90 95

Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His
 100 105 110

Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu
 115 120 125

Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala
 130 135 140

Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg
 145 150 155 160

Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu
 165 170 175

Gly Thr Val Phe Met Asn His Ala Gln Glu Arg Thr Ala Gly Thr Pro
 180 185 190

Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr
 195 200 205

Arg Ile Met Ile Lys Pro Val His Val Ala Gly Gly Tyr Gly His Leu
 210 215 220

Thr Tyr Gly Phe Asn Tyr Ile Gly Gln Pro Glu Ile Thr Ala Met Arg
 225 230 235 240

Ser Pro Glu Phe Val Ala Ala Pro Arg Arg Cys Ser Thr Asn Glu Gly
 245 250 255

His Gly Ser Asp Arg Asn Asp His Glu Leu Gly
 260 265

<210> 285
 <211> 692
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(669)
 <223> FRXA01309

<400> 285
 att gca gac cac gaa ggt acc cac atc aat tgg gac atg gtc aaa gaa 48
 Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu
 1 5 10 15

cgt tcc gcc gag gtg atc acc tca ccg gag tgg act ggt tcc aag aag 96
 Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys
 20 25 30

gac gga cgt cgc tac acc gcg ttt tcc atc aac att gaa tac gac aag 144
 Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys
 35 40 45

ccg tgg cac acc ctg tct ggt cgc atg cac tac tac ctc gac cac gat 192
 Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp
 50 55 60

tgg ttt att gat tac ggc gag cag ttg cca atc ttt agg cca ccg ttg 240
 Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu
 65 70 75 80

gac aag atc cac atc aat ggt gag gtc ggc cct ggc cag tcg gtc aca 288
 Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr
 85 90 95

ggc acc gac ggc gaa cca gaa gta acc gtg cgt tat ctg acc acc cac 336
 Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His
 100 105 110

aac aag tgg tcg att cac tcg cag tac tac gac aat ctg cat gtg ctt 384
 Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu
 115 120 125

tct att tct cgt ggc ggc cag gtg atc tgg atg tcc aac aag gat gca 432
 Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala
 130 135 140

gag aaa ctc ggt atc gct gac aac gat tgg atc gag gct tat aac cgc 480
 Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg
 145 150 155 160

aac ggc gtt gtt tct gct cgt gcg att gtc tcc cac cgc att cct gaa 528
 Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu
 165 170 175

ggc acc gtg ttt atg aac cac gcg cag gaa ccc acc gct ggc acc ccg 576
 Gly Thr Val Phe Met Asn His Ala Gln Glu Pro Thr Ala Gly Thr Pro
 180 185 190

ctg aac gag aag tct ggc agg cgc ggc gga act cac aac tct ctt act 624
 Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr
 195 200 205

cga atc atg att aaa acg gtc cat gtt gcc ggt ggc tac ggc act 669
 Arg Ile Met Ile Lys Thr Val His Val Ala Gly Gly Tyr Gly Thr
 210 215 220

taacctatgg cttaactaca tcg 692

<210> 286

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu
 1 5 10 15

Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys
 20 25 30

Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys
 35 40 45

Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp
 50 55 60

Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu
 65 70 75 80

Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr
 85 90 95

Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His
 100 105 110

Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu
 115 120 125

Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala
 130 135 140

Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg
 145 150 155 160

Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu
 165 170 175

Gly Thr Val Phe Met Asn His Ala Gln Glu Pro Thr Ala Gly Thr Pro
 180 185 190

Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr
 195 200 205
 Arg Ile Met Ile Lys Thr Val His Val Ala Gly Gly Tyr Gly Thr
 210 215 220

<210> 287
 <211> 807
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(784)
 <223> RXA02017

<400> 287
 gcctgtggca cgggagctcc cagcggcaag gtgagttctga cctcgtggaa cgttggcgaa 60
 cgccccgctg cgatgttccc accaaggaag gactaggcgg atg cgc acc cat act 115
 Met Arg Thr His Thr
 1 5
 ggc aaa att ccg gat cac ttt gtg cct cgc atc tcc atg acg gag gag 163
 Gly Lys Ile Pro Asp His Phe Val Pro Arg Ile Ser Met Thr Glu Glu
 10 15 20
 cag cgg cgc gtg gtg ttc atg ctg aat agt ttg ctg ttg gat tat cca 211
 Gln Arg Arg Val Val Phe Met Leu Asn Ser Leu Leu Leu Asp Tyr Pro
 25 30 35
 gag gag gga ttc gtc gac aag cta aat gcc gtc gag gcg cag ctt gat 259
 Glu Glu Gly Phe Val Asp Lys Leu Asn Ala Val Glu Ala Gln Leu Asp
 40 45 50
 gtc ctt ccg ctc ccc gtc gcg gcg cac gtg gtc gag ttc ctt gac gcg 307
 Val Leu Pro Leu Pro Val Ala Ala His Val Val Glu Phe Leu Asp Ala
 55 60 65
 gca cgc gtc gct ggg cta cgc gcc atg cag gaa gcc tac gtt gag acc 355
 Ala Arg Val Ala Gly Leu Arg Ala Met Gln Glu Ala Tyr Val Glu Thr
 70 75 80 85
 ttt gac cag cgc cga cgc tgc tca ctg ttt ctc acc tac tac gct gtg 403
 Phe Asp Gln Arg Arg Arg Cys Ser Leu Phe Leu Thr Tyr Tyr Ala Val
 90 95 100
 ggc gac acc cgg cag cgc ggc acg gcg atc ctc acc ttc cgt caa acg 451
 Gly Asp Thr Arg Gln Arg Gly Thr Ala Ile Leu Thr Phe Arg Gln Thr
 105 110 115
 ctg caa cag ctc gga ttt gaa tcc gag cgc gac gaa ttg ccc gac cac 499
 Leu Gln Gln Leu Gly Phe Glu Ser Glu Arg Asp Glu Leu Pro Asp His
 120 125 130
 ctc tgc gtc gtg ctt gag gcc gca gcg ctt gct gat tct tcg ctt ttc 547
 Leu Cys Val Val Leu Glu Ala Ala Ala Leu Ala Asp Ser Ser Leu Phe
 135 140 145

gac gcc gcc acc cag gtg tta tca gct cac cgc gac ggc atc gaa gtg 595
 Asp Ala Ala Thr Gln Val Leu Ser Ala His Arg Asp Gly Ile Glu Val
 150 155 160 165

ttg cgc gca gcc ctc gac aac ctc gac tcg ccc tac aga tac ctg atc 643
 Leu Arg Ala Ala Leu Asp Asn Leu Asp Ser Pro Tyr Arg Tyr Leu Ile
 170 175 180

atg tct ttg tgc cag gca ttg cca gaa atc gat gaa gaa acc gcc aac 691
 Met Ser Leu Cys Gln Ala Leu Pro Glu Ile Asp Glu Glu Thr Ala Asn
 185 190 195

agc tac atg gag ctc atc cgc agc ggt cca cca gca gaa atg gtg ggc 739
 Ser Tyr Met Glu Leu Ile Arg Ser Gly Pro Pro Ala Glu Met Val Gly
 200 205 210

atc ggc acg cct cta ccg ttc ccc acc tca caa ccg gac att cac 784
 Ile Gly Thr Pro Leu Pro Phe Pro Thr Ser Gln Pro Asp Ile His
 215 220 225

taggacacac tatgtcaaac ttt 807

<210> 288

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Met Arg Thr His Thr Gly Lys Ile Pro Asp His Phe Val Pro Arg Ile
 1 5 10 15

Ser Met Thr Glu Glu Gln Arg Arg Val Val Phe Met Leu Asn Ser Leu
 20 25 30

Leu Leu Asp Tyr Pro Glu Glu Gly Phe Val Asp Lys Leu Asn Ala Val
 35 40 45

Glu Ala Gln Leu Asp Val Leu Pro Leu Pro Val Ala Ala His Val Val
 50 55 60

Glu Phe Leu Asp Ala Ala Arg Val Ala Gly Leu Arg Ala Met Gln Glu
 65 70 75 80

Ala Tyr Val Glu Thr Phe Asp Gln Arg Arg Arg Cys Ser Leu Phe Leu
 85 90 95

Thr Tyr Tyr Ala Val Gly Asp Thr Arg Gln Arg Gly Thr Ala Ile Leu
 100 105 110

Thr Phe Arg Gln Thr Leu Gln Gln Leu Gly Phe Glu Ser Glu Arg Asp
 115 120 125

Glu Leu Pro Asp His Leu Cys Val Val Leu Glu Ala Ala Ala Leu Ala
 130 135 140

Asp Ser Ser Leu Phe Asp Ala Ala Thr Gln Val Leu Ser Ala His Arg
 145 150 155 160

Asp Gly Ile Glu Val Leu Arg Ala Ala Leu Asp Asn Leu Asp Ser Pro
 165 170 175

Tyr Arg Tyr Leu Ile Met Ser Leu Cys Gln Ala Leu Pro Glu Ile Asp
 180 185 190

Glu Glu Thr Ala Asn Ser Tyr Met Glu Leu Ile Arg Ser Gly Pro Pro
 195 200 205

Ala Glu Met Val Gly Ile Gly Thr Pro Leu Pro Phe Pro Thr Ser Gln
 210 215 220

Pro Asp Ile His
 225

<210> 289
 <211> 1073
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1050)
 <223> RXA02018

<400> 289

cgc atc tgc gag cac tgc ctc aac ccc acc tgt gtg tcc tcc tgc cca	48
Arg Ile Cys Glu His Cys Leu Asn Pro Thr Cys Val Ser Ser Cys Pro	
1 5 10 15	
tcc ggt gct atg tac aaa cgc gcc gaa gac ggc atc gtg ctg gtt gac	96
Ser Gly Ala Met Tyr Lys Arg Ala Glu Asp Gly Ile Val Leu Val Asp	
20 25 30	
cag gat caa tgc cgt ggc tgg cgc atg tgt gtt tcc ggc tgc ccc tac	144
Gln Asp Gln Cys Arg Gly Trp Arg Met Cys Val Ser Gly Cys Pro Tyr	
35 40 45	
aaa aag gtc tac ttc aat cac aaa tcg ggc aag gcc gaa aag tgt acg	192
Lys Lys Val Tyr Phe Asn His Lys Ser Gly Lys Ala Glu Lys Cys Thr	
50 55 60	
ctg tgc tat ccg cgc ctc gag gtc ggc cag ccg acc gtg tgc tcc gag	240
Leu Cys Tyr Pro Arg Leu Glu Val Gly Gln Pro Thr Val Cys Ser Glu	
65 70 75 80	
acg tgc gtg ggt cgc ttg cgc tac ttg ggc gtt ttg ctt tac gac gcc	288
Thr Cys Val Gly Arg Leu Arg Tyr Leu Gly Val Leu Leu Tyr Asp Ala	
85 90 95	
gac cgt gtc gct gaa gtc gcc gcc acg cca gac gaa aag gat ctt ttc	336
Asp Arg Val Ala Glu Val Ala Ala Thr Pro Asp Glu Lys Asp Leu Phe	
100 105 110	
gaa gcc caa aag acc ctc ttc cta gat ccc cac gac cca cag gtg atc	384
Glu Ala Gln Lys Thr Leu Phe Leu Asp Pro His Asp Pro Gln Val Ile	
115 120 125	
gcc gac gcc caa cgc aac ggc atc ccg cac tcc tgg ctc gaa gct gcg	432
Ala Asp Ala Gln Arg Asn Gly Ile Pro His Ser Trp Leu Glu Ala Ala	
130 135 140	

cag aac tct cca att tac gat ctc atc ttc aaa tac gag gtt gcc ctc	480
Gln Asn Ser Pro Ile Tyr Asp Leu Ile Phe Lys Tyr Glu Val Ala Leu	
145 150 155 160	
ccg ctt cac cct gaa tac cgc acc ttg ccg atg gtt tgg tac att ccg	528
Pro Leu His Pro Glu Tyr Arg Thr Leu Pro Met Val Trp Tyr Ile Pro	
165 170 175	
cca cta agc ccc atc gtt gat gag gtg acc gcg tcc ggc aac gac ggc	576
Pro Leu Ser Pro Ile Val Asp Glu Val Thr Ala Ser Gly Asn Asp Gly	
180 185 190	
gaa gac cac aag atc ctg ctc acc gcg ctg tcc acc atg cgc atc ccg	624
Glu Asp His Lys Ile Leu Leu Thr Ala Leu Ser Thr Met Arg Ile Pro	
195 200 205	
ctg gaa tac ctg gct gga ttg ttc act gcc ggt gat acc agg ccg gtg	672
Leu Glu Tyr Leu Ala Gly Leu Phe Thr Ala Gly Asp Thr Arg Pro Val	
210 215 220	
gaa aaa tcc ctc cga cgc cta gcc gcc atg cga tca tat atg cgc gat	720
Glu Lys Ser Leu Arg Arg Leu Ala Ala Met Arg Ser Tyr Met Arg Asp	
225 230 235 240	
atc agt ttg ggc cgc gaa cct cag gaa gaa atc gca gag gct gtc gga	768
Ile Ser Leu Gly Arg Glu Pro Gln Glu Glu Ile Ala Glu Ala Val Gly	
245 250 255	
atg acc ggc aag gtg gtg cag gaa atg tat cgc atc ctg gcc att gcc	816
Met Thr Gly Lys Val Val Gln Glu Met Tyr Arg Ile Leu Ala Ile Ala	
260 265 270	
aag tat gac gat cgc tat gtc atc ccc acc gcc tcc cct gag acc ccg	864
Lys Tyr Asp Asp Arg Tyr Val Ile Pro Thr Ala Ser Pro Glu Thr Pro	
275 280 285	
cgc gga att tct tcc ctg gat cct ttc ggc gat gtc gat cca gcc cga	912
Arg Gly Ile Ser Ser Leu Asp Pro Phe Gly Asp Val Asp Pro Ala Arg	
290 295 300	
gcc acc gag cag ctc aac atc ggt ttg ggc gaa ggc gct cca gag gcc	960
Ala Thr Glu Gln Leu Asn Ile Gly Leu Gly Glu Gly Ala Pro Glu Ala	
305 310 315 320	
tgt ggc acg gga gct ccc agc ggc aag gtg agt ctg acc tcg tgg aac	1008
Cys Gly Thr Gly Ala Pro Ser Gly Lys Val Ser Leu Thr Ser Trp Asn	
325 330 335	
gtt ggc gaa cgc ccc gct gcg atg ttc cca cca agg aag gac	1050
Val Gly Glu Arg Pro Ala Ala Met Phe Pro Pro Arg Lys Asp	
340 345 350	
taggcggatg cgcacccata ctg	1073

<210> 290

<211> 350

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Arg Ile Cys Glu His Cys Leu Asn Pro Thr Cys Val Ser Ser Cys Pro
 1 5 10 15
 Ser Gly Ala Met Tyr Lys Arg Ala Glu Asp Gly Ile Val Leu Val Asp
 20 25 30
 Gln Asp Gln Cys Arg Gly Trp Arg Met Cys Val Ser Gly Cys Pro Tyr
 35 40 45
 Lys Lys Val Tyr Phe Asn His Lys Ser Gly Lys Ala Glu Lys Cys Thr
 50 55 60
 Leu Cys Tyr Pro Arg Leu Glu Val Gly Gln Pro Thr Val Cys Ser Glu
 65 70 75 80
 Thr Cys Val Gly Arg Leu Arg Tyr Leu Gly Val Leu Leu Tyr Asp Ala
 85 90 95
 Asp Arg Val Ala Glu Val Ala Ala Thr Pro Asp Glu Lys Asp Leu Phe
 100 105 110
 Glu Ala Gln Lys Thr Leu Phe Leu Asp Pro His Asp Pro Gln Val Ile
 115 120 125
 Ala Asp Ala Gln Arg Asn Gly Ile Pro His Ser Trp Leu Glu Ala Ala
 130 135 140
 Gln Asn Ser Pro Ile Tyr Asp Leu Ile Phe Lys Tyr Glu Val Ala Leu
 145 150 155 160
 Pro Leu His Pro Glu Tyr Arg Thr Leu Pro Met Val Trp Tyr Ile Pro
 165 170 175
 Pro Leu Ser Pro Ile Val Asp Glu Val Thr Ala Ser Gly Asn Asp Gly
 180 185 190
 Glu Asp His Lys Ile Leu Leu Thr Ala Leu Ser Thr Met Arg Ile Pro
 195 200 205
 Leu Glu Tyr Leu Ala Gly Leu Phe Thr Ala Gly Asp Thr Arg Pro Val
 210 215 220
 Glu Lys Ser Leu Arg Arg Leu Ala Ala Met Arg Ser Tyr Met Arg Asp
 225 230 235 240
 Ile Ser Leu Gly Arg Glu Pro Gln Glu Glu Ile Ala Glu Ala Val Gly
 245 250 255
 Met Thr Gly Lys Val Val Gln Glu Met Tyr Arg Ile Leu Ala Ile Ala
 260 265 270
 Lys Tyr Asp Asp Arg Tyr Val Ile Pro Thr Ala Ser Pro Glu Thr Pro
 275 280 285
 Arg Gly Ile Ser Ser Leu Asp Pro Phe Gly Asp Val Asp Pro Ala Arg
 290 295 300
 Ala Thr Glu Gln Leu Asn Ile Gly Leu Gly Glu Gly Ala Pro Glu Ala
 305 310 315 320
 Cys Gly Thr Gly Ala Pro Ser Gly Lys Val Ser Leu Thr Ser Trp Asn

325

330

335

Val Gly Glu Arg Pro Ala Ala Met Phe Pro Pro Arg Lys Asp
 340 345 350

<210> 291

<211> 900

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(877)

<223> RXA02016

<400> 291

acatggagct catccgcagc ggtccaccag cagaaatggt gggcatcggc acgcctctac 60

cgttccccac ctcacaaccg gacattcact aggacacact atg tca aac ttt gaa 115
 Met Ser Asn Phe Glu
 1 5

acg ttc ctc tgg gtt gcc tac ccc tgg ctg tgt atc gcc gcc tac atc 163
 Thr Phe Leu Trp Val Ala Tyr Pro Trp Leu Cys Ile Ala Ala Tyr Ile
 10 15 20

atc ggc att tct tgg cgc tgg cgc gcc gac caa ttc ggt tgg acc acc 211
 Ile Gly Ile Ser Trp Arg Trp Arg Ala Asp Gln Phe Gly Trp Thr Thr
 25 30 35

cac tcc tcc caa atc tac gaa tcc aaa ctc ctc cgc atc gcc tcc cca 259
 His Ser Ser Gln Ile Tyr Glu Ser Lys Leu Leu Arg Ile Ala Ser Pro
 40 45 50

ctc ttc cac tgg ggc atg gtg ttc gtg gtg atc ggc cac ctc atg gga 307
 Leu Phe His Trp Gly Met Val Phe Val Val Ile Gly His Leu Met Gly
 55 60 65

ctt gcc atc ccc aag agc tgg acc caa gct gta gga att tct gac gcc 355
 Leu Ala Ile Pro Lys Ser Trp Thr Gln Ala Val Gly Ile Ser Asp Ala
 70 75 80 85

gct tac cac ctc atc gcc acc atc cca ggc acc att gcc ggc atc gct 403
 Ala Tyr His Leu Ile Ala Thr Ile Pro Gly Thr Ile Ala Gly Ile Ala
 90 95 100

gca gtc ctt gga ctc atc ggc ttg att atc cgt cgc gtg atc aac aaa 451
 Ala Val Leu Gly Leu Ile Gly Leu Ile Ile Arg Arg Val Ile Asn Lys
 105 110 115

acc gtc ttc ctg tcc acc tca cgc tcc gac aaa gtg atg tat gtg cta 499
 Thr Val Phe Leu Ser Thr Ser Arg Ser Asp Lys Val Met Tyr Val Leu
 120 125 130

ctc ggc gct gca att ttg tcc ggt ttc atc gcc acc gtc tcc acc cag 547
 Leu Gly Ala Ala Ile Leu Ser Gly Phe Ile Ala Thr Val Ser Thr Gln
 135 140 145

gtc ttc ggc ggc gca cac ggc tac gac tac cgc gaa acc atc tcc cca 595
 Val Phe Gly Gly Ala His Gly Tyr Asp Tyr Arg Glu Thr Ile Ser Pro

150	155	160	165	
tgg gtc cgc caa ctg ctc atc ttc aac gct caa cca gag ctc atg gct				643
Trp Val Arg Gln Leu Leu Ile Phe Asn Ala Gln Pro Glu Leu Met Ala				
	170	175	180	
gat gtc cct tgg gaa ttc aag gtc cac atc gtc gct gga ttc acc ctc				691
Asp Val Pro Trp Glu Phe Lys Val His Ile Val Ala Gly Phe Thr Leu				
	185	190	195	
atc gca ctg tgg cca ttc acc cgc cta gtc cac gcg ttc tcc gca cca				739
Ile Ala Leu Trp Pro Phe Thr Arg Leu Val His Ala Phe Ser Ala Pro				
	200	205	210	
gtt gga tac gtc acc cgc ccc tac gtg gtc tat cgc acc cgc gac acc				787
Val Gly Tyr Val Thr Arg Pro Tyr Val Val Tyr Arg Thr Arg Asp Thr				
	215	220	225	
acc tct gaa ccg gca cgc caa aac gtc gcc tgg gaa ccg atc cgc tcg				835
Thr Ser Glu Pro Ala Arg Gln Asn Val Ala Trp Glu Pro Ile Arg Ser				
	230	235	240	245
gtc aaa aat cag ctc gac aat gac tcg aaa tgg cac ggc gcc				877
Val Lys Asn Gln Leu Asp Asn Asp Ser Lys Trp His Gly Ala				
	250	255		
taaattcctc acaagcccc tag				900

<210> 292

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Ser Asn Phe Glu Thr Phe Leu Trp Val Ala Tyr Pro Trp Leu Cys				
1	5	10	15	
Ile Ala Ala Tyr Ile Ile Gly Ile Ser Trp Arg Trp Arg Ala Asp Gln				
	20	25	30	
Phe Gly Trp Thr Thr His Ser Ser Gln Ile Tyr Glu Ser Lys Leu Leu				
	35	40	45	
Arg Ile Ala Ser Pro Leu Phe His Trp Gly Met Val Phe Val Val Ile				
	50	55	60	
Gly His Leu Met Gly Leu Ala Ile Pro Lys Ser Trp Thr Gln Ala Val				
	65	70	75	80
Gly Ile Ser Asp Ala Ala Tyr His Leu Ile Ala Thr Ile Pro Gly Thr				
	85	90	95	
Ile Ala Gly Ile Ala Ala Val Leu Gly Leu Ile Gly Leu Ile Ile Arg				
	100	105	110	
Arg Val Ile Asn Lys Thr Val Phe Leu Ser Thr Ser Arg Ser Asp Lys				
	115	120	125	
Val Met Tyr Val Leu Leu Gly Ala Ala Ile Leu Ser Gly Phe Ile Ala				
	130	135	140	

Thr Val Ser Thr Gln Val Phe Gly Gly Ala His Gly Tyr Asp Tyr Arg
 145 150 155 160
 Glu Thr Ile Ser Pro Trp Val Arg Gln Leu Leu Ile Phe Asn Ala Gln
 165 170 175
 Pro Glu Leu Met Ala Asp Val Pro Trp Glu Phe Lys Val His Ile Val
 180 185 190
 Ala Gly Phe Thr Leu Ile Ala Leu Trp Pro Phe Thr Arg Leu Val His
 195 200 205
 Ala Phe Ser Ala Pro Val Gly Tyr Val Thr Arg Pro Tyr Val Val Tyr
 210 215 220
 Arg Thr Arg Asp Thr Thr Ser Glu Pro Ala Arg Gln Asn Val Ala Trp
 225 230 235 240
 Glu Pro Ile Arg Ser Val Lys Asn Gln Leu Asp Asn Asp Ser Lys Trp
 245 250 255
 His Gly Ala

<210> 293
 <211> 813
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(790)
 <223> RXA00471

<400> 293
 acgcatcaaa tctgaaatcg gcgaaggcac cgaagtggca atcaccatgg atgtgtagtt 60
 ggctgtacgc gcgtgtcttc ggggctgtaa cctgaaaggc atg gtt gat gtg ttt 115
 Met Val Asp Val Phe
 1 5
 ttg gtc gat gac cac tcc gtg ttt cgc tcc ggc gtc aaa gca gaa cta 163
 Leu Val Asp Asp His Ser Val Phe Arg Ser Gly Val Lys Ala Glu Leu
 10 15 20
 ggc aac gcc gtc aca gta gtc ggc gaa gca ggg acg gtg gcc gac gcc 211
 Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly Thr Val Ala Asp Ala
 25 30 35
 gta gcc ggc atc aag gca agc aaa cca gag gta gtg ctt ctc gac gtc 259
 Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val Val Leu Leu Asp Val
 40 45 50
 cac atg ccc gac ggc ggc ggc ctc gca gtg ctc cag cag atc aac gac 307
 His Met Pro Asp Gly Gly Gly Leu Ala Val Leu Gln Gln Ile Asn Asp
 55 60 65
 tcc gat gtg gac acc att ttc ttg gca ctc agt gtc tct gat gct gcg 355
 Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser Val Ser Asp Ala Ala

70	75	80	85	
gaa gat gtc atc gcc atc atc cgt ggc ggt gcc agg gga tac gtg acc				403
Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala Arg Gly Tyr Val Thr				
	90	95	100	
aaa tca atc tcc ggt gaa gaa ctc atc gaa gcc atc aac cgc gtg aaa				451
Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala Ile Asn Arg Val Lys				
	105	110	115	
tcc ggc gac gca ttc ttc tca cca cgc ctg gca ggc ttt gtc ctc gac				499
Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala Gly Phe Val Leu Asp				
	120	125	130	
gcc ttc gcc gcc ccc gat tcc gca gct ggc gca ggc att gtc gac gca				547
Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala Gly Ile Val Asp Ala				
	135	140	145	
ccc gaa aaa gac gcc gcc gta gaa tcc gga aaa atc ctc gac gac cca				595
Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys Ile Leu Asp Asp Pro				
	150	155	160	165
gtt gtc gac gcc ctc acc cgc cgc gaa ctc gaa gtc ctc cgc cta cta				643
Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu Val Leu Arg Leu Leu				
	170	175	180	
gcc cgc ggc tac acc tac aaa gaa atc ggc aaa gaa ctg ttc att tcc				691
Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys Glu Leu Phe Ile Ser				
	185	190	195	
gtc aaa acc gtg gaa acc cac gcc tca aac att ctg cgg aaa acc caa				739
Val Lys Thr Val Glu Thr His Ala Ser Asn Ile Leu Arg Lys Thr Gln				
	200	205	210	
caa tcc aac cgc cac gcg ttg acc cgg tgg gct cac tcg agg gat ctt				787
Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala His Ser Arg Asp Leu				
	215	220	225	
gac taatggcggc taaaaagagt ggc				813
Asp				
230				

<210> 294

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met	Val	Asp	Val	Phe	Leu	Val	Asp	Asp	His	Ser	Val	Phe	Arg	Ser	Gly
1				5					10					15	

Val	Lys	Ala	Glu	Leu	Gly	Asn	Ala	Val	Thr	Val	Val	Gly	Glu	Ala	Gly
			20					25					30		

Thr	Val	Ala	Asp	Ala	Val	Ala	Gly	Ile	Lys	Ala	Ser	Lys	Pro	Glu	Val
			35				40					45			

Val	Leu	Leu	Asp	Val	His	Met	Pro	Asp	Gly	Gly	Gly	Leu	Ala	Val	Leu
	50					55					60				

Gln Gln Ile Asn Asp Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser
 65 70 75 80
 Val Ser Asp Ala Ala Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala
 85 90 95
 Arg Gly Tyr Val Thr Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala
 100 105 110
 Ile Asn Arg Val Lys Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala
 115 120 125
 Gly Phe Val Leu Asp Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala
 130 135 140
 Gly Ile Val Asp Ala Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys
 145 150 155 160
 Ile Leu Asp Asp Pro Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu
 165 170 175
 Val Leu Arg Leu Leu Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys
 180 185 190
 Glu Leu Phe Ile Ser Val Lys Thr Val Glu Thr His Ala Ser Asn Ile
 195 200 205
 Leu Arg Lys Thr Gln Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala
 210 215 220
 His Ser Arg Asp Leu Asp
 225 230

<210> 295

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXA00133

<400> 295

gttacatcag atgaggatgc cctatgggtg tacacatgcg acgggtgtat tgcaggagga 60

aatttgaagg tggataccca gcggattaa gatgatgaag atg cta ttc gtt cgg 115
 Met Leu Phe Val Arg
 1 5

cgg ctg aca tcg ctg aaa acc gca aca ggc atc cca gtc acc atg ttc 163
 Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile Pro Val Thr Met Phe
 10 15 20

gcc act gtg ttg cag gac aat cgc ctg caa att act cag tgg gtt ggg 211
 Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile Thr Gln Trp Val Gly
 25 30 35

ttg cgt acc ccg gct ctg cag aat ctg gtc att gaa cca ggt gtg ggc 259
 Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile Glu Pro Gly Val Gly

40				45				50								
gtt	ggg	gga	cgc	gtc	gtc	gca	acc	cgt	cgt	ccg	gtt	ggg	gtg	agt	gat	307
Val	Gly	Gly	Arg	Val	Val	Ala	Thr	Arg	Arg	Pro	Val	Gly	Val	Ser	Asp	
55				60				65								
tac	acc	agg	gca	aat	gtc	att	tca	cat	gag	aag	gat	tcc	gcg	att	cag	355
Tyr	Thr	Arg	Ala	Asn	Val	Ile	Ser	His	Glu	Lys	Asp	Ser	Ala	Ile	Gln	
70				75				80				85				
gat	gag	ggc	ctt	cat	tcc	att	gtc	gca	gtt	ccc	gtg	atc	gtg	cac	cgc	403
Asp	Glu	Gly	Leu	His	Ser	Ile	Val	Ala	Val	Pro	Val	Ile	Val	His	Arg	
90				95				100								
gaa	att	cgt	ggc	gtt	ttg	tat	gtt	ggc	gtt	cac	tct	gcg	gtg	cgt	ctc	451
Glu	Ile	Arg	Gly	Val	Leu	Tyr	Val	Gly	Val	His	Ser	Ala	Val	Arg	Leu	
105				110				115								
ggc	gac	act	gtt	att	gaa	gaa	gtc	acc	atg	act	gcg	cgc	acg	ttg	gaa	499
Gly	Asp	Thr	Val	Ile	Glu	Glu	Val	Thr	Met	Thr	Ala	Arg	Thr	Leu	Glu	
120				125				130								
caa	aac	ctg	gcg	atc	aac	tcc	gcg	ctt	cgc	cgc	aat	ggc	gtt	cct	gat	547
Gln	Asn	Leu	Ala	Ile	Asn	Ser	Ala	Leu	Arg	Arg	Asn	Gly	Val	Pro	Asp	
135				140				145								
ggg	cgc	ggg	tcc	ctc	aaa	gct	aac	cgc	gtg	atg	aat	ggg	gcg	gag	tgg	595
Gly	Arg	Gly	Ser	Leu	Lys	Ala	Asn	Arg	Val	Met	Asn	Gly	Ala	Glu	Trp	
150				155				160				165				
gag	cag	gtt	cgt	tcc	act	cat	tcc	aag	ctg	cgc	atg	ctg	gca	aat	cgt	643
Glu	Gln	Val	Arg	Ser	Thr	His	Ser	Lys	Leu	Arg	Met	Leu	Ala	Asn	Arg	
170				175				180								
gtg	acc	gat	gag	gat	ctg	cgc	cgc	gat	ttg	gaa	gag	ctt	tgc	gat	cag	691
Val	Thr	Asp	Glu	Asp	Leu	Arg	Arg	Asp	Leu	Glu	Glu	Leu	Cys	Asp	Gln	
185				190				195								
atg	gtc	acc	cca	gtc	cgc	atc	aag	cag	acc	acc	aag	ctg	tcc	gcg	cgt	739
Met	Val	Thr	Pro	Val	Arg	Ile	Lys	Gln	Thr	Thr	Lys	Leu	Ser	Ala	Arg	
200				205				210								
gag	ttg	gac	gtg	ctg	gct	tgt	gtc	gcg	ctc	ggg	cac	acc	aac	gtc	gaa	787
Glu	Leu	Asp	Val	Leu	Ala	Cys	Val	Ala	Leu	Gly	His	Thr	Asn	Val	Glu	
215				220				225								
gct	gct	gaa	gag	atg	ggc	atc	ggc	gcg	gaa	acc	gtc	aag	agc	tac	ctg	835
Ala	Ala	Glu	Glu	Met	Gly	Ile	Gly	Ala	Glu	Thr	Val	Lys	Ser	Tyr	Leu	
230				235				240				245				
cgc	tcg	gtc	atg	cgc	aag	ctc	ggc	gcc	cac	acg	cgc	tac	gag	gca	gtc	883
Arg	Ser	Val	Met	Arg	Lys	Leu	Gly	Ala	His	Thr	Arg	Tyr	Glu	Ala	Val	
250				255				260								
aac	gca	gca	cgc	cgg	atc	ggc	gca	ctg	cct	taaaaagatt ttgctttacg						933
Asn	Ala	Ala	Arg	Arg	Ile	Gly	Ala	Leu	Pro							
265				270												
acg																936

<210> 296
 <211> 271
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 296

```

Met Leu Phe Val Arg Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile
 1           5           10           15

Pro Val Thr Met Phe Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile
      20           25           30

Thr Gln Trp Val Gly Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile
      35           40           45

Glu Pro Gly Val Gly Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro
      50           55           60

Val Gly Val Ser Asp Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys
      65           70           75           80

Asp Ser Ala Ile Gln Asp Glu Gly Leu His Ser Ile Val Ala Val Pro
      85           90           95

Val Ile Val His Arg Glu Ile Arg Gly Val Leu Tyr Val Gly Val His
      100          105          110

Ser Ala Val Arg Leu Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr
      115          120          125

Ala Arg Thr Leu Glu Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg
      130          135          140

Asn Gly Val Pro Asp Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met
      145          150          155          160

Asn Gly Ala Glu Trp Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg
      165          170          175

Met Leu Ala Asn Arg Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu
      180          185          190

Glu Leu Cys Asp Gln Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr
      195          200          205

Lys Leu Ser Ala Arg Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly
      210          215          220

His Thr Asn Val Glu Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr
      225          230          235          240

Val Lys Ser Tyr Leu Arg Ser Val Met Arg Lys Leu Gly Ala His Thr
      245          250          255

Arg Tyr Glu Ala Val Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro
      260          265          270

```

<210> 297
 <211> 759
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXA00650

<400> 297

```

aaggctagac taaagtaga ttcattctgct catcgatact cttgaaggcg cattttcatt 60

cgaaacgaag tgcgccattg ggaaggacct agttcaaaca atg att cgc gtg ctg 115
                                         Met Ile Arg Val Leu
                                         1           5

ctt gct gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg 163
Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu
                        10                        15                        20

gaa agc gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa 211
Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu
                        25                        30                        35

ggt gcg gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg 259
Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met
                        40                        45                        50

gac ctc cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc 307
Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly
                        55                        60                        65

gca gac gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa 355
Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys
                        70                        75                        80                        85

gtc ctg gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca 403
Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala
                        90                        95                        100

atc gaa gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc 451
Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser
                        105                        110                        115

gaa ctc ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg 499
Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu
                        120                        125                        130

tca ccc atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa 547
Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys
                        135                        140                        145

acc tca ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt 595
Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly
                        150                        155                        160                        165

gga tcc tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc 643
Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala
                        170                        175                        180

acg gtg aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg 691
Thr Val Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg
                        185                        190                        195

```

tca cgt acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg 736
 Ser Arg Thr Ser Ala Val Ala Ala Arg Glu Gln Gly Leu Leu
 200 205 210

tagcgggggt tgctgcaagg ctt 759

<210> 298
 <211> 212
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 298
 Met Ile Arg Val Leu Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly
 1 5 10 15
 Leu Arg Ala Val Leu Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu
 20 25 30
 Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile
 35 40 45
 Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr
 50 55 60
 Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile
 65 70 75 80
 Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr
 85 90 95
 Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys
 100 105 110
 Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu
 115 120 125
 Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg
 130 135 140
 Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu
 145 150 155 160
 Lys Leu Val Ala Gly Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu
 165 170 175
 Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp
 180 185 190
 Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu
 195 200 205
 Gln Gly Leu Leu
 210

<210> 299
 <211> 655
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (24)..(632)

<223> RXA01189

<400> 299

```

cacctgcaga aaaggaagct taaatg att tcc att tcc atc gcc gac gac gaa 53
                Met Ile Ser Ile Ser Ile Ala Asp Asp Glu
                  1                      5                      10

gcc ctg atc gca agc tcc ctg gca acc ttg ctc agc ttg gaa ccc gat 101
Ala Leu Ile Ala Ser Ser Leu Ala Thr Leu Leu Ser Leu Glu Pro Asp
                  15                      20                      25

tta gac gtc cga cct acc gca gga tcc ggt gaa gaa ctc att gaa acg 149
Leu Asp Val Arg Pro Thr Ala Gly Ser Gly Glu Glu Leu Ile Glu Thr
                  30                      35                      40

tgg gcg gat cca agc aac cga acc gat gta tgc gtc ctt gac ctt caa 197
Trp Ala Asp Pro Ser Asn Arg Thr Asp Val Cys Val Leu Asp Leu Gln
                  45                      50                      55

ctc gga ggc atc gac ggc atc gac acc gcc acc cgg ctc atg gaa acc 245
Leu Gly Gly Ile Asp Gly Ile Asp Thr Ala Thr Arg Leu Met Glu Thr
                  60                      65                      70

acc cca gat ttg gcc gtg ctc atc gtg acc agc cac gcc agg ccc cga 293
Thr Pro Asp Leu Ala Val Leu Ile Val Thr Ser His Ala Arg Pro Arg
                  75                      80                      85                      90

caa ctc aaa cgc gcg ctt gca gca ggt gtt tta gga ttc ttg ccc aaa 341
Gln Leu Lys Arg Ala Leu Ala Ala Gly Val Leu Gly Phe Leu Pro Lys
                  95                      100                      105

aca tcc acc gca gat gaa ttc gcc acc gca atc cgc acc gtt cac gct 389
Thr Ser Thr Ala Asp Glu Phe Ala Thr Ala Ile Arg Thr Val His Ala
                  110                      115                      120

gga cga cgc tac atc gac ccc gaa cta gcc gcc atg acg atc agc gcc 437
Gly Arg Arg Tyr Ile Asp Pro Glu Leu Ala Ala Met Thr Ile Ser Ala
                  125                      130                      135

ggt gaa tcc cca tta acc aac cgt gaa gaa gaa gtc ctc gaa cta gca 485
Gly Glu Ser Pro Leu Thr Asn Arg Glu Glu Glu Val Leu Glu Leu Ala
                  140                      145                      150

ggc caa gga cta agc gcc gaa gaa att gcg gtg gca gcg cac ctc gcg 533
Gly Gln Gly Leu Ser Ala Glu Glu Ile Ala Val Ala Ala His Leu Ala
                  155                      160                      165                      170

ccg gga acc acc cgc aac tat tta tcc caa gct atg aca aaa gta ggc 581
Pro Gly Thr Thr Arg Asn Tyr Leu Ser Gln Ala Met Thr Lys Val Gly
                  175                      180                      185

gcg cag aat cgc ttt gaa gcg ttc acg cgc gcc agg gaa ttg ggc tgg 629
Ala Gln Asn Arg Phe Glu Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp
                  190                      195                      200

ttg tagcttggtg cttatctcct att 655
Leu

```

<210> 300
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 300
 Met Ile Ser Ile Ser Ile Ala Asp Asp Glu Ala Leu Ile Ala Ser Ser
 1 5 10 15
 Leu Ala Thr Leu Leu Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr
 20 25 30
 Ala Gly Ser Gly Glu Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn
 35 40 45
 Arg Thr Asp Val Cys Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly
 50 55 60
 Ile Asp Thr Ala Thr Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val
 65 70 75 80
 Leu Ile Val Thr Ser His Ala Arg Pro Arg Gln Leu Lys Arg Ala Leu
 85 90 95
 Ala Ala Gly Val Leu Gly Phe Leu Pro Lys Thr Ser Thr Ala Asp Glu
 100 105 110
 Phe Ala Thr Ala Ile Arg Thr Val His Ala Gly Arg Arg Tyr Ile Asp
 115 120 125
 Pro Glu Leu Ala Ala Met Thr Ile Ser Ala Gly Glu Ser Pro Leu Thr
 130 135 140
 Asn Arg Glu Glu Glu Val Leu Glu Leu Ala Gly Gln Gly Leu Ser Ala
 145 150 155 160
 Glu Glu Ile Ala Val Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn
 165 170 175
 Tyr Leu Ser Gln Ala Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu
 180 185 190
 Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp Leu
 195 200

<210> 301
 <211> 753
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(730)
 <223> RXA01607

<400> 301
 gggctgaagg gctgggcgga acaataatta ttgaatctac aatcggatcg ggaactggaa 60

```

tttccgccccg ttttccctat ccacaaaagg accaagataa gtg atc cgt att ctg 115
Val Ile Arg Ile Leu
1 5

ttg gct gat gat cat ccc gtt gtt cgc gca ggc ctt gcc tcc ttg ctg 163
Leu Ala Asp Asp His Pro Val Val Arg Ala Gly Leu Ala Ser Leu Leu
10 15 20

gtg agt gaa gat gat ttt gag ata gtg gac atg gtg ggc acc cca gat 211
Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met Val Gly Thr Pro Asp
25 30 35

gat gcc gtt gcg cgc gcc gcg gaa ggc ggg gtg gat gtg gtg ttg atg 259
Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val Asp Val Val Leu Met
40 45 50

gat ctg cgt ttt ggt gat caa cca ggc atc gag gtc gcc ggc ggg gta 307
Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu Val Ala Gly Gly Val
55 60 65

gag gca acg cgt cgc atc cgt gcg ctg gac aac ccg cca cag gta ctg 355
Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn Pro Pro Gln Val Leu
70 75 80 85

gtg gtg acc aac tac tcc aca gac ggc gat gtg gtg ggc gca gta tct 403
Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val Val Gly Ala Val Ser
90 95 100

gct ggt gcc gtg ggg tat ttg ctc aaa gat agc tcc cca gaa gat ctc 451
Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser Ser Pro Glu Asp Leu
105 110 115

att gcc ggt gtt cgc gat gcc gcg cgg gga gaa tca gtg ctt tca aag 499
Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu Ser Val Leu Ser Lys
120 125 130

cag gtc gcc agc aag atc atg ggg cgg atg aac aac ccc atg act gct 547
Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn Asn Pro Met Thr Ala
135 140 145

ctc agt gcc aga gaa att gaa gtg ctg tcc ttg gtg gcg caa ggg caa 595
Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu Val Ala Gln Gly Gln
150 155 160 165

agc aat aga gaa atc ggc aag aaa ctt ttc ctc act gag gcc acg gtg 643
Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu Thr Glu Ala Thr Val
170 175 180

aaa agt cac atg ggg cat gtg ttc aac aag ctg gat gtc acc tct aga 691
Lys Ser His Met Gly His Val Phe Asn Lys Leu Asp Val Thr Ser Arg
185 190 195

aca gct gcg gta gct gaa gcc aga cag cgc gga att atc tagacgcaca 740
Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly Ile Ile
200 205 210

cgtgttggtgta acc 753

```

<210> 302

<211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 302
 Val Ile Arg Ile Leu Leu Ala Asp Asp His Pro Val Val Arg Ala Gly
 1 5 10 15
 Leu Ala Ser Leu Leu Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met
 20 25 30
 Val Gly Thr Pro Asp Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val
 35 40 45
 Asp Val Val Leu Met Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu
 50 55 60
 Val Ala Gly Gly Val Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn
 65 70 75 80
 Pro Pro Gln Val Leu Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val
 85 90 95
 Val Gly Ala Val Ser Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser
 100 105 110
 Ser Pro Glu Asp Leu Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu
 115 120 125
 Ser Val Leu Ser Lys Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn
 130 135 140
 Asn Pro Met Thr Ala Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu
 145 150 155 160
 Val Ala Gln Gly Gln Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu
 165 170 175
 Thr Glu Ala Thr Val Lys Ser His Met Gly His Val Phe Asn Lys Leu
 180 185 190
 Asp Val Thr Ser Arg Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly
 195 200 205
 Ile Ile
 210

<210> 303
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1369)
 <223> RXN00470

<400> 303
 tcataaccag gttgggcaaa agggatgaat ccctggttgt ggtggggctc ctgaaaagta 60

ctcatagact	ctattgtgga	gtgttgaggc	tgataagtga	atg Met 1	ggg Gly	gaa Glu	agc Ser	cct Pro 5	115							
gaa Glu	aag Lys	gtg Val	gcg Ala	ttc Phe 10	agg Arg	gtc Val	ttc Phe	cct Pro 15	gat Asp	ggt Gly	ttg Leu	gtg Val	tcg Ser	cag Gln 20	ggg Gly	163
cat His	gac Asp	atg Met	atc Ile 25	gaa Glu	gat Asp	atg Met	agt Ser	aac Asn 30	aca Thr	cct Pro	gcg Ala	cct Pro	tat Tyr 35	acc Thr	ccg Pro	211
cag Gln	cct Pro	gcg Ala	ggg Gly	caa Gln	gcg Ala	gtg Val	cct Pro 45	tta Leu	tat Tyr	ccc Pro	acg Thr	ttt Phe 50	acc Thr	cgg Arg	tca Ser	259
aga Arg	gat Asp 55	ggt Gly	cgg Arg	gtt Val	gtt Val	gcg Ala 60	ggt Gly	gtc Val	gca Ala	tcg Ser	ggg Gly 65	ctg Leu	gca Ala	aag Lys	cat His	307
ctt Leu 70	aat Asn	gtg Val	tcg Ser	gtg Val	ttt Phe 75	tgg Trp	gtt Val	cgt Arg	gcg Ala	ctg Leu 80	ctg Leu	att Ile	ttt Phe	gcg Ala	gcg Ala 85	355
ttg Leu	ctg Leu	agc Ser	ggt Gly	gcg Ala 90	ggt Gly	ctt Leu	ttt Phe	gcg Ala	tat Tyr 95	gcc Ala	ttg Leu	att Ile	tgg Trp 100	att Ile	ttt Phe	403
acg Thr	cgc Arg	att Ile	gag Glu 105	aaa Lys	aag Lys	ggg Gly	agt Ser	ggg Gly 110	gag Glu	gcg Ala	tcg Ser	aca Thr	agc Ser 115	aag Lys	cgc Arg	451
tgg Trp	gtg Val	tcg Ser 120	tgg Trp	tgc Cys	ctg Leu	gtg Val	ctg Leu 125	ctc Leu	gct Ala	atc Ile	ggt Gly	ggt Gly 130	gct Ala	gcg Ala	gcg Ala	499
tcg Ser	gtg Val 135	atg Met	ctg Leu	agc Ser	acc Thr	ggc Gly 140	ttc Phe	gcg Ala	gtg Val	ggc Gly	acg Thr 145	ttg Leu	gtg Val	ccc Pro	atc Ile	547
ggc Gly 150	gtg Val	gtc Val	ggt Gly	gtg Val	ggc Gly 155	ctg Leu	ttg Leu	atg Met	gtg Val	tgg Trp 160	ctg Leu	gcg Ala	tat Tyr	gac Asp	cgc Arg 165	595
ggg Gly	gtg Val	gaa Glu	tcc Ser	ggc Gly 170	ccg Pro	aat Asn	ctg Leu	ctg Leu	att Ile 175	att Ile	gcc Ala	acc Thr	ggc Gly	ggt Gly 180	gtg Val	643
ttg Leu	atg Met	ctg Leu	gtg Val 185	gcg Ala	atc Ile	gtg Val	ctg Leu	atc Ile	gtg Val	atg Met	aat Asn	tgg Trp 195	aac Asn	acc Thr	cag Gln	691
gac Asp	ggc Gly	ttc Phe 200	gtc Val	atg Met	gcg Ala	ctg Leu	gtg Val	gcc Ala	gtg Val	gtg Val	ctc Leu	acg Thr 210	ctg Leu	gtg Val	ggt Gly	739
gtg Val	gct Ala	gcg Ala	ctg Leu	ggc Gly	gtt Val	ccg Pro 220	ctg Leu	tgg Trp	gtg Val	cgg Arg	atg Met 225	tgg Trp	gat Asp	cag Gln	ctg Leu	787
ggc	gag	gag	cgc	gcg	gaa	aaa	gcc	gca	gct	gct	qag	cgc	gca	gat	att	835

Gly 230	Glu	Glu	Arg	Ala	Glu 235	Lys	Ala	Ala	Ala	Ala 240	Glu	Arg	Ala	Asp	Ile 245	
gct	tcc	cgc	ctg	cat	gat	tcg	gta	ctg	cag	acc	ttg	gcg	ctg	att	caa	883
Ala	Ser	Arg	Leu	His 250	Asp	Ser	Val	Leu	Gln 255	Thr	Leu	Ala	Leu	Ile 260	Gln	
aag	cgt	gcc	gac	gac	ccc	gcc	gaa	gtc	gcc	cgc	ctg	gcc	cgc	ggg	cag	931
Lys	Arg	Ala	Asp 265	Asp	Pro	Ala	Glu	Val 270	Ala	Arg	Leu	Ala	Arg	Gly 275	Gln	
gaa	cgc	gag	ctg	cgt	caa	tgg	ctg	ttt	gat	tcc	caa	gat	aaa	aca	cct	979
Glu	Arg	Glu 280	Leu	Arg	Gln	Trp	Leu 285	Phe	Asp	Ser	Gln	Asp 290	Lys	Thr	Pro	
caa	aca	acc	ggc	act	gtc	ttt	act	gcg	ttg	gag	cgc	gcc	tgc	ggg	gaa	1027
Gln	Thr	Thr	Gly	Thr	Val	Phe 300	Thr	Ala	Leu	Glu	Arg 305	Ala	Cys	Gly	Glu	
gtc	gag	gat	att	tac	gct	ctg	cgt	atc	gtg	cct	gtg	acc	gtg	gga	acc	1075
Val	Glu	Asp	Ile	Tyr	Ala	Leu 315	Arg	Ile	Val	Pro 320	Val	Thr	Val	Gly 325	Thr	
gat	gaa	gcg	ctg	act	gag	aaa	acg	cag	gca	gcg	gtg	atg	gca	gtc	cgc	1123
Asp	Glu	Ala	Leu	Thr 330	Glu	Lys	Thr	Gln	Ala 335	Ala	Val	Met	Ala	Val 340	Arg	
gaa	gca	ctc	gtg	aac	gtg	gcc	aag	cat	gcc	ggc	gtg	gaa	acc	gcc	gat	1171
Glu	Ala	Leu	Val 345	Asn	Val	Ala	Lys	His 350	Ala	Gly	Val	Glu	Thr 355	Ala	Asp	
gtg	tac	gcc	gaa	att	atg	ctc	ggc	gaa	ctg	aac	att	ttc	gtc	cgc	gac	1219
Val	Tyr	Ala	Glu	Ile	Met	Leu 365	Gly	Glu	Leu	Asn	Ile	Phe 370	Val	Arg	Asp	
cgc	ggt	gca	gga	ttc	gac	ccc	gac	aac	atc	ccc	gac	ggg	cac	cac	ggg	1267
Arg	Gly	Ala	Gly	Phe	Asp 380	Pro	Asp	Asn	Ile	Pro 385	Asp	Gly	His	His	Gly	
ctc	gcc	gaa	tcc	gtc	caa	ggc	cgc	gtc	gaa	cga	gcc	ggc	gga	aaa	gta	1315
Leu	Ala	Glu	Ser	Val	Gln 395	Gly	Arg	Val	Glu	Arg 400	Ala	Gly	Gly	Lys	Val 405	
cgc	atc	aaa	tct	gaa	atc	ggc	gaa	ggc	acc	gaa	gtg	gca	atc	acc	atg	1363
Arg	Ile	Lys	Ser	Glu 410	Ile	Gly	Glu	Gly	Thr 415	Glu	Val	Ala	Ile	Thr 420	Met	
gat	gtg	tagttggtcg	tacgcgcgtg	tct												1392
Asp	Val															

<210> 304

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met	Gly	Glu	Ser	Pro	Glu	Lys	Val	Ala	Phe	Arg	Val	Phe	Pro	Asp	Gly
1					5				10					15	

Leu Val Ser Gln Gly His Asp Met Ile Glu Asp Met Ser Asn Thr Pro
 20 25 30
 Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro
 35 40 45
 Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser
 50 55 60
 Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu
 65 70 75 80
 Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala
 85 90 95
 Leu Ile Trp Ile Phe Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala
 100 105 110
 Ser Thr Ser Lys Arg Trp Val Ser Trp Cys Leu Val Leu Leu Ala Ile
 115 120 125
 Gly Gly Ala Ala Ala Ser Val Met Leu Ser Thr Gly Phe Ala Val Gly
 130 135 140
 Thr Leu Val Pro Ile Gly Val Val Gly Val Gly Leu Leu Met Val Trp
 145 150 155 160
 Leu Ala Tyr Asp Arg Gly Val Glu Ser Gly Pro Asn Leu Leu Ile Ile
 165 170 175
 Ala Thr Gly Gly Val Leu Met Leu Val Ala Ile Val Leu Ile Val Met
 180 185 190
 Asn Trp Asn Thr Gln Asp Gly Phe Val Met Ala Leu Val Ala Val Val
 195 200 205
 Leu Thr Leu Val Gly Val Ala Ala Leu Gly Val Pro Leu Trp Val Arg
 210 215 220
 Met Trp Asp Gln Leu Gly Glu Glu Arg Ala Glu Lys Ala Ala Ala Ala
 225 230 235 240
 Glu Arg Ala Asp Ile Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr
 245 250 255
 Leu Ala Leu Ile Gln Lys Arg Ala Asp Asp Pro Ala Glu Val Ala Arg
 260 265 270
 Leu Ala Arg Gly Gln Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser
 275 280 285
 Gln Asp Lys Thr Pro Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu
 290 295 300
 Arg Ala Cys Gly Glu Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro
 305 310 315 320
 Val Thr Val Gly Thr Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Ala
 325 330 335
 Val Met Ala Val Arg Glu Ala Leu Val Asn Val Ala Lys His Ala Gly

340	345	350
Val Glu Thr Ala Asp Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn		
355	360	365
Ile Phe Val Arg Asp Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro		
370	375	380
Asp Gly His His Gly Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg		
385	390	395
Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu		
405	410	415
Val Ala Ile Thr Met Asp Val		
420		

<210> 305
 <211> 1323
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1300)
 <223> FRXA00470

<400> 305
 tctattgtgg agtgttgagg ctgataagtg aatgggggaa agccctgaaa aggtggcggtt 60
 cagggtcttc cctgatgggt tgggtgcgca ggggcatgac atg atc gaa gat atg 115
 Met Ile Glu Asp Met
 1 5
 agt aac aca cct gcg cct tat acc ccg cag cct gcg ggg caa gcg gtg 163
 Ser Asn Thr Pro Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val
 10 15 20
 cct tta tat ccc acg ttt acc cgg tca aga gat ggt cgg gtt gtt gcg 211
 Pro Leu Tyr Pro Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala
 25 30 35
 ggt gtc gca tcg ggg ctg gca aag cat ctt aat gtg tcg gtg ttt tgg 259
 Gly Val Ala Ser Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp
 40 45 50
 gtt cgt gcg ctg ctg att ttt gcg gcg ttg ctg agc ggt gcg ggt ctt 307
 Val Arg Ala Leu Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu
 55 60 65
 ttt gcg tat gcc ttg att tgg att ttt acg cgc att gag aaa aag ggg 355
 Phe Ala Tyr Ala Leu Ile Trp Ile Phe Thr Arg Ile Glu Lys Lys Gly
 70 75 80 85
 agt ggg gag gcg tcg aca agc aag cgc tgg gtg tcg tgg tgc ctg gtg 403
 Ser Gly Glu Ala Ser Thr Ser Lys Arg Trp Val Ser Trp Cys Leu Val
 90 95 100
 ctg ctc gct atc ggt ggt gct gcg gcg tcg gtg atg ctg agc acc ggc 451
 Leu Leu Ala Ile Gly Gly Ala Ala Ala Ser Val Met Leu Ser Thr Gly

105							110					115					
ttc	gcg	gtg	ggc	acg	ttg	gtg	ccc	atc	ggc	gtg	gtc	ggc	gtg	ggc	ctg	499	
Phe	Ala	Val	Gly	Thr	Leu	Val	Pro	Ile	Gly	Val	Val	Gly	Val	Gly	Leu		
		120					125					130					
ttg	atg	gtg	tgg	ctg	gcg	tat	gac	cgc	ggg	gtg	gaa	tcc	ggc	ccg	aat	547	
Leu	Met	Val	Trp	Leu	Ala	Tyr	Asp	Arg	Gly	Val	Glu	Ser	Gly	Pro	Asn		
		135				140					145						
ctg	ctg	att	att	gcc	acc	ggc	ggc	gtg	ttg	atg	ctg	gtg	gcg	atc	gtg	595	
Leu	Leu	Ile	Ile	Ala	Thr	Gly	Gly	Val	Leu	Met	Leu	Val	Ala	Ile	Val		
					155					160					165		
ctg	atc	gtg	atg	aat	tgg	aac	acc	cag	gac	ggc	ttc	gtc	atg	gcg	ctg	643	
Leu	Ile	Val	Met	Asn	Trp	Asn	Thr	Gln	Asp	Gly	Phe	Val	Met	Ala	Leu		
				170					175					180			
gtg	gcc	gtg	gtg	ctc	acg	ctg	gtg	ggc	gtg	gct	gcg	ctg	ggc	gtt	ccg	691	
Val	Ala	Val	Val	Leu	Thr	Leu	Val	Gly	Val	Ala	Ala	Leu	Gly	Val	Pro		
				185				190					195				
ctg	tgg	gtg	cgg	atg	tgg	gat	cag	ctg	ggc	gag	gag	cgc	gcg	gaa	aaa	739	
Leu	Trp	Val	Arg	Met	Trp	Asp	Gln	Leu	Gly	Glu	Glu	Arg	Ala	Glu	Lys		
		200					205					210					
gcc	gca	gct	gct	gag	cgc	gca	gat	att	gct	tcc	cgc	ctg	cat	gat	tcg	787	
Ala	Ala	Ala	Ala	Glu	Arg	Ala	Asp	Ile	Ala	Ser	Arg	Leu	His	Asp	Ser		
		215				220					225						
gta	ctg	cag	acc	ttg	gcg	ctg	att	caa	aag	cgt	gcc	gac	gac	ccc	gcc	835	
Val	Leu	Gln	Thr	Leu	Ala	Leu	Ile	Gln	Lys	Arg	Ala	Asp	Asp	Pro	Ala		
		230			235					240					245		
gaa	gtc	gcc	cgc	ctg	gcc	cgc	ggg	cag	gaa	cgc	gag	ctg	cgt	caa	tgg	883	
Glu	Val	Ala	Arg	Leu	Ala	Arg	Gly	Gln	Glu	Arg	Glu	Leu	Arg	Gln	Trp		
				250				255						260			
ctg	ttt	gat	tcc	caa	gat	aaa	aca	cct	caa	aca	acc	ggc	act	gtc	ttt	931	
Leu	Phe	Asp	Ser	Gln	Asp	Lys	Thr	Pro	Gln	Thr	Thr	Gly	Thr	Val	Phe		
			265					270					275				
act	gcg	ttg	gag	cgc	gcc	tgc	ggc	gaa	gtc	gag	gat	att	tac	gct	ctg	979	
Thr	Ala	Leu	Glu	Arg	Ala	Cys	Gly	Glu	Val	Glu	Asp	Ile	Tyr	Ala	Leu		
		280				285						290					
cgt	atc	gtg	cct	gtg	acc	gtg	gga	acc	gat	gaa	gcg	ctg	act	gag	aaa	1027	
Arg	Ile	Val	Pro	Val	Thr	Val	Gly	Thr	Asp	Glu	Ala	Leu	Thr	Glu	Lys		
		295				300					305						
acg	cag	gca	gcg	gtg	atg	gca	gtc	cgc	gaa	gca	ctc	gtg	aac	gtg	gcc	1075	
Thr	Gln	Ala	Ala	Val	Met	Ala	Val	Arg	Glu	Ala	Leu	Val	Asn	Val	Ala		
					315					320					325		
aag	cat	gcc	ggc	gtg	gaa	acc	gcc	gat	gtg	tac	gcc	gaa	att	atg	ctc	1123	
Lys	His	Ala	Gly	Val	Glu	Thr	Ala	Asp	Val	Tyr	Ala	Glu	Ile	Met	Leu		
				330					335					340			
ggc	gaa	ctg	aac	att	ttc	gtc	cgc	gac	cgc	ggc	gca	gga	ttc	gac	ccc	1171	
Gly	Glu	Leu	Asn	Ile	Phe	Val	Arg	Asp	Arg	Gly	Ala	Gly	Phe	Asp	Pro		
			345					350					355				

gac aac atc ccc gac ggg cac cac ggg ctc gcc gaa tcc gtc caa ggc 1219
 Asp Asn Ile Pro Asp Gly His His Gly Leu Ala Glu Ser Val Gln Gly
 360 365 370

cgc gtc gaa cga gcc ggc gga aaa gta cgc atc aaa tct gaa atc ggc 1267
 Arg Val Glu Arg Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly
 375 380 385

gaa ggc acc gaa gtg gca atc acc atg gat gtg tagttggtcg tacgcgcgtg 1320
 Glu Gly Thr Glu Val Ala Ile Thr Met Asp Val
 390 395 400

tct 1323

<210> 306

<211> 400

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

Met Ile Glu Asp Met Ser Asn Thr Pro Ala Pro Tyr Thr Pro Gln Pro
 1 5 10 15

Ala Gly Gln Ala Val Pro Leu Tyr Pro Thr Phe Thr Arg Ser Arg Asp
 20 25 30

Gly Arg Val Val Ala Gly Val Ala Ser Gly Leu Ala Lys His Leu Asn
 35 40 45

Val Ser Val Phe Trp Val Arg Ala Leu Leu Ile Phe Ala Ala Leu Leu
 50 55 60

Ser Gly Ala Gly Leu Phe Ala Tyr Ala Leu Ile Trp Ile Phe Thr Arg
 65 70 75 80

Ile Glu Lys Lys Gly Ser Gly Glu Ala Ser Thr Ser Lys Arg Trp Val
 85 90 95

Ser Trp Cys Leu Val Leu Leu Ala Ile Gly Gly Ala Ala Ala Ser Val
 100 105 110

Met Leu Ser Thr Gly Phe Ala Val Gly Thr Leu Val Pro Ile Gly Val
 115 120 125

Val Gly Val Gly Leu Leu Met Val Trp Leu Ala Tyr Asp Arg Gly Val
 130 135 140

Glu Ser Gly Pro Asn Leu Leu Ile Ile Ala Thr Gly Gly Val Leu Met
 145 150 155 160

Leu Val Ala Ile Val Leu Ile Val Met Asn Trp Asn Thr Gln Asp Gly
 165 170 175

Phe Val Met Ala Leu Val Ala Val Val Leu Thr Leu Val Gly Val Ala
 180 185 190

Ala Leu Gly Val Pro Leu Trp Val Arg Met Trp Asp Gln Leu Gly Glu
 195 200 205

Glu Arg Ala Glu Lys Ala Ala Ala Glu Arg Ala Asp Ile Ala Ser
 210 215 220
 Arg Leu His Asp Ser Val Leu Gln Thr Leu Ala Leu Ile Gln Lys Arg
 225 230 235 240
 Ala Asp Asp Pro Ala Glu Val Ala Arg Leu Ala Arg Gly Gln Glu Arg
 245 250 255
 Glu Leu Arg Gln Trp Leu Phe Asp Ser Gln Asp Lys Thr Pro Gln Thr
 260 265 270
 Thr Gly Thr Val Phe Thr Ala Leu Glu Arg Ala Cys Gly Glu Val Glu
 275 280 285
 Asp Ile Tyr Ala Leu Arg Ile Val Pro Val Thr Val Gly Thr Asp Glu
 290 295 300
 Ala Leu Thr Glu Lys Thr Gln Ala Ala Val Met Ala Val Arg Glu Ala
 305 310 315 320
 Leu Val Asn Val Ala Lys His Ala Gly Val Glu Thr Ala Asp Val Tyr
 325 330 335
 Ala Glu Ile Met Leu Gly Glu Leu Asn Ile Phe Val Arg Asp Arg Gly
 340 345 350
 Ala Gly Phe Asp Pro Asp Asn Ile Pro Asp Gly His His Gly Leu Ala
 355 360 365
 Glu Ser Val Gln Gly Arg Val Glu Arg Ala Gly Gly Lys Val Arg Ile
 370 375 380
 Lys Ser Glu Ile Gly Glu Gly Thr Glu Val Ala Ile Thr Met Asp Val
 385 390 395 400

<210> 307
 <211> 1119
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1096)
 <223> RXA00756

<400> 307
 attcgctaaa cctgcgcagg atgagactgc cctgcgcagaa agcacattcg acgaagccac 60
 cgcgtaaaca gtacgtggtg gaagcttgag aggaagacaa gtg aat att gat gtc 115
 Val Asn Ile Asp Val
 1 5
 cag gct tta aaa gcc atc gag tct gaa aaa gga atc cca gtt cca gac 163
 Gln Ala Leu Lys Ala Ile Glu Ser Glu Lys Gly Ile Pro Val Pro Asp
 10 15 20

ttg	ctg	cgc	acc	atc	gcc	tct	gca	ctt	ttg	cat	tcg	tac	atg	gat	aat	211
Leu	Leu	Arg	Thr	Ile	Ala	Ser	Ala	Leu	Leu	His	Ser	Tyr	Met	Asp	Asn	
			25					30					35			
cgc	gaa	act	gtt	gcg	tct	gcg	aac	ctg	aaa	cca	cgc	gtg	gac	atc	gat	259
Arg	Glu	Thr	Val	Ala	Ser	Ala	Asn	Leu	Lys	Pro	Arg	Val	Asp	Ile	Asp	
		40					45					50				
tcc	aca	act	ggc	acg	gtc	aac	gtc	atc	gtc	tca	gaa	ttc	gac	gaa	aac	307
Ser	Thr	Thr	Gly	Thr	Val	Asn	Val	Ile	Val	Ser	Glu	Phe	Asp	Glu	Asn	
		55				60					65					
gga	gag	ctc	gct	tcc	gaa	tac	gac	gac	acc	cca	tcc	aac	ttc	gga	cga	355
Gly	Glu	Leu	Ala	Ser	Glu	Tyr	Asp	Asp	Thr	Pro	Ser	Asn	Phe	Gly	Arg	
70					75					80					85	
gtc	agc	gcc	cgc	gct	gtt	cgc	gac	gcg	atc	gtt	aag	tcc	ctg	cgc	gaa	403
Val	Ser	Ala	Arg	Ala	Val	Arg	Asp	Ala	Ile	Val	Lys	Ser	Leu	Arg	Glu	
				90					95					100		
gca	gaa	gca	agc	cga	gca	ttc	gat	gcg	tac	gca	gat	tat	gaa	ggc	acc	451
Ala	Glu	Ala	Ser	Arg	Ala	Phe	Asp	Ala	Tyr	Ala	Asp	Tyr	Glu	Gly	Thr	
			105					110					115			
gtt	gtg	tcc	ggc	atc	gtt	caa	gca	gat	gcc	cgc	gca	gct	gaa	cgc	gga	499
Val	Val	Ser	Gly	Ile	Val	Gln	Ala	Asp	Ala	Arg	Ala	Ala	Glu	Arg	Gly	
		120					125					130				
atc	atc	atc	gtg	cag	ctg	ggt	acc	gaa	gcg	gac	aac	caa	gac	ggc	gtt	547
Ile	Ile	Ile	Val	Gln	Leu	Gly	Thr	Glu	Ala	Asp	Asn	Gln	Asp	Gly	Val	
	135					140					145					
ttg	ctc	cca	gcc	gag	cag	atc	cct	ggc	gaa	aag	ctc	aag	cac	ggc	gac	595
Leu	Leu	Pro	Ala	Glu	Gln	Ile	Pro	Gly	Glu	Lys	Leu	Lys	His	Gly	Asp	
150					155					160					165	
cgc	gtc	aag	tgc	ttc	gtc	gtt	ggc	gtg	ggc	aag	ggc	aac	act	gac	atc	643
Arg	Val	Lys	Cys	Phe	Val	Val	Gly	Val	Gly	Lys	Gly	Asn	Thr	Asp	Ile	
				170					175					180		
cag	atc	aac	ctg	tct	cgt	act	cac	cct	gag	ctg	gtg	cgc	cga	ctg	ttt	691
Gln	Ile	Asn	Leu	Ser	Arg	Thr	His	Pro	Glu	Leu	Val	Arg	Arg	Leu	Phe	
			185					190					195			
gaa	ctg	gaa	atc	cca	gaa	gtt	gct	gac	gga	tcc	gtg	gaa	att	gtt	gct	739
Glu	Leu	Glu	Ile	Pro	Glu	Val	Ala	Asp	Gly	Ser	Val	Glu	Ile	Val	Ala	
		200					205					210				
atc	tcc	cgc	gaa	gcc	gga	cac	cgc	tcc	aag	gtt	gct	gtt	caa	gcc	aag	787
Ile	Ser	Arg	Glu	Ala	Gly	His	Arg	Ser	Lys	Val	Ala	Val	Gln	Ala	Lys	
	215					220					225					
gtg	aag	aac	ctc	aac	gcc	aag	ggc	gct	tgc	att	ggc	cca	cgt	gga	cag	835
Val	Lys	Asn	Leu	Asn	Ala	Lys	Gly	Ala	Cys	Ile	Gly	Pro	Arg	Gly	Gln	
230					235					240					245	
cgt	gtg	tcc	aac	atc	atg	cgt	gaa	ctc	ggt	gga	gaa	aaa	atc	gac	atc	883
Arg	Val	Ser	Asn	Ile	Met	Arg	Glu	Leu	Gly	Gly	Glu	Lys	Ile	Asp	Ile	
				250					255					260		
atc	gat	tac	tcc	gaa	gat	cca	gca	acc	ttc	gtt	gga	aat	gca	ctg	gca	931

Ile Asp Tyr Ser Glu Asp Pro Ala Thr Phe Val Gly Asn Ala Leu Ala
 265 270 275

cca tcc aag gtt gtc aac gta gag gtc acc gat ctt gaa gct caa acc 979
 Pro Ser Lys Val Val Asn Val Glu Val Thr Asp Leu Glu Ala Gln Thr
 280 285 290

gcg cgc gta act gtc cct gac tac cag ctt tca cta gca atc ggt aaa 1027
 Ala Arg Val Thr Val Pro Asp Tyr Gln Leu Ser Leu Ala Ile Gly Lys
 295 300 305

gaa ggt caa aac gcc cgc ttg gct gcc cgc ctg acc ggc tgg aag atc 1075
 Glu Gly Gln Asn Ala Arg Leu Ala Ala Arg Leu Thr Gly Trp Lys Ile
 310 315 320 325

gac atc cac tct gac atc gat taaaagtcgc ttgaaccggc atg 1119
 Asp Ile His Ser Asp Ile Asp
 330

<210> 308

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

Val Asn Ile Asp Val Gln Ala Leu Lys Ala Ile Glu Ser Glu Lys Gly
 1 5 10 15

Ile Pro Val Pro Asp Leu Leu Arg Thr Ile Ala Ser Ala Leu Leu His
 20 25 30

Ser Tyr Met Asp Asn Arg Glu Thr Val Ala Ser Ala Asn Leu Lys Pro
 35 40 45

Arg Val Asp Ile Asp Ser Thr Thr Gly Thr Val Asn Val Ile Val Ser
 50 55 60

Glu Phe Asp Glu Asn Gly Glu Leu Ala Ser Glu Tyr Asp Asp Thr Pro
 65 70 75 80

Ser Asn Phe Gly Arg Val Ser Ala Arg Ala Val Arg Asp Ala Ile Val
 85 90 95

Lys Ser Leu Arg Glu Ala Glu Ala Ser Arg Ala Phe Asp Ala Tyr Ala
 100 105 110

Asp Tyr Glu Gly Thr Val Val Ser Gly Ile Val Gln Ala Asp Ala Arg
 115 120 125

Ala Ala Glu Arg Gly Ile Ile Ile Val Gln Leu Gly Thr Glu Ala Asp
 130 135 140

Asn Gln Asp Gly Val Leu Leu Pro Ala Glu Gln Ile Pro Gly Glu Lys
 145 150 155 160

Leu Lys His Gly Asp Arg Val Lys Cys Phe Val Val Gly Val Gly Lys
 165 170 175

Gly Asn Thr Asp Ile Gln Ile Asn Leu Ser Arg Thr His Pro Glu Leu
 180 185 190

Val Arg Arg Leu Phe Glu Leu Glu Ile Pro Glu Val Ala Asp Gly Ser
 195 200 205

Val Glu Ile Val Ala Ile Ser Arg Glu Ala Gly His Arg Ser Lys Val
 210 215 220

Ala Val Gln Ala Lys Val Lys Asn Leu Asn Ala Lys Gly Ala Cys Ile
 225 230 235 240

Gly Pro Arg Gly Gln Arg Val Ser Asn Ile Met Arg Glu Leu Gly Gly
 245 250 255

Glu Lys Ile Asp Ile Ile Asp Tyr Ser Glu Asp Pro Ala Thr Phe Val
 260 265 270

Gly Asn Ala Leu Ala Pro Ser Lys Val Val Asn Val Glu Val Thr Asp
 275 280 285

Leu Glu Ala Gln Thr Ala Arg Val Thr Val Pro Asp Tyr Gln Leu Ser
 290 295 300

Leu Ala Ile Gly Lys Glu Gly Gln Asn Ala Arg Leu Ala Ala Arg Leu
 305 310 315 320

Thr Gly Trp Lys Ile Asp Ile His Ser Asp Ile Asp
 325 330

<210> 309
 <211> 834
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(811)
 <223> RXA00139

<400> 309
 gaccggaac gtactcaagg tagacacccg cgacggttcc tacctctccc gcgttaacaa 60

ctaagattct taaaaccttt aagaatcagc cagaaacatt ttg att gaa cag gaa 115
 Leu Ile Glu Gln Glu
 1 5

caa aga gaa caa aac gtg agc gag cgt cga caa gat tac aag cga cac 163
 Gln Arg Glu Gln Asn Val Ser Glu Arg Arg Gln Asp Tyr Lys Arg His
 10 15 20

gga tcc cgc tac aag gcg cgc atg cgt gcc gta gac atc cta ttt gaa 211
 Gly Ser Arg Tyr Lys Ala Arg Met Arg Ala Val Asp Ile Leu Phe Glu
 25 30 35

gcg gaa tcc cgc gat gtt gat ccc gtg gcc atc atc gat gac cgc cac 259
 Ala Glu Ser Arg Asp Val Asp Pro Val Ala Ile Ile Asp Asp Arg His
 40 45 50

aag ttg gcg cgc gat acc aac ccc atc gtt gca ccg gta gcg gaa tac 307
 Lys Leu Ala Arg Asp Thr Asn Pro Ile Val Ala Pro Val Ala Glu Tyr
 55 60 65


```

acc gaa acc atc atc aat ggc gtt gcc gtt gaa ctc gat acc ctc gat 355
Thr Glu Thr Ile Ile Asn Gly Val Ala Val Glu Leu Asp Thr Leu Asp
70 75 80 85

gtc ttc ctc gcg gaa cac atc gca gaa acc tgg act ctc gga cga ctc 403
Val Phe Leu Ala Glu His Ile Ala Glu Thr Trp Thr Leu Gly Arg Leu
90 95 100

cca tcc gtc gac cgc gca atc ctg cgc gtc gct tcc tgg gaa atg atc 451
Pro Ser Val Asp Arg Ala Ile Leu Arg Val Ala Ser Trp Glu Met Ile
105 110 115

tac aac gcc gac gtt cct gtc acc acc gca atc gtt gaa gcc gtg gaa 499
Tyr Asn Ala Asp Val Pro Val Thr Thr Ala Ile Val Glu Ala Val Glu
120 125 130

att gcc tcc gaa tac tcc gga gac aaa tcc agt gcc tac atc aac gcg 547
Ile Ala Ser Glu Tyr Ser Gly Asp Lys Ser Ser Ala Tyr Ile Asn Ala
135 140 145

aca ctt gac gcc atg gca tca aag gtg gag acc ctc cgc gag cgc gcc 595
Thr Leu Asp Ala Met Ala Ser Lys Val Glu Thr Leu Arg Glu Arg Ala
150 155 160 165

gcc aac cca gaa gca gtt ctg gcg gaa gct tcc gaa tct ctc gat gat 643
Ala Asn Pro Glu Ala Val Leu Ala Glu Ala Ser Glu Ser Leu Asp Asp
170 175 180

gct ccg gtc gcg ccg tgg gat gac tcg gat gct ttg gat gac tcg gat 691
Ala Pro Val Ala Pro Trp Asp Asp Ser Asp Ala Leu Asp Asp Ser Asp
185 190 195

gaa gat ttt gag gct gta gat gct gct gag gtt ttt gag gct gaa gag 739
Glu Asp Phe Glu Ala Val Asp Ala Ala Glu Val Phe Glu Ala Glu Glu
200 205 210

act gta gag gtt tcc gaa gtc gca gaa gac tct gaa gtt tca aag gtt 787
Thr Val Glu Val Ser Glu Val Ala Glu Asp Ser Glu Val Ser Lys Val
215 220 225

tca gaa gaa aag gct gac gag agc taaatctttt ctggctaaca cca 834
Ser Glu Glu Lys Ala Asp Glu Ser
230 235

```

<210> 310

<211> 237

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

```

Leu Ile Glu Gln Glu Gln Arg Glu Gln Asn Val Ser Glu Arg Arg Gln
1 5 10 15

Asp Tyr Lys Arg His Gly Ser Arg Tyr Lys Ala Arg Met Arg Ala Val
20 25 30

Asp Ile Leu Phe Glu Ala Glu Ser Arg Asp Val Asp Pro Val Ala Ile
35 40 45

```

Ile Asp Asp Arg His Lys Leu Ala Arg Asp Thr Asn Pro Ile Val Ala
 50 55 60

Pro Val Ala Glu Tyr Thr Glu Thr Ile Ile Asn Gly Val Ala Val Glu
 65 70 75 80

Leu Asp Thr Leu Asp Val Phe Leu Ala Glu His Ile Ala Glu Thr Trp
 85 90 95

Thr Leu Gly Arg Leu Pro Ser Val Asp Arg Ala Ile Leu Arg Val Ala
 100 105 110

Ser Trp Glu Met Ile Tyr Asn Ala Asp Val Pro Val Thr Thr Ala Ile
 115 120 125

Val Glu Ala Val Glu Ile Ala Ser Glu Tyr Ser Gly Asp Lys Ser Ser
 130 135 140

Ala Tyr Ile Asn Ala Thr Leu Asp Ala Met Ala Ser Lys Val Glu Thr
 145 150 155 160

Leu Arg Glu Arg Ala Ala Asn Pro Glu Ala Val Leu Ala Glu Ala Ser
 165 170 175

Glu Ser Leu Asp Asp Ala Pro Val Ala Pro Trp Asp Asp Ser Asp Ala
 180 185 190

Leu Asp Asp Ser Asp Glu Asp Phe Glu Ala Val Asp Ala Ala Glu Val
 195 200 205

Phe Glu Ala Glu Glu Thr Val Glu Val Ser Glu Val Ala Glu Asp Ser
 210 215 220

Glu Val Ser Lys Val Ser Glu Glu Lys Ala Asp Glu Ser
 225 230 235

<210> 311
 <211> 1458
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1435)
 <223> RXA01303

<400> 311
 aacatgcggg cgcaggtcag agctgttatc ttagtactta tcacagccat agggcgggct 60

tgacggaaag cctttccgcg taaccatgaa gaggcatac gtg aca caa ctc aac 115
 Val Thr Gln Leu Asn
 1 5

acc aaa ggc gtt gtt ctg caa ggg tgg gat cca gaa gat cct gaa cat 163
 Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro Glu Asp Pro Glu His
 10 15 20

tgg gac tcg aaa att gca tgg cga acc ctg tgg att acc acc ttc tcc 211
 Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp Ile Thr Thr Phe Ser
 25 30 35

atg att att ggg ttc tgc gtg tgg tat ttg gtt tct gcc atc gct ccc	259
Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val Ser Ala Ile Ala Pro	
40 45 50	
cta ctc aat cga att gga ttt gat ctc tca gca ggt cag ctt tat tgg	307
Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala Gly Gln Leu Tyr Trp	
55 60 65	
ctc gca tct atc ccc ggt ttg gcc ggc gga tta atc cga ttg att tac	355
Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu Ile Arg Leu Ile Tyr	
70 75 80 85	
atg ttc ctt cca ccg att ctt gga acc cgc aaa ttg gtc gga att tcc	403
Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys Leu Val Gly Ile Ser	
90 95 100	
tcc ggt cta ttt ttg atc ccc atg ttt ggg tgg ttc ctg gct gtc caa	451
Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp Phe Leu Ala Val Gln	
105 110 115	
gat tca agc act ccc tac tgg tgg ctt ctc aca ctc gct gca ctc act	499
Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr Leu Ala Ala Leu Thr	
120 125 130	
ggc att ggt ggt ggc gtg ttc tct gga tat atg ccg tcc acg gga tac	547
Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met Pro Ser Thr Gly Tyr	
135 140 145	
ttc ttc ccc aag gca aaa tcg ggc act gcg ctg ggc att cag gca ggt	595
Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu Gly Ile Gln Ala Gly	
150 155 160 165	
atc ggc aac ctc ggc gtc tcg ata att cag ttc atg ggc cca tgg gtc	643
Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe Met Gly Pro Trp Val	
170 175 180	
atg ggt ttc ggt ctg ctg ggc att ggt ttc ctc acc ccg cag cgc acc	691
Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu Thr Pro Gln Arg Thr	
185 190 195	
att gaa ggc acc acg gtg ttt gtg cac aat gct gcg att gtg ttg gtc	739
Ile Glu Gly Thr Thr Val Phe Val His Asn Ala Ala Ile Val Leu Val	
200 205 210	
ccg tgg act att ctc gcg gcc gtt tta tcc ttc ctg ttt ctt aaa gat	787
Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe Leu Phe Leu Lys Asp	
215 220 225	
gtc cca gtc acc gca aat ttc cgg caa cag atc gat atc ttt ggc aac	835
Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile Asp Ile Phe Gly Asn	
230 235 240 245	
aag aac aca tgg att ttg tcc att atc tac ttg atg aca ttc ggt gcc	883
Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu Met Thr Phe Gly Ala	
250 255 260	
ttc gcc ggt ttc gcc gcg cag ttc ggt ctg atc atc aac aac aac ttc	931
Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile Ile Asn Asn Asn Phe	
265 270 275	

ggc atc gct tcc ccg atg gca gag act tat cca gct gag atg ctt cac 979
 Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro Ala Glu Met Leu His
 280 285 290

gcc ggt gct acg ttc gcg ttt ctt gga cct ttg att ggt gct ttg gtg 1027
 Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu Ile Gly Ala Leu Val
 295 300 305

cgt gct gca tgg ggt cca ctg tgt gac aga ttc ggt gga gct atc tgg 1075
 Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe Gly Gly Ala Ile Trp
 310 315 320 325

acc ttt gtc ggt ggc atc gga atg act atc gcc act gca gct gcc gca 1123
 Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala Thr Ala Ala Ala Ala
 330 335 340

atc ttc cta agc aga gcg gag aca cct gat gat ttc tgg cca ttc ctg 1171
 Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp Phe Trp Pro Phe Leu
 345 350 355

tgg tcc atg ctt gcc ctg ttc ttc ttc acc ggt ctg ggc aat gct ggc 1219
 Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly Leu Gly Asn Ala Gly
 360 365 370

acc ttc aaa caa atg ccc atg att ttg cct aaa cgc caa gca ggt ggc 1267
 Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys Arg Gln Ala Gly Gly
 375 380 385

gtg atc ggc tgg acc ggt gcc att ggt gcc ttc ggc ccc ttc att gtc 1315
 Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe Gly Pro Phe Ile Val
 390 395 400 405

ggt gtc ttg ctc tcc ttc act cca act gtc gcg ttc ttc tgg ggc tgc 1363
 Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala Phe Phe Trp Gly Cys
 410 415 420

gtg gtg ttc ttc atc atc gcc acc gct ttg acc tgg atc tac tac gcc 1411
 Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr Trp Ile Tyr Tyr Ala
 425 430 435

cgc ccg aac gct cca ttc ccg gga taaaccgaaa ggccaatcca tga 1458
 Arg Pro Asn Ala Pro Phe Pro Gly
 440 445

<210> 312

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Val Thr Gln Leu Asn Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro
 1 5 10 15

Glu Asp Pro Glu His Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp
 20 25 30

Ile Thr Thr Phe Ser Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val
 35 40 45

Ser Ala Ile Ala Pro Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala

50					55					60					
Gly	Gln	Leu	Tyr	Trp	Leu	Ala	Ser	Ile	Pro	Gly	Leu	Ala	Gly	Gly	Leu
65					70					75					80
Ile	Arg	Leu	Ile	Tyr	Met	Phe	Leu	Pro	Pro	Ile	Leu	Gly	Thr	Arg	Lys
				85					90					95	
Leu	Val	Gly	Ile	Ser	Ser	Gly	Leu	Phe	Leu	Ile	Pro	Met	Phe	Gly	Trp
			100					105					110		
Phe	Leu	Ala	Val	Gln	Asp	Ser	Ser	Thr	Pro	Tyr	Trp	Trp	Leu	Leu	Thr
		115					120					125			
Leu	Ala	Ala	Leu	Thr	Gly	Ile	Gly	Gly	Gly	Val	Phe	Ser	Gly	Tyr	Met
	130					135					140				
Pro	Ser	Thr	Gly	Tyr	Phe	Phe	Pro	Lys	Ala	Lys	Ser	Gly	Thr	Ala	Leu
145						150					155				160
Gly	Ile	Gln	Ala	Gly	Ile	Gly	Asn	Leu	Gly	Val	Ser	Ile	Ile	Gln	Phe
				165					170					175	
Met	Gly	Pro	Trp	Val	Met	Gly	Phe	Gly	Leu	Leu	Gly	Ile	Gly	Phe	Leu
			180					185					190		
Thr	Pro	Gln	Arg	Thr	Ile	Glu	Gly	Thr	Thr	Val	Phe	Val	His	Asn	Ala
			195				200					205			
Ala	Ile	Val	Leu	Val	Pro	Trp	Thr	Ile	Leu	Ala	Ala	Val	Leu	Ser	Phe
	210					215					220				
Leu	Phe	Leu	Lys	Asp	Val	Pro	Val	Thr	Ala	Asn	Phe	Arg	Gln	Gln	Ile
225						230					235				240
Asp	Ile	Phe	Gly	Asn	Lys	Asn	Thr	Trp	Ile	Leu	Ser	Ile	Ile	Tyr	Leu
				245					250					255	
Met	Thr	Phe	Gly	Ala	Phe	Ala	Gly	Phe	Ala	Ala	Gln	Phe	Gly	Leu	Ile
			260					265					270		
Ile	Asn	Asn	Asn	Phe	Gly	Ile	Ala	Ser	Pro	Met	Ala	Glu	Thr	Tyr	Pro
			275				280					285			
Ala	Glu	Met	Leu	His	Ala	Gly	Ala	Thr	Phe	Ala	Phe	Leu	Gly	Pro	Leu
	290					295					300				
Ile	Gly	Ala	Leu	Val	Arg	Ala	Ala	Trp	Gly	Pro	Leu	Cys	Asp	Arg	Phe
305						310					315				320
Gly	Gly	Ala	Ile	Trp	Thr	Phe	Val	Gly	Gly	Ile	Gly	Met	Thr	Ile	Ala
				325					330					335	
Thr	Ala	Ala	Ala	Ala	Ile	Phe	Leu	Ser	Arg	Ala	Glu	Thr	Pro	Asp	Asp
			340					345					350		
Phe	Trp	Pro	Phe	Leu	Trp	Ser	Met	Leu	Ala	Leu	Phe	Phe	Phe	Thr	Gly
		355					360					365			
Leu	Gly	Asn	Ala	Gly	Thr	Phe	Lys	Gln	Met	Pro	Met	Ile	Leu	Pro	Lys
	370					375					380				

Arg Gln Ala Gly Gly Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe
385 390 395 400

Gly Pro Phe Ile Val Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala
405 410 415

Phe Phe Trp Gly Cys Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr
420 425 430

Trp Ile Tyr Tyr Ala Arg Pro Asn Ala Pro Phe Pro Gly
435 440 445

<210> 313

<211> 327

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(304)

<223> RXA01412

<400> 313

cgcccttcttt gcagctgaga attaactcac ccttgccctt ataccccata ggggtatagc 60
cttgagggag agagtacttc acctgaaagg ggccagtgc atg gca tta aag aac 115
Met Ala Leu Lys Asn
1 5
tac acc gtt gag ggc atg acc tgc gca cac tgc gtg gca tcg gta act 163
Tyr Thr Val Glu Gly Met Thr Cys Ala His Cys Val Ala Ser Val Thr
10 15 20
gaa gag gta agc gaa gtt aat ggc gtt agc gct gtt gac gtc act cta 211
Glu Glu Val Ser Glu Val Asn Gly Val Ser Ala Val Asp Val Thr Leu
25 30 35
gaa tca gga aac gtc gct gtc agt ggc gaa ggt ttc agc gat gca gag 259
Glu Ser Gly Asn Val Ala Val Ser Gly Glu Gly Phe Ser Asp Ala Glu
40 45 50
atc cag gct gct gta gag gaa gcc ggc tac aag atc gtt gcc tcc 304
Ile Gln Ala Ala Val Glu Glu Ala Gly Tyr Lys Ile Val Ala Ser
55 60 65
taaagcaccc aagaacattt aaa 327

<210> 314

<211> 68

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Ala Leu Lys Asn Tyr Thr Val Glu Gly Met Thr Cys Ala His Cys
1 5 10 15
Val Ala Ser Val Thr Glu Glu Val Ser Glu Val Asn Gly Val Ser Ala
20 25 30

Val Asp Val Thr Leu Glu Ser Gly Asn Val Ala Val Ser Gly Glu Gly
 35 40 45
 Phe Ser Asp Ala Glu Ile Gln Ala Ala Val Glu Glu Ala Gly Tyr Lys
 50 55 60
 Ile Val Ala Ser
 65

<210> 315
 <211> 1266
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1243)
 <223> RXA00773

<400> 315
 gcccccaaaa agtgaaagca caccactttc ctagttgctgc cctgctcaca atttgcttca 60
 aatattttgc ccaacctgat tcacggggga caatagttag gtg act tta aaa atc 115
 Val Thr Leu Lys Ile
 1 5
 ggc ccc ttt gac ctt gcc tcc cct gtg gtt cta gcc ccc atg gct ggt 163
 Gly Pro Phe Asp Leu Ala Ser Pro Val Val Leu Ala Pro Met Ala Gly
 10 15 20
 gta acc aac gtt gct ttc cgc acg ctg tgc cgt gaa cag gaa atg caa 211
 Val Thr Asn Val Ala Phe Arg Thr Leu Cys Arg Glu Gln Glu Met Gln
 25 30 35
 cgc acg gga aca atc tcg ggg ctg tac gtc tgt gaa atg gtg act gcg 259
 Arg Thr Gly Thr Ile Ser Gly Leu Tyr Val Cys Glu Met Val Thr Ala
 40 45 50
 cgt gct ctt gtt gag cgc aat gag aaa acc atg cac atg acc acc ttc 307
 Arg Ala Leu Val Glu Arg Asn Glu Lys Thr Met His Met Thr Thr Phe
 55 60 65
 gcg ccg gat gaa aat ccc cga agc ttg cag ctg tac acg gtt gac ccg 355
 Ala Pro Asp Glu Asn Pro Arg Ser Leu Gln Leu Tyr Thr Val Asp Pro
 70 75 80 85
 aag tac acc tac gaa gcg gcg aag atg atc gtt gat gaa aac ttg gcg 403
 Lys Tyr Thr Tyr Glu Ala Ala Lys Met Ile Val Asp Glu Asn Leu Ala
 90 95 100
 gat cat att gat atg aac ttt ggc tgc ccg gtt cca aag gtc acg gcg 451
 Asp His Ile Asp Met Asn Phe Gly Cys Pro Val Pro Lys Val Thr Arg
 105 110 115
 cgg ggt ggc ggt tct gcg att cct tac aag cgc cgt ttg ttt gaa aac 499
 Arg Gly Gly Gly Ser Ala Ile Pro Tyr Lys Arg Arg Leu Phe Glu Asn
 120 125 130
 atc gtt tcc gcg gct gtg aag gct acg gaa ggc acg gac att ccg gtg 547

Ile	Val	Ser	Ala	Ala	Val	Lys	Ala	Thr	Glu	Gly	Thr	Asp	Ile	Pro	Val	
135						140					145					
acg	gtg	aag	ttc	cgc	gtt	ggc	att	gat	gat	gag	cac	cat	act	cac	ttg	595
Thr	Val	Lys	Phe	Arg	Val	Gly	Ile	Asp	Asp	Glu	His	His	Thr	His	Leu	
150					155					160					165	
gat	gct	gga	cgc	att	gct	gtc	gac	gcc	ggc	gcg	aag	tcc	gta	gcg	ctt	643
Asp	Ala	Gly	Arg	Ile	Ala	Val	Asp	Ala	Gly	Ala	Lys	Ser	Val	Ala	Leu	
				170					175					180		
cac	gcc	cgc	act	gcg	gcg	cag	cgc	tat	tcc	ggc	gag	gct	gat	tgg	aac	691
His	Ala	Arg	Thr	Ala	Ala	Gln	Arg	Tyr	Ser	Gly	Glu	Ala	Asp	Trp	Asn	
			185					190					195			
gag	atc	gcg	cgc	ctg	aag	gag	cat	ttg	gca	gat	acc	ggc	atc	cca	gtt	739
Glu	Ile	Ala	Arg	Leu	Lys	Glu	His	Leu	Ala	Asp	Thr	Gly	Ile	Pro	Val	
	200						205					210				
ttg	ggc	aat	ggc	gat	att	ttc	gcg	gca	tcc	gat	gca	acg	cgc	atg	atg	787
Leu	Gly	Asn	Gly	Asp	Ile	Phe	Ala	Ala	Ser	Asp	Ala	Thr	Arg	Met	Met	
	215					220					225					
gag	caa	act	ggc	tgc	gat	ggc	gtc	gtg	gtt	ggg	cgt	ggc	tgc	ctg	ggc	835
Glu	Gln	Thr	Gly	Cys	Asp	Gly	Val	Val	Val	Gly	Arg	Gly	Cys	Leu	Gly	
230					235					240					245	
agg	cct	tgg	ctc	ttt	gct	gag	ctg	tct	gct	gct	gtt	cgt	gga	gaa	gaa	883
Arg	Pro	Trp	Leu	Phe	Ala	Glu	Leu	Ser	Ala	Ala	Val	Arg	Gly	Glu	Glu	
				250					255					260		
atc	cca	gag	gag	cct	acc	ttc	ggc	gaa	gtt	acc	caa	atc	atc	ctg	cgc	931
Ile	Pro	Glu	Glu	Pro	Thr	Phe	Gly	Glu	Val	Thr	Gln	Ile	Ile	Leu	Arg	
			265					270					275			
cac	gca	gaa	ctc	ctc	atg	cag	cat	gat	ggc	gaa	acc	aag	ggg	ctg	cgc	979
His	Ala	Glu	Leu	Leu	Met	Gln	His	Asp	Gly	Glu	Thr	Lys	Gly	Leu	Arg	
		280					285					290				
gat	ctg	cgt	aag	cac	atg	ggc	tgg	tac	ctg	cgc	ggc	ttc	cct	gtt	ggc	1027
Asp	Leu	Arg	Lys	His	Met	Gly	Trp	Tyr	Leu	Arg	Gly	Phe	Pro	Val	Gly	
	295					300					305					
ggc	gaa	ttc	cgc	tcc	aat	ctg	gcc	aag	gtt	tcc	acc	tat	gtg	gag	ctt	1075
Gly	Glu	Phe	Arg	Ser	Asn	Leu	Ala	Lys	Val	Ser	Thr	Tyr	Val	Glu	Leu	
310					315					320					325	
gag	gat	ctc	cta	gca	cca	tgg	gct	gac	tcc	acc	gcc	aag	gca	gag	gac	1123
Glu	Asp	Leu	Leu	Ala	Pro	Trp	Ala	Asp	Ser	Thr	Ala	Lys	Ala	Glu	Asp	
				330					335					340		
gcg	gaa	ggc	gca	cga	ggc	cga	cag	ggc	gct	cct	gca	aag	gtg	gca	ctt	1171
Ala	Glu	Gly	Ala	Arg	Gly	Arg	Gln	Gly	Ala	Pro	Ala	Lys	Val	Ala	Leu	
			345					350					355			
cca	gat	ggc	tgg	ttg	gac	gat	cct	gag	gat	gcc	act	gtt	cct	aaa	ggc	1219
Pro	Asp	Gly	Trp	Leu	Asp	Asp	Pro	Glu	Asp	Ala	Thr	Val	Pro	Lys	Gly	
		360					365					370				
gca	gaa	atg	gaa	aac	tcc	gga	ggg	tagttaattt	aatacttacc	ccc						1266
Ala	Glu	Met	Glu	Asn	Ser	Gly	Gly									

375

380

<210> 316

<211> 381

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 316

Val Thr Leu Lys Ile Gly Pro Phe Asp Leu Ala Ser Pro Val Val Leu
 1 5 10 15

Ala Pro Met Ala Gly Val Thr Asn Val Ala Phe Arg Thr Leu Cys Arg
 20 25 30

Glu Gln Glu Met Gln Arg Thr Gly Thr Ile Ser Gly Leu Tyr Val Cys
 35 40 45

Glu Met Val Thr Ala Arg Ala Leu Val Glu Arg Asn Glu Lys Thr Met
 50 55 60

His Met Thr Thr Phe Ala Pro Asp Glu Asn Pro Arg Ser Leu Gln Leu
 65 70 75 80

Tyr Thr Val Asp Pro Lys Tyr Thr Tyr Glu Ala Ala Lys Met Ile Val
 85 90 95

Asp Glu Asn Leu Ala Asp His Ile Asp Met Asn Phe Gly Cys Pro Val
 100 105 110

Pro Lys Val Thr Arg Arg Gly Gly Gly Ser Ala Ile Pro Tyr Lys Arg
 115 120 125

Arg Leu Phe Glu Asn Ile Val Ser Ala Ala Val Lys Ala Thr Glu Gly
 130 135 140

Thr Asp Ile Pro Val Thr Val Lys Phe Arg Val Gly Ile Asp Asp Glu
 145 150 155 160

His His Thr His Leu Asp Ala Gly Arg Ile Ala Val Asp Ala Gly Ala
 165 170 175

Lys Ser Val Ala Leu His Ala Arg Thr Ala Ala Gln Arg Tyr Ser Gly
 180 185 190

Glu Ala Asp Trp Asn Glu Ile Ala Arg Leu Lys Glu His Leu Ala Asp
 195 200 205

Thr Gly Ile Pro Val Leu Gly Asn Gly Asp Ile Phe Ala Ala Ser Asp
 210 215 220

Ala Thr Arg Met Met Glu Gln Thr Gly Cys Asp Gly Val Val Val Gly
 225 230 235 240

Arg Gly Cys Leu Gly Arg Pro Trp Leu Phe Ala Glu Leu Ser Ala Ala
 245 250 255

Val Arg Gly Glu Glu Ile Pro Glu Glu Pro Thr Phe Gly Glu Val Thr
 260 265 270

Gln Ile Ile Leu Arg His Ala Glu Leu Leu Met Gln His Asp Gly Glu

275	280	285
Thr Lys Gly Leu Arg Asp Leu Arg Lys His Met Gly Trp Tyr Leu Arg		
290	295	300
Gly Phe Pro Val Gly Gly Glu Phe Arg Ser Asn Leu Ala Lys Val Ser		
305	310	315
Thr Tyr Val Glu Leu Glu Asp Leu Leu Ala Pro Trp Ala Asp Ser Thr		
	325	330
Ala Lys Ala Glu Asp Ala Glu Gly Ala Arg Gly Arg Gln Gly Ala Pro		
	340	345
Ala Lys Val Ala Leu Pro Asp Gly Trp Leu Asp Asp Pro Glu Asp Ala		
	355	360
Thr Val Pro Lys Gly Ala Glu Met Glu Asn Ser Gly Gly		
	370	375
		380

<210> 317
 <211> 290
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(267)
 <223> RXA02746

<400> 317
 ggt gtg cag ggc atg act gtc acc gaa acc caa ggc ttt ggc cag cag 48
 Gly Val Gln Gly Met Thr Val Thr Glu Thr Gln Gly Phe Gly Gln Gln
 1 5 10 15
 aaa ggc cac acc gag gtg tac cgt ggt gct gaa tac gct gtc gat ttt 96
 Lys Gly His Thr Glu Val Tyr Arg Gly Ala Glu Tyr Ala Val Asp Phe
 20 25 30
 gtg cct aag gtc aag att gaa gtt att atc tcc gat gct cag gct gag 144
 Val Pro Lys Val Lys Ile Glu Val Ile Ile Ser Asp Ala Gln Ala Glu
 35 40 45
 gaa gtc atc aac att atc gtc gag acc gca cgc acc ggc aaa gtc ggc 192
 Glu Val Ile Asn Ile Ile Val Glu Thr Ala Arg Thr Gly Lys Val Gly
 50 55 60
 gac ggc aaa gtg tgg atg act aac atc gaa gag ctg gtt cgt gtt cgt 240
 Asp Gly Lys Val Trp Met Thr Asn Ile Glu Glu Leu Val Arg Val Arg
 65 70 75 80
 acc ggt gag cgc ggc gaa gca gcc ctt taaaaactta tgaataatcc 287
 Thr Gly Glu Arg Gly Glu Ala Ala Leu
 85
 agc 290

<210> 318
 <211> 89

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Gly Val Gln Gly Met Thr Val Thr Glu Thr Gln Gly Phe Gly Gln Gln
 1 5 10 15

Lys Gly His Thr Glu Val Tyr Arg Gly Ala Glu Tyr Ala Val Asp Phe
 20 25 30

Val Pro Lys Val Lys Ile Glu Val Ile Ile Ser Asp Ala Gln Ala Glu
 35 40 45

Glu Val Ile Asn Ile Ile Val Glu Thr Ala Arg Thr Gly Lys Val Gly
 50 55 60

Asp Gly Lys Val Trp Met Thr Asn Ile Glu Glu Leu Val Arg Val Arg
 65 70 75 80

Thr Gly Glu Arg Gly Glu Ala Ala Leu
 85

<210> 319

<211> 902

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(879)

<223> RXA02745

<400> 319

gcc gga atc tcc ttc gaa gtc ccc cgc ggt caa gtt ttg gcc ctc ctg 48
 Ala Gly Ile Ser Phe Glu Val Pro Arg Gly Gln Val Leu Ala Leu Leu
 1 5 10 15

gga cct aat ggc gca ggc aaa acc acc acc att gaa atg tgc gaa ggt 96
 Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Ile Glu Met Cys Glu Gly
 20 25 30

ttt acc gcc ccc acc tct ggc agc atc cga gtc ttg ggc atc gat cca 144
 Phe Thr Ala Pro Thr Ser Gly Ser Ile Arg Val Leu Gly Ile Asp Pro
 35 40 45

gcc aca gaa cca gac cag gtg cgc cga cgc atc ggc atc atg ctt caa 192
 Ala Thr Glu Pro Asp Gln Val Arg Arg Arg Ile Gly Ile Met Leu Gln
 50 55 60

ggt ggc ggt tcc tac agc gga atc cgc gtg ttt gaa atg ctc aag ctt 240
 Gly Gly Gly Ser Tyr Ser Gly Ile Arg Val Phe Glu Met Leu Lys Leu
 65 70 75 80

gcg gcg tcc tac aac gac aac cca cac gat cct gaa tgg ctg ctt gat 288
 Ala Ala Ser Tyr Asn Asp Asn Pro His Asp Pro Glu Trp Leu Leu Asp
 85 90 95

ctt gta gga ctg cgt gaa caa cgc aaa acc acc tac cga cgt ctg tca 336
 Leu Val Gly Leu Arg Glu Gln Arg Lys Thr Thr Tyr Arg Arg Leu Ser
 100 105 110

ggt ggc caa cag caa cgc ctt tct ttg gcc tta gca tta att ggt cgc 384
 Gly Gly Gln Gln Gln Arg Leu Ser Leu Ala Leu Ala Leu Ile Gly Arg
 115 120 125

cct gag att atc ttc ctc gac gaa ccc acc gct ggc atg gat gcg caa 432
 Pro Glu Ile Ile Phe Leu Asp Glu Pro Thr Ala Gly Met Asp Ala Gln
 130 135 140

tca cgc aac atg gtg tgg gag ctt gtc aac gat ctc cgc cgc gac ggc 480
 Ser Arg Asn Met Val Trp Glu Leu Val Asn Asp Leu Arg Arg Asp Gly
 145 150 155 160

gtc acc atc gtg ctc acc acc cac ctg atg gat gag gcc gaa gca cta 528
 Val Thr Ile Val Leu Thr Thr His Leu Met Asp Glu Ala Glu Ala Leu
 165 170 175

gct gac cac gtg atc atc gtt gcc aac ggt caa atc ctt gcc agt ggc 576
 Ala Asp His Val Ile Ile Val Ala Asn Gly Gln Ile Leu Ala Ser Gly
 180 185 190

aca cct gat gaa ctc act gcg caa cgc gat cat ctt gaa att aat gtc 624
 Thr Pro Asp Glu Leu Thr Ala Gln Arg Asp His Leu Glu Ile Asn Val
 195 200 205

tcc gta gag acc acg agc ccg ctt gat ctt gat cgc ttg gtg gat gat 672
 Ser Val Glu Thr Thr Ser Pro Leu Asp Leu Asp Arg Leu Val Asp Asp
 210 215 220

ctc agc agc tta aac atc ggt gat gtg aaa gca cga gcc aac cgg cca 720
 Leu Ser Ser Leu Asn Ile Gly Asp Val Lys Ala Arg Ala Asn Arg Pro
 225 230 235 240

ctg cat tat tca ctt cgg acg caa caa gcc acc ccg gat tcc ttg gcg 768
 Leu His Tyr Ser Leu Arg Thr Gln Gln Ala Thr Pro Asp Ser Leu Ala
 245 250 255

cac atc gtc cag gct gtc gcc cgc caa aac gtc atg att cgc tct ttg 816
 His Ile Val Gln Ala Val Ala Arg Gln Asn Val Met Ile Arg Ser Leu
 260 265 270

gat acg gga cac cgc tca ttg gaa gat gtc ttc ctg gac atc acc gga 864
 Asp Thr Gly His Arg Ser Leu Glu Asp Val Phe Leu Asp Ile Thr Gly
 275 280 285

aaa gaa ctg agg agt taacgcacac catgtctaaa cct 902
 Lys Glu Leu Arg Ser
 290

<210> 320

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Ala Gly Ile Ser Phe Glu Val Pro Arg Gly Gln Val Leu Ala Leu Leu
 1 5 10 15

Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Ile Glu Met Cys Glu Gly
 20 25 30

Phe Thr Ala Pro Thr Ser Gly Ser Ile Arg Val Leu Gly Ile Asp Pro
 35 40 45
 Ala Thr Glu Pro Asp Gln Val Arg Arg Arg Ile Gly Ile Met Leu Gln
 50 55 60
 Gly Gly Gly Ser Tyr Ser Gly Ile Arg Val Phe Glu Met Leu Lys Leu
 65 70 75 80
 Ala Ala Ser Tyr Asn Asp Asn Pro His Asp Pro Glu Trp Leu Leu Asp
 85 90 95
 Leu Val Gly Leu Arg Glu Gln Arg Lys Thr Thr Tyr Arg Arg Leu Ser
 100 105 110
 Gly Gly Gln Gln Gln Arg Leu Ser Leu Ala Leu Ala Leu Ile Gly Arg
 115 120 125
 Pro Glu Ile Ile Phe Leu Asp Glu Pro Thr Ala Gly Met Asp Ala Gln
 130 135 140
 Ser Arg Asn Met Val Trp Glu Leu Val Asn Asp Leu Arg Arg Asp Gly
 145 150 155 160
 Val Thr Ile Val Leu Thr Thr His Leu Met Asp Glu Ala Glu Ala Leu
 165 170 175
 Ala Asp His Val Ile Ile Val Ala Asn Gly Gln Ile Leu Ala Ser Gly
 180 185 190
 Thr Pro Asp Glu Leu Thr Ala Gln Arg Asp His Leu Glu Ile Asn Val
 195 200 205
 Ser Val Glu Thr Thr Ser Pro Leu Asp Leu Asp Arg Leu Val Asp Asp
 210 215 220
 Leu Ser Ser Leu Asn Ile Gly Asp Val Lys Ala Arg Ala Asn Arg Pro
 225 230 235 240
 Leu His Tyr Ser Leu Arg Thr Gln Gln Ala Thr Pro Asp Ser Leu Ala
 245 250 255
 His Ile Val Gln Ala Val Ala Arg Gln Asn Val Met Ile Arg Ser Leu
 260 265 270
 Asp Thr Gly His Arg Ser Leu Glu Asp Val Phe Leu Asp Ile Thr Gly
 275 280 285
 Lys Glu Leu Arg Ser
 290

<210> 321
 <211> 486
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(463)

<223> RXN00820

<400> 321

acttccacca ccccaaacca tcgtttcttt cgaagacgca ccaaccctca ccggccagga 60

cctgggcttt tcgcagtggc gcactgtcac ccaggagatg gtg aac acc ttg gcg 115
 Val Asn Thr Leu Ala
 1 5

gac gca act gat gat cag cag tgg att cac act gat cct gag cgc gcc 163
 Asp Ala Thr Asp Asp Gln Gln Trp Ile His Thr Asp Pro Glu Arg Ala
 10 15 20

aag gac ggt cct ttt ggt ggc gca att gcc cac ggt ttc ctc acc ttg 211
 Lys Asp Gly Pro Phe Gly Gly Ala Ile Ala His Gly Phe Leu Thr Leu
 25 30 35

tcc atg atc att ccg ttc tgg ggc gag ctt ctc gat gtc acc ggc gtg 259
 Ser Met Ile Ile Pro Phe Trp Gly Glu Leu Leu Asp Val Thr Gly Val
 40 45 50

acc acc aag gtg aac tat ggc ctg gat aag gtg cgt ttc acc tct ccc 307
 Thr Thr Lys Val Asn Tyr Gly Leu Asp Lys Val Arg Phe Thr Ser Pro
 55 60 65

gtc aag gtc ggt tcc cgc atc cgc atg ggc gct gtg gtc cgt gag atc 355
 Val Lys Val Gly Ser Arg Ile Arg Met Gly Ala Val Val Arg Glu Ile
 70 75 80 85

tct gag gtg aag ggc aat ggc ctg cac ctg gtc gcc gat ggc act att 403
 Ser Glu Val Lys Gly Asn Gly Leu His Leu Val Ala Asp Gly Thr Ile
 90 95 100

gag atc gaa ggg cag gag cgc ccg gcc gtc gta gct acc ttc ctc acc 451
 Glu Ile Glu Gly Gln Glu Arg Pro Ala Val Val Ala Thr Phe Leu Thr
 105 110 115

cgc ttc tac gct taaaagcttg cttctcgacg caa 486
 Arg Phe Tyr Ala
 120

<210> 322

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Val Asn Thr Leu Ala Asp Ala Thr Asp Asp Gln Gln Trp Ile His Thr
 1 5 10 15

Asp Pro Glu Arg Ala Lys Asp Gly Pro Phe Gly Gly Ala Ile Ala His
 20 25 30

Gly Phe Leu Thr Leu Ser Met Ile Ile Pro Phe Trp Gly Glu Leu Leu
 35 40 45

Asp Val Thr Gly Val Thr Thr Lys Val Asn Tyr Gly Leu Asp Lys Val
 50 55 60

Arg Phe Thr Ser Pro Val Lys Val Gly Ser Arg Ile Arg Met Gly Ala

435

<210> 324
 <211> 121
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 324

Val	Asn	Thr	Phe	Ala	Asp	Ala	Thr	Asp	Asp	Gln	Gln	Trp	Ile	His	Thr
1				5					10					15	
Asp	Pro	Glu	Arg	Ala	Lys	Asp	Gly	Pro	Phe	Gly	Gly	Ala	Ile	Ala	His
			20					25					30		
Gly	Phe	Leu	Thr	Leu	Ser	Met	Ile	Ile	Pro	Phe	Trp	Gly	Glu	Leu	Leu
	35						40					45			
Asp	Val	Thr	Gly	Val	Thr	Thr	Lys	Val	Asn	Tyr	Gly	Leu	Asp	Lys	Val
	50					55					60				
Arg	Phe	Thr	Ser	Pro	Val	Lys	Val	Gly	Ser	Arg	Ile	Arg	Met	Gly	Ala
	65				70				75						80
Val	Val	Arg	Glu	Ile	Ser	Glu	Val	Lys	Gly	Asn	Gly	Leu	His	Leu	Val
				85					90					95	
Ala	Asp	Gly	Thr	Ile	Glu	Ile	Glu	Gly	Gln	Glu	Arg	Pro	Ala	Val	Val
		100						105					110		
Ala	Thr	Phe	Leu	Thr	Arg	Phe	Tyr	Ala							
	115						120								

<210> 325
 <211> 732
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(709)

<223> RXA01059

<400> 325

aattattagc	tttccaatac	aaaattttaaa	tcccagagcg	atctgccccca	cacttacttg	60
atgcgggaac	aaatttgaag	gttttttcagt	tgctataggt	atg act aca gtt act	115	
				Met Thr Thr Val Thr		
				1	5	
caa gac ctt cta gca ctt gac gaa gac gca cag aac ctc ctt ttc cgt	163					
Gln Asp Leu Leu Ala Leu Asp Glu Asp Ala Gln Asn Leu Leu Phe Arg						
	10		15		20	
gag gct cgc acc gca aat gct ttc act gat gaa cca atc tct gac gag	211					
Glu Ala Arg Thr Ala Asn Ala Phe Thr Asp Glu Pro Ile Ser Asp Glu						
	25		30		35	
cag atc gaa gca atc ttc gac cta gtt aag tgg gca cca acc gca atg	259					
Gln Ile Glu Ala Ile Phe Asp Leu Val Lys Trp Ala Pro Thr Ala Met						
	40		45		50	

aac tcc cag cct ctg cgc gtg gta att gtt cgt tcc gaa gaa gcc aaa 307
 Asn Ser Gln Pro Leu Arg Val Val Ile Val Arg Ser Glu Glu Ala Lys
 55 60 65
 gct cgc ctc gtg cca ttg atg gca gaa ggc aac cag gcc aag gtt gct 355
 Ala Arg Leu Val Pro Leu Met Ala Glu Gly Asn Gln Ala Lys Val Ala
 70 75 80 85
 gca gct cct gcg gtc gca ctt ctt gca gcc gac atc gac ttc cac gaa 403
 Ala Ala Pro Ala Val Ala Leu Leu Ala Ala Asp Ile Asp Phe His Glu
 90 95 100
 gaa atg ccc aag ctc ttc cca cct ttc cca ggc gca cgc gac atg ttc 451
 Glu Met Pro Lys Leu Phe Pro Pro Phe Pro Gly Ala Arg Asp Met Phe
 105 110 115
 gaa gcc gat gaa gct tca cgt gct tcc tcc gca gaa ctc aat gct ggc 499
 Glu Ala Asp Glu Ala Ser Arg Ala Ser Ser Ala Glu Leu Asn Ala Gly
 120 125 130
 ctt cag atc gga tac gcc atc atc ggt atc cgc gca gca ggt ctc gcc 547
 Leu Gln Ile Gly Tyr Ala Ile Ile Gly Ile Arg Ala Ala Gly Leu Ala
 135 140 145
 gct ggc cca atg acc ggc atg gat gca gac gct atc tcc aag gag ttc 595
 Ala Gly Pro Met Thr Gly Met Asp Ala Asp Ala Ile Ser Lys Glu Phe
 150 155 160 165
 ttc cca gac ggc cgc cac cgc gtt ctg gtt gcc atc aac atg ggt aag 643
 Phe Pro Asp Gly Arg His Arg Val Leu Val Ala Ile Asn Met Gly Lys
 170 175 180
 cca gct gac aat gct tgg tac gac cgc ctg cca cgc ctt gag cag gac 691
 Pro Ala Asp Asn Ala Trp Tyr Asp Arg Leu Pro Arg Leu Glu Gln Asp
 185 190 195
 gaa gtt gtc gaa acc ctc tagaaaccac tctagaaata gct 732
 Glu Val Val Glu Thr Leu
 200

<210> 326

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Thr Thr Val Thr Gln Asp Leu Leu Ala Leu Asp Glu Asp Ala Gln
 1 5 10 15
 Asn Leu Leu Phe Arg Glu Ala Arg Thr Ala Asn Ala Phe Thr Asp Glu
 20 25 30
 Pro Ile Ser Asp Glu Gln Ile Glu Ala Ile Phe Asp Leu Val Lys Trp
 35 40 45
 Ala Pro Thr Ala Met Asn Ser Gln Pro Leu Arg Val Val Ile Val Arg
 50 55 60
 Ser Glu Glu Ala Lys Ala Arg Leu Val Pro Leu Met Ala Glu Gly Asn
 65 70 75 80

<400> 327														
ctctattgtg	gtacgcacca	tgactgctca	accagcccac	gagccgccaa	ggcatctccg	60								
gttcagtacg agcgggatcc tcccggacaa tcgcgtccaa						atg	tgg	gag	ggc	cac	115			
						Met	Trp	Glu	Gly	His				
						1				5				
aat gct cgc gca ttg ctt ccg ctc gac att aga acc att gac gat cgc	163													
Asn Ala Arg Ala Leu Leu Pro Leu Asp Ile Arg Thr Ile Asp Asp Arg														
10 15 20														
ccc atg cag gcc tcc gaa acc aac ctg cac ctc cca tca atg cgg atg	211													
Pro Met Gln Ala Ser Glu Thr Asn Leu His Leu Pro Ser Met Arg Met														
25 30 35														
gcg agc gta ttc ggg act tcg caa ttt gtc gag cgt tca gag agt ttc	259													
Ala Ser Val Phe Gly Thr Ser Gln Phe Val Glu Arg Ser Glu Ser Phe														
40 45 50														
atc tca gaa aac ccc acg ggt gtg gtt gcg atc ttc ttt gcg act gaa	307													
Ile Ser Glu Asn Pro Thr Gly Val Val Ala Ile Phe Phe Ala Thr Glu														
55 60 65														
ggg gaa gca gtc ttc ttc cac cgt ggt gga cat gta gcg ctt cgg cca	355													
Gly Glu Ala Val Phe Phe His Arg Gly Gly His Val Ala Leu Arg Pro														

70	75	80	85	
ggt cag gcc att gtt tac gac gcc gat agg cca ttc ctc cgc gga ttc				403
Gly Gln Ala Ile Val Tyr Asp Ala Asp Arg Pro Phe Leu Arg Gly Phe				
	90	95	100	
aac aat cgc ttc cgc gag cta gtt ctc acc atc ccg aag cag cgc tac				451
Asn Asn Arg Phe Arg Glu Leu Val Leu Thr Ile Pro Lys Gln Arg Tyr				
	105	110	115	
ctt gaa att gtt ggc tca aaa ggc cct gag ctt ccc gct att ttt gag				499
Leu Glu Ile Val Gly Ser Lys Gly Pro Glu Leu Pro Ala Ile Phe Glu				
	120	125	130	
ttc gga gca aca gga acc gcc aat gaa caa gct tta gcg cga cta gtt				547
Phe Gly Ala Thr Gly Thr Ala Asn Glu Gln Ala Leu Ala Arg Leu Val				
	135	140	145	
cag gaa tct cta cac agg att gaa agt ggc gag ccg aag cat atc gat				595
Gln Glu Ser Leu His Arg Ile Glu Ser Gly Glu Pro Lys His Ile Asp				
	150	155	160	165
tcc agt gga cct tta gga aaa ccg tgg agc gat atc gag cac gag gcc				643
Ser Ser Gly Pro Leu Gly Lys Pro Trp Ser Asp Ile Glu His Glu Ala				
	170	175	180	
cac gga ctt atc cgc aat gta ctt ggc gac gcc aca agt agc gaa gaa				691
His Gly Leu Ile Arg Asn Val Leu Gly Asp Ala Thr Ser Ser Glu Glu				
	185	190	195	
ggc tta att tct gca gcc cag aga ttt att gac atc aat att tcc gaa				739
Gly Leu Ile Ser Ala Ala Gln Arg Phe Ile Asp Ile Asn Ile Ser Glu				
	200	205	210	
agt gac tta caa gcg tcg cgg att gct gca gcc gtg gga atc agc gaa				787
Ser Asp Leu Gln Ala Ser Arg Ile Ala Ala Ala Val Gly Ile Ser Glu				
	215	220	225	
cgc caa cta agt cga atc ttc tca gac tca gga caa act atc gga cgc				835
Arg Gln Leu Ser Arg Ile Phe Ser Asp Ser Gly Gln Thr Ile Gly Arg				
	230	235	240	245
tac gtc cta aac acc cga ctg gat ttt gca aag gaa gcg ctg tcg aca				883
Tyr Val Leu Asn Thr Arg Leu Asp Phe Ala Lys Glu Ala Leu Ser Thr				
	250	255	260	
ccg gag cga gac aag gtt tcg gtc agt gag atc ggt aag cgc ttt ggg				931
Pro Glu Arg Asp Lys Val Ser Val Ser Glu Ile Gly Lys Arg Phe Gly				
	265	270	275	
ttc gct tcc cca agt cat ttc agt cgc acc ttc cgc gag cgg ttt gaa				979
Phe Ala Ser Pro Ser His Phe Ser Arg Thr Phe Arg Glu Arg Phe Glu				
	280	285	290	
atg acg ccg ctt caa tgg agg aag gaa tcg cag cgt caa tcc ttt caa				1027
Met Thr Pro Leu Gln Trp Arg Lys Glu Ser Gln Arg Gln Ser Phe Gln				
	295	300	305	
gag tgagggttttt gttctcaggc gga				1053
Glu				
310				

<210> 328

<211> 310

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 328

```

Met Trp Glu Gly His Asn Ala Arg Ala Leu Leu Pro Leu Asp Ile Arg
 1           5           10           15

Thr Ile Asp Asp Arg Pro Met Gln Ala Ser Glu Thr Asn Leu His Leu
      20           25           30

Pro Ser Met Arg Met Ala Ser Val Phe Gly Thr Ser Gln Phe Val Glu
      35           40           45

Arg Ser Glu Ser Phe Ile Ser Glu Asn Pro Thr Gly Val Val Ala Ile
      50           55           60

Phe Phe Ala Thr Glu Gly Glu Ala Val Phe Phe His Arg Gly Gly His
      65           70           75           80

Val Ala Leu Arg Pro Gly Gln Ala Ile Val Tyr Asp Ala Asp Arg Pro
      85           90           95

Phe Leu Arg Gly Phe Asn Asn Arg Phe Arg Glu Leu Val Leu Thr Ile
      100          105          110

Pro Lys Gln Arg Tyr Leu Glu Ile Val Gly Ser Lys Gly Pro Glu Leu
      115          120          125

Pro Ala Ile Phe Glu Phe Gly Ala Thr Gly Thr Ala Asn Glu Gln Ala
      130          135          140

Leu Ala Arg Leu Val Gln Glu Ser Leu His Arg Ile Glu Ser Gly Glu
      145          150          155          160

Pro Lys His Ile Asp Ser Ser Gly Pro Leu Gly Lys Pro Trp Ser Asp
      165          170          175

Ile Glu His Glu Ala His Gly Leu Ile Arg Asn Val Leu Gly Asp Ala
      180          185          190

Thr Ser Ser Glu Glu Gly Leu Ile Ser Ala Ala Gln Arg Phe Ile Asp
      195          200          205

Ile Asn Ile Ser Glu Ser Asp Leu Gln Ala Ser Arg Ile Ala Ala Ala
      210          215          220

Val Gly Ile Ser Glu Arg Gln Leu Ser Arg Ile Phe Ser Asp Ser Gly
      225          230          235          240

Gln Thr Ile Gly Arg Tyr Val Leu Asn Thr Arg Leu Asp Phe Ala Lys
      245          250          255

Glu Ala Leu Ser Thr Pro Glu Arg Asp Lys Val Ser Val Ser Glu Ile
      260          265          270

Gly Lys Arg Phe Gly Phe Ala Ser Pro Ser His Phe Ser Arg Thr Phe
      275          280          285

```

Arg Glu Arg Phe Glu Met Thr Pro Leu Gln Trp Arg Lys Glu Ser Gln
 290 295 300

Arg Gln Ser Phe Gln Glu
 305 310

<210> 329

<211> 1806

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1783)

<223> RXN00073

<400> 329

gaatctaagt gttggtctag acagagcggg acgtctaagt ttgcggatag atcaaaccga 60

gtgacatgta cttcactagc tctttaagga ttaactcccc atg aca aca acc acc 115
 Met Thr Thr Thr Thr
 1 5

gga agt gcc cgg cca gca cgt gcc gcc agg aag cct aag ccc gaa ggc 163
 Gly Ser Ala Arg Pro Ala Arg Ala Ala Arg Lys Pro Lys Pro Glu Gly
 10 15 20

caa tgg aaa atc gac ggc acc gag ccg ctt aac cat gcc gag gaa att 211
 Gln Trp Lys Ile Asp Gly Thr Glu Pro Leu Asn His Ala Glu Glu Ile
 25 30 35

aag caa gaa gaa ccc gct ttt gct gtc aag cag ccg gtc att gat att 259
 Lys Gln Glu Glu Pro Ala Phe Ala Val Lys Gln Arg Val Ile Asp Ile
 40 45 50

tac tcc aag cag ggt ttt tct tcc att gca ccg gat gac att gcc cca 307
 Tyr Ser Lys Gln Gly Phe Ser Ser Ile Ala Pro Asp Asp Ile Ala Pro
 55 60 65

cgc ttt aag tgg ttg ggc att tac acc cag ccg aag cag gat ctg ggc 355
 Arg Phe Lys Trp Leu Gly Ile Tyr Thr Gln Arg Lys Gln Asp Leu Gly
 70 75 80 85

ggt gaa ctg acc ggt cag ctt cct gat gat gag ctg cag gat gag tac 403
 Gly Glu Leu Thr Gly Gln Leu Pro Asp Asp Glu Leu Gln Asp Glu Tyr
 90 95 100

ttc atg atg cgt gtg cgt ttt gat ggc gga ctg gct tcc cct gag cgc 451
 Phe Met Met Arg Val Arg Phe Asp Gly Gly Leu Ala Ser Pro Glu Arg
 105 110 115

ctg cgt gcc gtg ggt gaa att tct agg gat tat gct cgt tcc acc gcg 499
 Leu Arg Ala Val Gly Glu Ile Ser Arg Asp Tyr Ala Arg Ser Thr Ala
 120 125 130

gac ttc acc gac cgc cag aac att cag ctg cac tgg att cgt att gaa 547
 Asp Phe Thr Asp Arg Gln Asn Ile Gln Leu His Trp Ile Arg Ile Glu
 135 140 145

gat	gtg	cct	gcg	atc	tgg	gag	aag	cta	gaa	acc	gtc	gga	ctg	tcc	acc	595
Asp	Val	Pro	Ala	Ile	Trp	Glu	Lys	Leu	Glu	Thr	Val	Gly	Leu	Ser	Thr	
150					155					160					165	
atg	ctt	ggt	tgc	ggt	gac	gtt	cca	cgt	gtt	atc	ttg	ggc	tcc	cca	gtt	643
Met	Leu	Gly	Cys	Gly	Asp	Val	Pro	Arg	Val	Ile	Leu	Gly	Ser	Pro	Val	
			170						175						180	
tct	ggc	gta	gct	gct	gaa	gag	ctg	atc	gat	gcc	acc	ccg	gct	atc	gat	691
Ser	Gly	Val	Ala	Ala	Glu	Glu	Leu	Ile	Asp	Ala	Thr	Pro	Ala	Ile	Asp	
			185					190					195			
gcg	att	cgt	gag	cgc	tac	cta	gac	aag	gaa	gag	ttc	cac	aac	ctt	cct	739
Ala	Ile	Arg	Glu	Arg	Tyr	Leu	Asp	Lys	Glu	Glu	Phe	His	Asn	Leu	Pro	
		200					205					210				
cgt	aag	ttt	aag	act	gct	atc	act	ggc	aac	cag	cgc	cag	gat	gtt	acc	787
Arg	Lys	Phe	Lys	Thr	Ala	Ile	Thr	Gly	Asn	Gln	Arg	Gln	Asp	Val	Thr	
	215					220					225					
cac	gaa	atc	cag	gac	gtt	tcc	ttc	gtt	cct	tgc	att	cac	cca	gaa	ttc	835
His	Glu	Ile	Gln	Asp	Val	Ser	Phe	Val	Pro	Ser	Ile	His	Pro	Glu	Phe	
230					235					240					245	
ggc	cca	gga	ttt	gag	tgc	ttt	gtg	ggc	ggt	ggc	ctg	tcc	acc	aac	cca	883
Gly	Pro	Gly	Phe	Glu	Cys	Phe	Val	Gly	Gly	Gly	Leu	Ser	Thr	Asn	Pro	
				250				255						260		
atg	ctt	gct	cag	cca	ctt	ggt	tct	tgg	att	cca	ctt	gat	gag	gtt	cca	931
Met	Leu	Ala	Gln	Pro	Leu	Gly	Ser	Trp	Ile	Pro	Leu	Asp	Glu	Val	Pro	
			265					270					275			
gaa	gtg	tgg	gct	ggc	gtc	gcc	gga	att	ttc	cgc	gac	tac	ggc	ttc	cga	979
Glu	Val	Trp	Ala	Gly	Val	Ala	Gly	Ile	Phe	Arg	Asp	Tyr	Gly	Phe	Arg	
		280					285					290				
cgc	ctg	cgt	aac	cgt	gct	cgc	ctc	aag	ttc	ttg	gtg	gca	cag	tgg	ggt	1027
Arg	Leu	Arg	Asn	Arg	Ala	Arg	Leu	Lys	Phe	Leu	Val	Ala	Gln	Trp	Gly	
	295					300					305					
att	gag	aag	ttc	cgt	gaa	gtt	ctt	gag	acc	gaa	tac	ctc	gag	cgc	aag	1075
Ile	Glu	Lys	Phe	Arg	Glu	Val	Leu	Glu	Thr	Glu	Tyr	Leu	Glu	Arg	Lys	
310					315					320					325	
ctg	atc	gat	ggc	cca	gtt	gtt	acc	acc	aac	cct	ggc	tac	cgt	gac	cac	1123
Leu	Ile	Asp	Gly	Pro	Val	Val	Thr	Thr	Asn	Pro	Gly	Tyr	Arg	Asp	His	
				330					335					340		
att	ggc	att	cac	cca	caa	aag	gac	ggc	aag	ttc	tac	ctc	ggt	gtg	aag	1171
Ile	Gly	Ile	His	Pro	Gln	Lys	Asp	Gly	Lys	Phe	Tyr	Leu	Gly	Val	Lys	
			345					350					355			
cca	acc	gtt	gga	cac	acc	acc	ggt	gag	cag	ctc	att	gcc	att	gct	gat	1219
Pro	Thr	Val	Gly	His	Thr	Thr	Gly	Glu	Gln	Leu	Ile	Ala	Ile	Ala	Asp	
		360					365					370				
gtt	gca	gaa	aag	cac	ggc	atc	acc	agg	att	cgt	acc	acg	gcg	gaa	aag	1267
Val	Ala	Glu	Lys	His	Gly	Ile	Thr	Arg	Ile	Arg	Thr	Thr	Ala	Glu	Lys	
		375				380					385					
gaa	ctg	ctc	ttc	ctc	gat	att	gag	aga	aag	aac	ctt	act	acc	gtt	gca	1315

Glu	Leu	Leu	Phe	Leu	Asp	Ile	Glu	Arg	Lys	Asn	Leu	Thr	Thr	Val	Ala	
390					395					400					405	
cgc	gac	ctg	gat	gaa	atc	gga	ctg	tac	tct	tca	cct	tcc	gag	ttc	cgc	1363
Arg	Asp	Leu	Asp	Glu	Ile	Gly	Leu	Tyr	Ser	Ser	Pro	Ser	Glu	Phe	Arg	
				410					415					420		
cgc	ggc	atc	att	tcc	tgc	acc	ggc	ttg	gag	ttc	tgc	aag	ctt	gcg	cac	1411
Arg	Gly	Ile	Ile	Ser	Cys	Thr	Gly	Leu	Glu	Phe	Cys	Lys	Leu	Ala	His	
				425				430						435		
gca	acc	acc	aag	tca	cga	gca	att	gag	ctt	gtc	gac	gaa	ctg	gaa	gag	1459
Ala	Thr	Thr	Lys	Ser	Arg	Ala	Ile	Glu	Leu	Val	Asp	Glu	Leu	Glu	Glu	
			440				445					450				
cgc	ctc	ggc	gat	ttg	gat	gtt	ccc	atc	aag	att	gca	ctg	aac	ggg	tgc	1507
Arg	Leu	Gly	Asp	Leu	Asp	Val	Pro	Ile	Lys	Ile	Ala	Leu	Asn	Gly	Cys	
	455					460					465					
cct	aac	tct	tgt	gca	cgc	acc	cag	gtt	tcc	gac	atc	gga	ttc	aag	gga	1555
Pro	Asn	Ser	Cys	Ala	Arg	Thr	Gln	Val	Ser	Asp	Ile	Gly	Phe	Lys	Gly	
470					475					480					485	
cag	acc	gtc	act	gat	gct	gac	ggc	aac	cgc	gtt	gaa	ggg	ttc	cag	gtt	1603
Gln	Thr	Val	Thr	Asp	Ala	Asp	Gly	Asn	Arg	Val	Glu	Gly	Phe	Gln	Val	
				490					495					500		
cac	ctg	ggc	ggg	tcc	atg	aac	ttg	gat	cca	aac	ttc	gga	cgc	aag	ctc	1651
His	Leu	Gly	Gly	Ser	Met	Asn	Leu	Asp	Pro	Asn	Phe	Gly	Arg	Lys	Leu	
			505					510					515			
aag	ggc	cac	aag	gtt	att	gcc	gat	gaa	gtg	gga	gag	tac	gtc	act	cgc	1699
Lys	Gly	His	Lys	Val	Ile	Ala	Asp	Glu	Val	Gly	Glu	Tyr	Val	Thr	Arg	
			520				525					530				
gtt	gtt	acc	cac	ttc	aag	gaa	cag	cgc	cac	gag	gac	gag	cac	ttc	cgc	1747
Val	Val	Thr	His	Phe	Lys	Glu	Gln	Arg	His	Glu	Asp	Glu	His	Phe	Arg	
			535				540				545					
gat	tgg	gtc	cag	cgg	gcc	gct	gag	gaa	gat	ttg	gtg	tgagtcttcg				1793
Asp	Trp	Val	Gln	Arg	Ala	Glu	Glu	Asp	Leu	Val						
550					555				560							
gaggaaaccc	aat															1806

<210> 330

<211> 561

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Met	Thr	Thr	Thr	Thr	Gly	Ser	Ala	Arg	Pro	Ala	Arg	Ala	Ala	Arg	Lys	
1					5				10					15		
Pro	Lys	Pro	Glu	Gly	Gln	Trp	Lys	Ile	Asp	Gly	Thr	Glu	Pro	Leu	Asn	
			20					25					30			
His	Ala	Glu	Glu	Ile	Lys	Gln	Glu	Glu	Pro	Ala	Phe	Ala	Val	Lys	Gln	
			35				40						45			

Arg Val Ile Asp Ile Tyr Ser Lys Gln Gly Phe Ser Ser Ile Ala Pro
 50 55 60
 Asp Asp Ile Ala Pro Arg Phe Lys Trp Leu Gly Ile Tyr Thr Gln Arg
 65 70 75 80
 Lys Gln Asp Leu Gly Gly Glu Leu Thr Gly Gln Leu Pro Asp Asp Glu
 85 90 95
 Leu Gln Asp Glu Tyr Phe Met Met Arg Val Arg Phe Asp Gly Gly Leu
 100 105 110
 Ala Ser Pro Glu Arg Leu Arg Ala Val Gly Glu Ile Ser Arg Asp Tyr
 115 120 125
 Ala Arg Ser Thr Ala Asp Phe Thr Asp Arg Gln Asn Ile Gln Leu His
 130 135 140
 Trp Ile Arg Ile Glu Asp Val Pro Ala Ile Trp Glu Lys Leu Glu Thr
 145 150 155 160
 Val Gly Leu Ser Thr Met Leu Gly Cys Gly Asp Val Pro Arg Val Ile
 165 170 175
 Leu Gly Ser Pro Val Ser Gly Val Ala Ala Glu Glu Leu Ile Asp Ala
 180 185 190
 Thr Pro Ala Ile Asp Ala Ile Arg Glu Arg Tyr Leu Asp Lys Glu Glu
 195 200 205
 Phe His Asn Leu Pro Arg Lys Phe Lys Thr Ala Ile Thr Gly Asn Gln
 210 215 220
 Arg Gln Asp Val Thr His Glu Ile Gln Asp Val Ser Phe Val Pro Ser
 225 230 235 240
 Ile His Pro Glu Phe Gly Pro Gly Phe Glu Cys Phe Val Gly Gly Gly
 245 250 255
 Leu Ser Thr Asn Pro Met Leu Ala Gln Pro Leu Gly Ser Trp Ile Pro
 260 265 270
 Leu Asp Glu Val Pro Glu Val Trp Ala Gly Val Ala Gly Ile Phe Arg
 275 280 285
 Asp Tyr Gly Phe Arg Arg Leu Arg Asn Arg Ala Arg Leu Lys Phe Leu
 290 295 300
 Val Ala Gln Trp Gly Ile Glu Lys Phe Arg Glu Val Leu Glu Thr Glu
 305 310 315 320
 Tyr Leu Glu Arg Lys Leu Ile Asp Gly Pro Val Val Thr Thr Asn Pro
 325 330 335
 Gly Tyr Arg Asp His Ile Gly Ile His Pro Gln Lys Asp Gly Lys Phe
 340 345 350
 Tyr Leu Gly Val Lys Pro Thr Val Gly His Thr Thr Gly Glu Gln Leu
 355 360 365
 Ile Ala Ile Ala Asp Val Ala Glu Lys His Gly Ile Thr Arg Ile Arg


```
<210> 331
<211> 373
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(373)  
<223> RXN03131
```

445

Arg Ile Gly Thr Ala Pro Asp Ser Trp Gly Val Trp Phe Pro Glu Asp
 25 30 35

cca aag cag atc cct tgg gag cgt ttt ctc tac gag gtc gtg aaa gct 259
 Pro Lys Gln Ile Pro Trp Glu Arg Phe Leu Tyr Glu Val Val Lys Ala
 40 45 50

ggc tac acc tgg atc gag ctt ggc cca tac ggc tac ctg cca acc gat 307
 Gly Tyr Thr Trp Ile Glu Leu Gly Pro Tyr Gly Tyr Leu Pro Thr Asp
 55 60 65

gcc aac cag ctt gaa gat gaa ctg ggc aag cgc ggc ctg aag ctg tcc 355
 Ala Asn Gln Leu Glu Asp Glu Leu Gly Lys Arg Gly Leu Lys Leu Ser
 70 75 80 85

gct ggc acc gag ttc acc 373
 Ala Gly Thr Glu Phe Thr
 90

<210> 332
 <211> 91
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 332
 Met Thr Thr Ser Val Pro Ala Ser Thr Lys Ala Leu Ser Val Ala Gly
 1 5 10 15

Glu Asn Pro Gly Leu Arg Ile Gly Thr Ala Pro Asp Ser Trp Gly Val
 20 25 30

Trp Phe Pro Glu Asp Pro Lys Gln Ile Pro Trp Glu Arg Phe Leu Tyr
 35 40 45

Glu Val Val Lys Ala Gly Tyr Thr Trp Ile Glu Leu Gly Pro Tyr Gly
 50 55 60

Tyr Leu Pro Thr Asp Ala Asn Gln Leu Glu Asp Glu Leu Gly Lys Arg
 65 70 75 80

Gly Leu Lys Leu Ser Ala Gly Thr Glu Phe Thr
 85 90

<210> 333
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(526)
 <223> RXS00153

<400> 333
 cctcgatttg agtaaagagg acgtcctcgc ctgatttttc ggggtgtgttt ttgcgtggcg 60

agccctgcct ggcccttcca aattatgtag ggtggcctgc gtg gga gca ata att 115
 Val Gly Ala Ile Ile
 1 5

tgg ttt atc gga gca ttg gtt ctt gct ggc ttg gaa ttg gca gta ggt 163
 Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu Glu Leu Ala Val Gly
 10 15 20

gag ttc acc tta ttg atg ctc ggc ggt gca gct ttg gca acc gcc ggc 211
 Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala Leu Ala Thr Ala Gly
 25 30 35

gtg gca ctc atc ggt gtc cca gta tgg gct gaa ttt gtc acc ttc gcg 259
 Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu Phe Val Thr Phe Ala
 40 45 50

gtg gcc tca gct gct cta ctg atg ttc att agg ccg gcc att aga aag 307
 Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg Pro Ala Ile Arg Lys
 55 60 65

cgt ctg ctg aaa cca aag gtt ctg gac tct tca cca cga gca ctt gtt 355
 Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser Pro Arg Ala Leu Val
 70 75 80 85

ggc cac cgt gct gaa gtg ctc gaa gat gtc gga gcg acc agc ggg cag 403
 Gly His Arg Ala Glu Val Leu Glu Asp Val Gly Ala Thr Ser Gly Gln
 90 95 100

gtc cgc ctg gat ggt tca att tgg tcc gcc cgc agc atg gat ccc aca 451
 Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg Ser Met Asp Pro Thr
 105 110 115

cac acc ttc gcg gaa ggt gaa att gtc agt gtc att gat atc caa ggc 499
 His Thr Phe Ala Glu Gly Glu Ile Val Ser Val Ile Asp Ile Gln Gly
 120 125 130

acg acc gcg att gta tgg aaa gaa gcc taaattttta acaatcaa 546
 Thr Thr Ala Ile Val Trp Lys Glu Ala
 135 140

agt 549

<210> 334
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 334
 Val Gly Ala Ile Ile Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu
 1 5 10 15

Glu Leu Ala Val Gly Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala
 20 25 30

Leu Ala Thr Ala Gly Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu
 35 40 45

Phe Val Thr Phe Ala Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg
 50 55 60

Pro Ala Ile Arg Lys Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser
 65 70 75 80

Pro Arg Ala Leu Val Gly His Arg Ala Glu Val Leu Glu Asp Val Gly
 85 90 95

Ala Thr Ser Gly Gln Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg
 100 105 110

Ser Met Asp Pro Thr His Thr Phe Ala Glu Gly Glu Ile Val Ser Val
 115 120 125

Ile Asp Ile Gln Gly Thr Thr Ala Ile Val Trp Lys Glu Ala
 130 135 140

<210> 335

<211> 509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(486)

<223> RXN01716

<400> 335

gaa gtc act cct gag gga ttc aaa gag atc acc cgt gaa aac acc atc	48
Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile	
1 5 10 15	
ggt cgc ctg ggc aaa ggc gtc gac gcc acc ggt cag cta gac ccc gag	96
Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu	
20 25 30	
gca atc gag cgc act cgt gtc gct ttg gaa aac tac gtt gaa ctc atg	144
Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met	
35 40 45	
gaa acc cat ggg gta gag gcc gta cga atg gtt gcc acc tcc gca acc	192
Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr	
50 55 60	
cgc gat gcg tcc aac cgc gat gaa ttc ttt tcg atg acc cgc cag ctt	240
Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu	
65 70 75 80	
ctg tcc aag atc cgt cct gga tac caa gct gaa gta att tcc ggc gaa	288
Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu	
85 90 95	
gag gaa gct ctg ctg tcc ttc cga ggt gca atc gtt gac ctg cct gaa	336
Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu	
100 105 110	
gac caa ggt cct ttc tgt gtt atc gac ctt ggc ggt gga tcc act gag	384
Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu	
115 120 125	
ttc atc gtt ggc acc tac gac ggt gaa atc cta ggc tcc cac tca acc	432
Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr	
130 135 140	
caa atg gga tgc gtg cgc ctg acc gaa cga atc atg cgc agc gac cca	480

Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160

ccc gac tgaaaccgaa gtggaaatcg ccc
 Pro Asp

509

<210> 336

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
 1 5 10 15

Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
 20 25 30

Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
 35 40 45

Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
 50 55 60

Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
 65 70 75 80

Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
 85 90 95

Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
 100 105 110

Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
 115 120 125

Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
 130 135 140

Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160

Pro Asp

<210> 337

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> RXN02972

<400> 337

acctacgacg gtgaaatcct aggctccac tcaacccaaa tgggatgcgt gcgcctgacc 60

gaacgaatca tgcgcagcga cccacccgac tgaaaccgaa gtg gaa atc gcc cgc 115
 Val Glu Ile Ala Arg
 1 5

gac tac gtt gca gaa cgc atc cag gaa gta aaa gcc atc gtc cca att 163
 Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys Ala Ile Val Pro Ile
 10 15 20

tca aag gca aaa acc ttt gtg gga tgc gca ggc acc ttc acc aca atc 211
 Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly Thr Phe Thr Thr Ile
 25 30 35

tcc gcc tgg gtg caa ggc cta gaa agc tac gac cgc gac gcg atc cac 259
 Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp Arg Asp Ala Ile His
 40 45 50

ctc tct gca ctc aac ttc gat gca ctg cga gtt gtc acc gat gag atc 307
 Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val Val Thr Asp Glu Ile
 55 60 65

att tca gaa tca tca tca cag cgc gcc agc aac cca gtt gtt gat cca 355
 Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn Pro Val Val Asp Pro
 70 75 80 85

ggg cgc gcc gac gtc atc ggt ggc gga tcc gtt gtt gtc caa gca gcg 403
 Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val Val Val Gln Ala Ala
 90 95 100

atc gac tta gcc tcc aaa gaa gcc ggt gta gac tac atc att att tcc 451
 Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp Tyr Ile Ile Ile Ser
 105 110 115

gaa aaa gac atc ctc gac ggc ctc atc ctt ggc ctg gta gaa gcc gac 499
 Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly Leu Val Glu Ala Asp
 120 125 130

tct ttg aag aaa taggacccta gttttaaacc act 534
 Ser Leu Lys Lys
 135

<210> 338

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Val Glu Ile Ala Arg Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys
 1 5 10 15

Ala Ile Val Pro Ile Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly
 20 25 30

Thr Phe Thr Thr Ile Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp
 35 40 45

Arg Asp Ala Ile His Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val
 50 55 60

Val Thr Asp Glu Ile Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn
 65 70 75 80

Pro Val Val Asp Pro Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val
 85 90 95

Val Val Gln Ala Ala Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp
 100 105 110

Tyr Ile Ile Ile Ser Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly
 115 120 125

Leu Val Glu Ala Asp Ser Leu Lys Lys
 130 135

<210> 339
 <211> 1497
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1474)
 <223> RXN00663

<400> 339
 ctgaacgatt ggtgaccggc tcatgaaaac ttgacgagtc cccggtattc gccagcgggtg 60

actactaccg tgggcgacaa gccacttag aggaggactt gtg aca acc acc tat 115
 Val Thr Thr Thr Tyr
 1 5

cca gat ttc ctt gga aat tct tcg ctc caa aca gat acg gag cac tgg 163
 Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr Asp Thr Glu His Trp
 10 15 20

gaa atg gaa gga ggt gcg cag gaa gtc tct gtt act tat gtt ttg gac 211
 Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val Thr Tyr Val Leu Asp
 25 30 35

acg tca gtg ttg ctg tct gat ccg ttg tcg ttg aca cgg ttc gcg gag 259
 Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu Thr Arg Phe Ala Glu
 40 45 50

cac gat gta gtt ctg cca att gtt gta att acg gaa tta gaa gcc aag 307
 His Asp Val Val Leu Pro Ile Val Val Ile Thr Glu Leu Glu Ala Lys
 55 60 65

cgt cat cac ccg gac ctt ggc ttt ttt gct cgc caa gcg ctt cgg atg 355
 Arg His His Pro Asp Leu Gly Phe Phe Ala Arg Gln Ala Leu Arg Met
 70 75 80 85

ctg gat gag ctg cgt gag atc cat ggg gat ttg tcc aag cca ctg cca 403
 Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu Ser Lys Pro Leu Pro
 90 95 100

att ggc gat gaa ggc gga cac atc cat gtt gag ctg aat cac caa aac 451
 Ile Gly Asp Glu Gly Gly His Ile His Val Glu Leu Asn His Gln Asn
 105 110 115

acg ggg tcc ttg ccc gtg gga ttc cgc ctt ggt gac aat gac acc cgc 499
 Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly Asp Asn Asp Thr Arg

120					125					130						
atc	ctt	gca	gtg	gcc	aag	aat	ctg	cag	gaa	gag	ggc	cac	aat	gtg	gtt	547
Ile	Leu	Ala	Val	Ala	Lys	Asn	Leu	Gln	Glu	Glu	Gly	His	Asn	Val	Val	
135					140					145						
ctg	gtg	tcg	aag	gac	ctg	ccg	atg	cgg	att	aag	gcg	tcg	gca	agc	gga	595
Leu	Val	Ser	Lys	Asp	Leu	Pro	Met	Arg	Ile	Lys	Ala	Ser	Ala	Ser	Gly	
150					155					160					165	
atc	gcc	gca	cag	gaa	tac	cgc	gct	gcc	ctg	gcg	cgc	gac	cgt	ggc	tac	643
Ile	Ala	Ala	Gln	Glu	Tyr	Arg	Ala	Ala	Leu	Ala	Arg	Asp	Arg	Gly	Tyr	
170					175					180						
acc	ggc	atg	acc	cac	gcc	aat	atc	acc	gat	gac	cag	ctc	agc	gag	ctc	691
Thr	Gly	Met	Thr	His	Ala	Asn	Ile	Thr	Asp	Asp	Gln	Leu	Ser	Glu	Leu	
185					190					195						
tac	gac	acc	ggc	gag	gtg	cgc	att	gag	gag	ctc	gaa	aag	ctg	ccc	gtc	739
Tyr	Asp	Thr	Gly	Glu	Val	Arg	Ile	Glu	Glu	Leu	Glu	Lys	Leu	Pro	Val	
200					205					210						
aac	cac	ggc	ttc	acc	ctc	aaa	tcc	aac	agc	ggc	tcg	gcg	ctt	ggc	cgt	787
Asn	His	Gly	Phe	Thr	Leu	Lys	Ser	Asn	Ser	Gly	Ser	Ala	Leu	Gly	Arg	
215					220					225						
atg	aat	tcc	gac	aag	atc	atc	gag	ctt	gtc	ccc	ggc	gac	cag	cag	gta	835
Met	Asn	Ser	Asp	Lys	Ile	Ile	Glu	Leu	Val	Pro	Gly	Asp	Gln	Gln	Val	
230					235					240					245	
ttc	ggc	atc	agc	ggg	cgt	agc	gct	gag	cag	cgc	gtt	gcc	att	gat	ttg	883
Phe	Gly	Ile	Ser	Gly	Arg	Ser	Ala	Glu	Gln	Arg	Val	Ala	Ile	Asp	Leu	
250					255					260						
ctt	aac	gac	gac	gcc	gtc	ggc	atc	gta	tcc	atc	ggc	ggc	ccc	gcg	ggc	931
Leu	Asn	Asp	Asp	Ala	Val	Gly	Ile	Val	Ser	Ile	Gly	Gly	Pro	Ala	Gly	
265					270					275						
aca	ggc	aaa	agc	gca	ctc	gca	ctg	tgt	gcc	ggc	ctg	gaa	gct	gtg	atg	979
Thr	Gly	Lys	Ser	Ala	Leu	Ala	Leu	Cys	Ala	Gly	Leu	Glu	Ala	Val	Met	
280					285					290						
gag	cgt	cgc	att	cag	cgc	aag	att	atc	gtg	ttc	cgc	cca	ctc	ttt	gcc	1027
Glu	Arg	Arg	Ile	Gln	Arg	Lys	Ile	Ile	Val	Phe	Arg	Pro	Leu	Phe	Ala	
295					300					305						
gtt	ggc	gga	cag	gaa	ctt	ggc	tac	ctg	cct	ggc	gac	caa	gaa	gaa	aaa	1075
Val	Gly	Gly	Gln	Glu	Leu	Gly	Tyr	Leu	Pro	Gly	Asp	Gln	Glu	Glu	Lys	
310					315					320					325	
atg	ggg	cct	tgg	gcg	caa	gcg	gtt	ttt	gac	acc	cta	agc	tcc	atg	gtc	1123
Met	Gly	Pro	Trp	Ala	Gln	Ala	Val	Phe	Asp	Thr	Leu	Ser	Ser	Met	Val	
330					335					340						
agc	caa	aac	atc	atc	gat	gaa	gcc	ctc	tcc	cgc	ggc	ctc	atc	gaa	gtt	1171
Ser	Gln	Asn	Ile	Ile	Asp	Glu	Ala	Leu	Ser	Arg	Gly	Leu	Ile	Glu	Val	
345					350					355						
ctc	cca	ctt	act	cac	atc	cgc	gga	cgc	tca	ctc	cac	gat	gct	ttc	gtc	1219
Leu	Pro	Leu	Thr	His	Ile	Arg	Gly	Arg	Ser	Leu	His	Asp	Ala	Phe	Val	
360					365					370						

atc gtc gac gag gcc caa tcc cta gaa cgc aac gtg ttg ctc acc atg 1267
 Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn Val Leu Leu Thr Met
 375 380 385

ctg tct cgc atc ggc cag aat tcc cga gta gtt ctc acc cat gac gta 1315
 Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val Leu Thr His Asp Val
 390 395 400 405

gcg cag cgc gac aac ctg cgc gtt ggt cgc tac gac ggc atc gtc tct 1363
 Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr Asp Gly Ile Val Ser
 410 415 420

gtg gtg gaa gca ctc aag gat cac gaa ctg ttt ggc cac atc acg ttg 1411
 Val Val Glu Ala Leu Lys Asp His Glu Leu Phe Gly His Ile Thr Leu
 425 430 435

cag cgt tcc gaa cgc tcc cga atc gct gag ttg gtc acc caa gtt ttg 1459
 Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu Val Thr Gln Val Leu
 440 445 450

gat gcg ccg tct ctg tagtcgcgca gtctgtggcg att 1497
 Asp Ala Pro Ser Leu
 455

<210> 340

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Val Thr Thr Thr Tyr Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr
 1 5 10 15

Asp Thr Glu His Trp Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val
 20 25 30

Thr Tyr Val Leu Asp Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu
 35 40 45

Thr Arg Phe Ala Glu His Asp Val Val Leu Pro Ile Val Val Ile Thr
 50 55 60

Glu Leu Glu Ala Lys Arg His His Pro Asp Leu Gly Phe Phe Ala Arg
 65 70 75 80

Gln Ala Leu Arg Met Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu
 85 90 95

Ser Lys Pro Leu Pro Ile Gly Asp Glu Gly Gly His Ile His Val Glu
 100 105 110

Leu Asn His Gln Asn Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly
 115 120 125

Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu
 130 135 140

Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys
 145 150 155 160

Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala
 165 170 175
 Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp
 180 185 190
 Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu
 195 200 205
 Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly
 210 215 220
 Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro
 225 230 235 240
 Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg
 245 250 255
 Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile
 260 265 270
 Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly
 275 280 285
 Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe
 290 295 300
 Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly
 305 310 315 320
 Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr
 325 330 335
 Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg
 340 345 350
 Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu
 355 360 365
 His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn
 370 375 380
 Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val
 385 390 395 400
 Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr
 405 410 415
 Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu Leu Phe
 420 425 430
 Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu
 435 440 445
 Val Thr Gln Val Leu Asp Ala Pro Ser Leu
 450 455

<210> 341

<211> 1248

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1225)

<223> RXN00778 .

<400> 341

```

aggtcttagg tttttaagtc gtgagcaatc cggagggaaa ctagcccgcc tacaggatct 60
gctcagacga tgtcttcact taaaccggaa aggcttcccc gtg aac ctc act ctt 115
                               Val Asn Leu Thr Leu
                               1 5
aag cgc tcc atc gcc ctt gtg ggc gca gtt act gca ggc tcc ttc gct 163
Lys Arg Ser Ile Ala Leu Val Gly Ala Val Thr Ala Gly Ser Phe Ala
                               10 15 20
ctt gta gct tgc tcc gac tcc aat gag tct gat tcc acc tcc tca tct 211
Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp Ser Thr Ser Ser Ser
                               25 30 35
gca gct tcc acc ggt tct tcc gat gct gca tcc att gag ggc ctt tcc 259
Ala Ala Ser Thr Gly Ser Ser Asp Ala Ala Ser Ile Glu Gly Leu Ser
                               40 45 50
ggt gtt acc ggt cag ctc gtt gct gaa ggt gca tct tcc cag cag tcc 307
Gly Val Thr Gly Gln Leu Val Ala Glu Gly Ala Ser Ser Gln Gln Ser
                               55 60 65
gca atg gac tac ttt ggt atc cgt tac tcc gag gct gtc agc ggt gca 355
Ala Met Asp Tyr Phe Gly Ile Arg Tyr Ser Glu Ala Val Ser Gly Ala
                               70 75 80 85
tct ctg gct tac acc cct tca ggt tcc ggt tcc ggc cgc acc aac ttc 403
Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser Gly Arg Thr Asn Phe
                               90 95 100
gct gca ggc cag gtt gct ttc ggt ggc tcc gac tcc gca atg aag gac 451
Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp Ser Ala Met Lys Asp
                               105 110 115
gac cag gct gca gaa gca gaa gca cgt tgc aac ggc aac gaa gca tgg 499
Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly Asn Glu Ala Trp
                               120 125 130
cac ctg cca ttc gtt atc ggc cca gtt gca gtt gct tac aac ctg cct 547
His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala Tyr Asn Leu Pro
                               135 140 145
ggc gtt gac acc ctg aac ctg gac acc aac atc atc gct cag atc ttc 595
Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile Ala Gln Ile Phe
                               150 155 160 165
aag ggc gag atc acc aag tgg aac gac gaa gca atc gct tcc cag aac 643
Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile Ala Ser Gln Asn
                               170 175 180
gag ggc acc gac ctc cca gac cag gac atc tcc gtt ctg tac cgt tcc 691
Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val Leu Tyr Arg Ser

```

185										190										195																			
gaa	gag	tcc	ggt	acc	tcc	gac	aac	ttc	cag	aag	ttc	ctc	gga	gct	tcc	739																							
Glu	Glu	Ser	Gly	Thr	Ser	Asp	Asn	Phe	Gln	Lys	Phe	Leu	Gly	Ala	Ser																								
200										205										210																			
acc	gac	atc	tgg	gag	acc	gaa	ggc	cag	cag	ttc	cca	acc	gag	gtt	ggc	787																							
Thr	Asp	Ile	Trp	Glu	Thr	Glu	Gly	Gln	Gln	Phe	Pro	Thr	Glu	Val	Gly																								
215										220										225																			
tcc	ggt	gcg	cag	ggc	tcc	aac	ggt	gta	gct	tct	gag	gct	tcc	aac	atc	835																							
Ser	Gly	Ala	Gln	Gly	Ser	Asn	Gly	Val	Ala	Ser	Glu	Ala	Ser	Asn	Ile																								
230										235										240										245									
gag	ggt	gca	atc	acc	tac	gtt	gaa	gct	ggc	ttc	gct	aac	cag	tcc	ggc	883																							
Glu	Gly	Ala	Ile	Thr	Tyr	Val	Glu	Ala	Gly	Phe	Ala	Asn	Gln	Ser	Gly																								
250										255										260																			
ctg	ggc	gtt	gca	aac	atc	gac	ttc	ggc	tcc	ggc	cca	gtt	gaa	ctc	aac	931																							
Leu	Gly	Val	Ala	Asn	Ile	Asp	Phe	Gly	Ser	Gly	Pro	Val	Glu	Leu	Asn																								
265										270										275																			
gct	gag	tcc	gtt	ggc	gtt	gca	ctt	ggc	gca	ctc	gac	ttc	ctg	act	gag	979																							
Ala	Glu	Ser	Val	Gly	Val	Ala	Leu	Gly	Ala	Leu	Asp	Phe	Leu	Thr	Glu																								
280										285										290																			
ggc	cac	aac	atg	gtt	gtt	gac	acc	gac	gct	atg	ttc	gca	atg	aac	gaa	1027																							
Gly	His	Asn	Met	Val	Val	Asp	Thr	Asp	Ala	Met	Phe	Ala	Met	Asn	Glu																								
295										300										305																			
gcc	ggt	gct	tac	cca	ctg	atc	ctc	acc	acc	tac	gaa	atc	gtc	tgc	tcc	1075																							
Ala	Gly	Ala	Tyr	Pro	Leu	Ile	Leu	Thr	Thr	Tyr	Glu	Ile	Val	Cys	Ser																								
310										315										320										325									
gca	ggc	tac	gac	gag	acc	acc	cgc	gac	cag	gtc	aag	gac	ttc	ctg	acc	1123																							
Ala	Gly	Tyr	Asp	Glu	Thr	Thr	Arg	Asp	Gln	Val	Lys	Asp	Phe	Leu	Thr																								
330										335										340																			
gtt	gca	ctg	gac	tcc	cag	gat	gac	cag	ctc	gag	gct	ctc	ggc	tac	atc	1171																							
Val	Ala	Leu	Asp	Ser	Gln	Asp	Asp	Gln	Leu	Glu	Ala	Leu	Gly	Tyr	Ile																								
345										350										355																			
cca	gtt	acc	ggc	gag	cac	tac	gat	cgc	ctc	gtt	gca	gca	gtt	gaa	gca	1219																							
Pro	Val	Thr	Gly	Glu	His	Tyr	Asp	Arg	Leu	Val	Ala	Ala	Val	Glu	Ala																								
360										365										370																			
att	cag	taataaaccg	ctgccgtagc	ttc												1248																							
Ile	Gln																																						
375																																							

<210> 342

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Val	Asn	Leu	Thr	Leu	Lys	Arg	Ser	Ile	Ala	Leu	Val	Gly	Ala	Val	Thr
1				5					10					15	

Ala Gly Ser Phe Ala Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp

20					25					30					
Ser	Thr	Ser	Ser	Ser	Ala	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ala	Ala	Ser
		35					40					45			
Ile	Glu	Gly	Leu	Ser	Gly	Val	Thr	Gly	Gln	Leu	Val	Ala	Glu	Gly	Ala
	50					55					60				
Ser	Ser	Gln	Gln	Ser	Ala	Met	Asp	Tyr	Phe	Gly	Ile	Arg	Tyr	Ser	Glu
	65					70					75				80
Ala	Val	Ser	Gly	Ala	Ser	Leu	Ala	Tyr	Thr	Pro	Ser	Gly	Ser	Gly	Ser
				85					90					95	
Gly	Arg	Thr	Asn	Phe	Ala	Ala	Gly	Gln	Val	Ala	Phe	Gly	Gly	Ser	Asp
			100					105					110		
Ser	Ala	Met	Lys	Asp	Asp	Gln	Ala	Glu	Ala	Glu	Ala	Arg	Cys	Asn	
		115				120					125				
Gly	Asn	Glu	Ala	Trp	His	Leu	Pro	Phe	Val	Ile	Gly	Pro	Val	Ala	Val
	130					135					140				
Ala	Tyr	Asn	Leu	Pro	Gly	Val	Asp	Thr	Leu	Asn	Leu	Asp	Thr	Asn	Ile
	145					150					155				160
Ile	Ala	Gln	Ile	Phe	Lys	Gly	Glu	Ile	Thr	Lys	Trp	Asn	Asp	Glu	Ala
				165					170					175	
Ile	Ala	Ser	Gln	Asn	Glu	Gly	Thr	Asp	Leu	Pro	Asp	Gln	Asp	Ile	Ser
			180					185					190		
Val	Leu	Tyr	Arg	Ser	Glu	Glu	Ser	Gly	Thr	Ser	Asp	Asn	Phe	Gln	Lys
		195						200				205			
Phe	Leu	Gly	Ala	Ser	Thr	Asp	Ile	Trp	Glu	Thr	Glu	Gly	Gln	Gln	Phe
	210					215					220				
Pro	Thr	Glu	Val	Gly	Ser	Gly	Ala	Gln	Gly	Ser	Asn	Gly	Val	Ala	Ser
	225					230					235				240
Glu	Ala	Ser	Asn	Ile	Glu	Gly	Ala	Ile	Thr	Tyr	Val	Glu	Ala	Gly	Phe
				245					250					255	
Ala	Asn	Gln	Ser	Gly	Leu	Gly	Val	Ala	Asn	Ile	Asp	Phe	Gly	Ser	Gly
			260					265					270		
Pro	Val	Glu	Leu	Asn	Ala	Glu	Ser	Val	Gly	Val	Ala	Leu	Gly	Ala	Leu
		275					280					285			
Asp	Phe	Leu	Thr	Glu	Gly	His	Asn	Met	Val	Val	Asp	Thr	Asp	Ala	Met
	290					295					300				
Phe	Ala	Met	Asn	Glu	Ala	Gly	Ala	Tyr	Pro	Leu	Ile	Leu	Thr	Thr	Tyr
	305					310					315				320
Glu	Ile	Val	Cys	Ser	Ala	Gly	Tyr	Asp	Glu	Thr	Thr	Arg	Asp	Gln	Val
				325					330					335	
Lys	Asp	Phe	Leu	Thr	Val	Ala	Leu	Asp	Ser	Gln	Asp	Asp	Gln	Leu	Glu
			340					345					350		

Ala Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val
 355 360 365

Ala Ala Val Glu Ala Ile Gln
 370 375

<210> 343
 <211> 870
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(847)
 <223> RXN00250

<400> 343
 acaacaccag accaccccaa ccctgaataa acccctatatt ttctaataaag tcacactttg 60
 ccgtatagaa attcagtcaa ccaagagtac tctgtccacc atg gtt ttt act ctt 115
 Met Val Phe Thr Leu
 1 5
 gcg gac tcc gtc tcc cag gtt gcg cta ggt ccg tcc tgg ctg gac cct 163
 Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro Ser Trp Leu Asp Pro
 10 15 20
 atg gaa ctt ctt tcc ggc tcc ggc ccg ttc ggt agc ttc att ctt ccg 211
 Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro
 25 30 35
 gcg atg ctt gcc att gtc ttt atc gaa tca ggc cta ctt ttc cca ctt 259
 Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu
 40 45 50
 cta cca ggt gat tct ctc ctt ttc acc ggt ggt ctc cta gct aac cag 307
 Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln
 55 60 65
 gct gac cct ttt gca ccg ctg tgg ctg gtg ctg atc ctc tgc cct atc 355
 Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu Ile Leu Cys Pro Ile
 70 75 80 85
 gcc gca att ctt ggc gat cag gtg ggt tac tgg att ggc cac aag ttc 403
 Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp Ile Gly His Lys Phe
 90 95 100
 cac cct cgc ctg gtc aat cgt ccg gat ggc agg att ttc aag cag gaa 451
 His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu
 105 110 115
 tac ctc aag cag act gag gat ttc ttt gag aag cat ggc ccc gtg acg 499
 Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys His Gly Pro Val Thr
 120 125 130
 atc att ttg tgc cgt ttc gtg ccc atc gtc cgt act tac gca cct ctg 547
 Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg Thr Tyr Ala Pro Leu
 135 140 145

```

gtc gca ggt atg gct ggc atg cgt tac cgc acg ttc att att tac aac 595
Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr Phe Ile Ile Tyr Asn
150                               155                               160                               165

atg atc ggt ggc att ttg tgg ggt tcc ggc gtg gtg gct ttg ggt gct 643
Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val Val Ala Leu Gly Ala
170                               175                               180

gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att gat ctg att ttc 691
Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile Asp Leu Ile Phe
185                               190                               195

ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg gtc ggc atg gcc 739
Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu Val Gly Met Ala
200                               205                               210

cgc aag ctg gct gac ggc cac aag caa gcc aac acc gag cca caa gaa 787
Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr Glu Pro Gln Glu
215                               220                               225

aac ccc gca gtc cag aca gcc cca gta aaa acc cag gaa gcc cag gaa 835
Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln Glu Ala Gln Glu
230                               235                               240                               245

gcc ccc cag aac taatctttcc ggccgccag ttc 870
Ala Pro Gln Asn

```

<210> 344
 <211> 249
 <212> PRT
 <213> *Corynebacterium glutamicum*

```

<400> 344
Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro
 1           5           10           15

Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly
20           25           30

Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly
35           40           45

Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly
50           55           60

Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu
65           70           75           80

Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp
85           90           95

Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg
100          105          110

Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys
115          120          125

His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg
130          135          140

```

Thr Tyr Ala Pro Leu Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr
 145 150 155 160
 Phe Ile Ile Tyr Asn Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val
 165 170 175
 Val Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn
 180 185 190
 Ile Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly
 195 200 205
 Leu Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn
 210 215 220
 Thr Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr
 225 230 235 240
 Gln Glu Ala Gln Glu Ala Pro Gln Asn
 245

<210> 345
 <211> 541
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> RXA00072

<400> 345
 acggccagga cgatccagtg cacaggccag caccagcaaa gtccacatcg caagcattaa 60
 aagaatctct cgaaagacac aaaagaggtg agtcgcaaca atg agc ttt caa cta 115
 Met Ser Phe Gln Leu 5
 1
 gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser 20
 10 15
 ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys 35
 25 30
 cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala 50
 40 45 50
 agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala 65
 55 60
 att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355
 Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala 85
 70 75 80
 gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403

Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr
 90 95 100

cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr
 105 110 115

tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499
 Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln
 120 125 130

gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541
 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala
 135 140 145

<210> 346
 <211> 147
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 346
 Met Ser Phe Gln Leu Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys
 1 5 10 15

Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser
 20 25 30

Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala
 35 40 45

Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu
 50 55 60

His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val
 65 70 75 80

Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe
 85 90 95

Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln
 100 105 110

Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu
 115 120 125

Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser
 130 135 140

Asn Pro Ala
 145

<210> 347
 <211> 1299
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1276)

<223> RXA00793

<400> 347

tcgctggttt ttagatgggt ttcaagccag cgagaccaca ttagtttcac gctgggtgaa 60

acctttgaga tcaatataga ccgtgtggtc tactcgagga atg agt gaa aac aat 115
 Met Ser Glu Asn Asn
 1 5

ccc act acc ttg cac tgg ttc cta ccc acc tat ggc gat tct cgc gga 163
 Pro Thr Thr Leu His Trp Phe Leu Pro Thr Tyr Gly Asp Ser Arg Gly
 10 15 20

atc aca gcc ggc ggg cat ggc ttc ggc ttc cac tcc gga agc cgg aca 211
 Ile Thr Ala Gly Gly His Gly Phe Gly Phe His Ser Gly Ser Arg Thr
 25 30 35

gca gac ctc gat tac ctc tcc caa att gcc ctg gcc gct gaa cga aac 259
 Ala Asp Leu Asp Tyr Leu Ser Gln Ile Ala Leu Ala Ala Glu Arg Asn
 40 45 50

ggg ttt gaa tcc gtc ctg act ccc act gga ttg tgg tgc gaa gat gcg 307
 Gly Phe Glu Ser Val Leu Thr Pro Thr Gly Leu Trp Cys Glu Asp Ala
 55 60 65

tgg atc acc acc gca gcg ctg ctg tct agg aca tca aaa ctg aaa ttc 355
 Trp Ile Thr Thr Ala Ala Leu Leu Ser Arg Thr Ser Lys Leu Lys Phe
 70 75 80 85

ctc gtt gct att cga cca ggc caa gtt agc ccc acc atc atc gcg cag 403
 Leu Val Ala Ile Arg Pro Gly Gln Val Ser Pro Thr Ile Ile Ala Gln
 90 95 100

cag ggt gct gcc ttc cag aaa ttc tca aat aac cgc ctg ctc atc aac 451
 Gln Gly Ala Ala Phe Gln Lys Phe Ser Asn Asn Arg Leu Leu Ile Asn
 105 110 115

gtc gtg gtg ggt ggc gaa gac cat gaa cag cgc gct ttc gct gat tat 499
 Val Val Val Gly Gly Glu Asp His Glu Gln Arg Ala Phe Ala Asp Tyr
 120 125 130

tct tcc aaa gag gag cgc tac cac aag gct gat gaa acc tta gag atc 547
 Ser Ser Lys Glu Glu Arg Tyr His Lys Ala Asp Glu Thr Leu Glu Ile
 135 140 145

atc gat cac cta tgg aac agc gca gaa cct cta aat ttc cag ggt gaa 595
 Ile Asp His Leu Trp Asn Ser Ala Glu Pro Leu Asn Phe Gln Gly Glu
 150 155 160 165

ttc ctc agt gtg gaa aac gcg gta ttg aag gaa cag ccc gag gtt tcc 643
 Phe Leu Ser Val Glu Asn Ala Val Leu Lys Glu Gln Pro Glu Val Ser
 170 175 180

cca ccg att tac ttt ggc gga tcc tca caa ctc ggc atc gaa atc gca 691
 Pro Pro Ile Tyr Phe Gly Gly Ser Ser Gln Leu Gly Ile Glu Ile Ala
 185 190 195

gcc caa cat tcc gat gtt tat ctc acc tgg ggt gaa cct gcg gaa aag 739
 Ala Gln His Ser Asp Val Tyr Leu Thr Trp Gly Glu Pro Ala Glu Lys
 200 205 210

gta gag gag aag ctt gcc cgg gtg cgc gcc gaa gca gat aag cga aac 787
 Val Glu Glu Lys Leu Ala Arg Val Arg Ala Glu Ala Asp Lys Arg Asn
 215 220 225

cgc gaa cta gac tat ggc atc cgc ctg cat gtc att gct cga cca act 835
 Arg Glu Leu Asp Tyr Gly Ile Arg Leu His Val Ile Ala Arg Pro Thr
 230 235 240 245

gag gat gaa gcc tgg tca gtg gct caa aat ctt ctt gac caa ctt gat 883
 Glu Asp Glu Ala Trp Ser Val Ala Gln Asn Leu Leu Asp Gln Leu Asp
 250 255 260

cag gaa gag gtt gcc cgc att cag gaa ggg ctt gcg cgt tct caa tcg 931
 Gln Glu Glu Val Ala Arg Ile Gln Glu Gly Leu Ala Arg Ser Gln Ser
 265 270 275

gaa ggt cag cgt cgc atg acg gaa ctt cat gga caa ggg gca gca ttc 979
 Glu Gly Gln Arg Arg Met Thr Glu Leu His Gly Gln Gly Ala Ala Phe
 280 285 290

aca gca gga gca gat gct cgc tcc ctt gaa att gca ccg aat ctc tgg 1027
 Thr Ala Gly Ala Asp Ala Arg Ser Leu Glu Ile Ala Pro Asn Leu Trp
 295 300 305

gca ggt gtt ggg cta gtc cgc ggt ggc gcc ggc aca gcg ttg gtg ggt 1075
 Ala Gly Val Gly Leu Val Arg Gly Gly Ala Gly Thr Ala Leu Val Gly
 310 315 320 325

tcc tat gag caa gtc gcg caa gca att ttg cga tac cgc gat att ggt 1123
 Ser Tyr Glu Gln Val Ala Gln Ala Ile Leu Arg Tyr Arg Asp Ile Gly
 330 335 340

ctg agc cac ttc att ttc tcc ggc tat cca cat ttg gag gaa acc tat 1171
 Leu Ser His Phe Ile Phe Ser Gly Tyr Pro His Leu Glu Glu Thr Tyr
 345 350 355

cac gtg ggc gaa gga gtg gta cct gag ctc ctc aaa ttg ggt gtt ccg 1219
 His Val Gly Glu Gly Val Val Pro Glu Leu Leu Lys Leu Gly Val Pro
 360 365 370

gtg aac aac cat gaa gaa caa cgc aac gac gtg gta gcg act ccg ttt 1267
 Val Asn Asn His Glu Glu Gln Arg Asn Asp Val Val Ala Thr Pro Phe
 375 380 385

att tcc aga tagatcacgg atcggctgct tta 1299
 Ile Ser Arg
 390

<210> 348

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Ser Glu Asn Asn Pro Thr Thr Leu His Trp Phe Leu Pro Thr Tyr
 1 5 10 15

Gly Asp Ser Arg Gly Ile Thr Ala Gly Gly His Gly Phe Gly Phe His
 20 25 30

Ser Gly Ser Arg Thr Ala Asp Leu Asp Tyr Leu Ser Gln Ile Ala Leu
 35 40 45
 Ala Ala Glu Arg Asn Gly Phe Glu Ser Val Leu Thr Pro Thr Gly Leu
 50 55 60
 Trp Cys Glu Asp Ala Trp Ile Thr Thr Ala Ala Leu Leu Ser Arg Thr
 65 70 75 80
 Ser Lys Leu Lys Phe Leu Val Ala Ile Arg Pro Gly Gln Val Ser Pro
 85 90 95
 Thr Ile Ile Ala Gln Gln Gly Ala Ala Phe Gln Lys Phe Ser Asn Asn
 100 105 110
 Arg Leu Leu Ile Asn Val Val Val Gly Gly Glu Asp His Glu Gln Arg
 115 120 125
 Ala Phe Ala Asp Tyr Ser Ser Lys Glu Glu Arg Tyr His Lys Ala Asp
 130 135 140
 Glu Thr Leu Glu Ile Ile Asp His Leu Trp Asn Ser Ala Glu Pro Leu
 145 150 155 160
 Asn Phe Gln Gly Glu Phe Leu Ser Val Glu Asn Ala Val Leu Lys Glu
 165 170 175
 Gln Pro Glu Val Ser Pro Pro Ile Tyr Phe Gly Gly Ser Ser Gln Leu
 180 185 190
 Gly Ile Glu Ile Ala Ala Gln His Ser Asp Val Tyr Leu Thr Trp Gly
 195 200 205
 Glu Pro Ala Glu Lys Val Glu Glu Lys Leu Ala Arg Val Arg Ala Glu
 210 215 220
 Ala Asp Lys Arg Asn Arg Glu Leu Asp Tyr Gly Ile Arg Leu His Val
 225 230 235 240
 Ile Ala Arg Pro Thr Glu Asp Glu Ala Trp Ser Val Ala Gln Asn Leu
 245 250 255
 Leu Asp Gln Leu Asp Gln Glu Glu Val Ala Arg Ile Gln Glu Gly Leu
 260 265 270
 Ala Arg Ser Gln Ser Glu Gly Gln Arg Arg Met Thr Glu Leu His Gly
 275 280 285
 Gln Gly Ala Ala Phe Thr Ala Gly Ala Asp Ala Arg Ser Leu Glu Ile
 290 295 300
 Ala Pro Asn Leu Trp Ala Gly Val Gly Leu Val Arg Gly Gly Ala Gly
 305 310 315 320
 Thr Ala Leu Val Gly Ser Tyr Glu Gln Val Ala Gln Ala Ile Leu Arg
 325 330 335
 Tyr Arg Asp Ile Gly Leu Ser His Phe Ile Phe Ser Gly Tyr Pro His
 340 345 350
 Leu Glu Glu Thr Tyr His Val Gly Glu Gly Val Val Pro Glu Leu Leu

355

360

365

Lys Leu Gly Val Pro Val Asn Asn His Glu Glu Gln Arg Asn Asp Val
 370 375 380

Val Ala Thr Pro Phe Ile Ser Arg
 385 390

<210> 349

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA01192

<400> 349

ccacggtgaa cacctgcagg tggagcaagc tagccttgcg catccgccag agattattcc 60

ggagattcctt tttggtggat cgctgccagc tgcaggtgag gtg gct gca cgt tat 115
 Val Ala Ala Arg Tyr
 1 5

gcg gac acc tat ctc acg tgg ggt gaa act ccc gat cag gtg gcg cag 163
 Ala Asp Thr Tyr Leu Thr Trp Gly Glu Thr Pro Asp Gln Val Ala Gln
 10 15 20

aaa atc aac tgg atc aac gag cta gca gca cag cgc ggc cgg gaa ctg 211
 Lys Ile Asn Trp Ile Asn Glu Leu Ala Ala Gln Arg Gly Arg Glu Leu
 25 30 35

cgc cat gga atc cgc ttc cat gtg atc acc cgc gat acg tct gaa gaa 259
 Arg His Gly Ile Arg Phe His Val Ile Thr Arg Asp Thr Ser Glu Glu
 40 45 50

gca tgg gtg gtg gca gag aag ttg att agc ggg gtc act cca gaa cag 307
 Ala Trp Val Val Ala Glu Lys Leu Ile Ser Gly Val Thr Pro Glu Gln
 55 60 65

gtc gct aag gct caa gcc ggg ttt gca acg tct aag tcg gag ggg cag 355
 Val Ala Lys Ala Gln Ala Gly Phe Ala Thr Ser Lys Ser Glu Gly Gln
 70 75 80 85

cgc cgg atg gct gag ctg cac agc aag ggt cgt gcc ttt act agt ggc 403
 Arg Arg Met Ala Glu Leu His Ser Lys Gly Arg Ala Phe Thr Ser Gly
 90 95 100

tca act gct cgt gat ctg gag gtg tat ccc aat gtg tgg gca ggc gtc 451
 Ser Thr Ala Arg Asp Leu Glu Val Tyr Pro Asn Val Trp Ala Gly Val
 105 110 115

ggt ttg ctt cgc gga ggt gca gga aca gcc ctt gtg ggc tcg cat gaa 499
 Gly Leu Leu Arg Gly Gly Ala Gly Thr Ala Leu Val Gly Ser His Glu
 120 125 130

gag gtc gcc gat cgc atc gaa gaa tac gca gca ctc ggc ttg gat cag 547
 Glu Val Ala Asp Arg Ile Glu Glu Tyr Ala Ala Leu Gly Leu Asp Gln
 135 140 145

ttt gta ctg tcg ggt tat cca aac ttg gag gag gcc ttc cac ttc ggt 595
 Phe Val Leu Ser Gly Tyr Pro Asn Leu Glu Glu Ala Phe His Phe Gly
 150 155 160 165

gag ggt gtg att ccg aaa ctg ctg cgc cgc ggt gtg gat atc aaa aat 643
 Glu Gly Val Ile Pro Lys Leu Leu Arg Arg Gly Val Asp Ile Lys Asn
 170 175 180

caa gaa tca cga gtt ttg gaa cct gtt ggg taaacggg 681
 Gln Glu Ser Arg Val Leu Glu Pro Val Gly
 185 190

<210> 350

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Val Ala Ala Arg Tyr Ala Asp Thr Tyr Leu Thr Trp Gly Glu Thr Pro
 1 5 10 15

Asp Gln Val Ala Gln Lys Ile Asn Trp Ile Asn Glu Leu Ala Ala Gln
 20 25 30

Arg Gly Arg Glu Leu Arg His Gly Ile Arg Phe His Val Ile Thr Arg
 35 40 45

Asp Thr Ser Glu Glu Ala Trp Val Val Ala Glu Lys Leu Ile Ser Gly
 50 55 60

Val Thr Pro Glu Gln Val Ala Lys Ala Gln Ala Gly Phe Ala Thr Ser
 65 70 75 80

Lys Ser Glu Gly Gln Arg Arg Met Ala Glu Leu His Ser Lys Gly Arg
 85 90 95

Ala Phe Thr Ser Gly Ser Thr Ala Arg Asp Leu Glu Val Tyr Pro Asn
 100 105 110

Val Trp Ala Gly Val Gly Leu Leu Arg Gly Gly Ala Gly Thr Ala Leu
 115 120 125

Val Gly Ser His Glu Glu Val Ala Asp Arg Ile Glu Glu Tyr Ala Ala
 130 135 140

Leu Gly Leu Asp Gln Phe Val Leu Ser Gly Tyr Pro Asn Leu Glu Glu
 145 150 155 160

Ala Phe His Phe Gly Glu Gly Val Ile Pro Lys Leu Leu Arg Arg Gly
 165 170 175

Val Asp Ile Lys Asn Gln Glu Ser Arg Val Leu Glu Pro Val Gly
 180 185 190

<210> 351

<211> 918

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(895)

<223> RXA00715

<400> 351

```

gtggtgttaa gcactaagat ggcaggttat gacttctctt aaagtaactt cgtccgcaga 60

tgcaaccaat aacaatgatg cccattttcc tgaaggtcca gtg gta acc gtt gac 115
Val Val Thr Val Asp
1 5

tgg ttg tca cac aac ctt gac cgg gat gat gtc atc gtg ttg tgt gcc 163
Trp Leu Ser His Asn Leu Asp Arg Asp Asp Val Ile Val Leu Cys Ala
10 15 20

aca atg gag gat gat gaa att gca cgt caa gcg gga att ccg ggg gca 211
Thr Met Glu Asp Asp Glu Ile Ala Arg Gln Ala Gly Ile Pro Gly Ala
25 30 35

ttt ctc gct gac ttg gaa gga gat ttc tca gat cca cat tcc gag ctt 259
Phe Leu Ala Asp Leu Glu Gly Asp Phe Ser Asp Pro His Ser Glu Leu
40 45 50

cca cac acc gcg cca cca aat ttg gtg ggt ttg cta gaa agc tac ggc 307
Pro His Thr Ala Pro Pro Asn Leu Val Gly Leu Leu Glu Ser Tyr Gly
55 60 65

att agc acc gat tcc acg gtg gtt gtt tat gat ctg cac ggc ctc atg 355
Ile Ser Thr Asp Ser Thr Val Val Val Tyr Asp Leu His Gly Leu Met
70 75 80 85

gtt gca ccg ccg gtg tgg tgg ctt ctc cgt gtt gct gga tta agc agc 403
Val Ala Pro Arg Val Trp Trp Leu Leu Arg Val Ala Gly Leu Ser Ser
90 95 100

att ggc gtg ctt gat ggc gga ttg cca gcc tgg gtt gat gct ggc ctt 451
Ile Gly Val Leu Asp Gly Gly Leu Pro Ala Trp Val Asp Ala Gly Leu
105 110 115

cca acg gaa ccg ctg tcg cta cct aca agt ggt gga agg atc agc gca 499
Pro Thr Glu Pro Leu Ser Leu Pro Thr Ser Gly Gly Arg Ile Ser Ala
120 125 130

gaa cca cag cca gat tta ctc gtt ggt gcc tcc ggc gtt gaa ccg gcg 547
Glu Pro Gln Pro Asp Leu Leu Val Gly Ala Ser Gly Val Glu Arg Ala
135 140 145

atc gcg cgc tca agc aag gca gtg att gat gct cgt aat gcg agc cga 595
Ile Ala Arg Ser Ser Lys Ala Val Ile Asp Ala Arg Asn Ala Ser Arg
150 155 160 165

ttc gct ggc gtt gaa gaa gag ccc cgt cca ggc ctt cga aaa ggg tcg 643
Phe Ala Gly Val Glu Glu Glu Pro Arg Pro Gly Leu Arg Lys Gly Ser
170 175 180

atc cct gga agc gtc aac att ccc ttc act gac att tct gat gag cat 691
Ile Pro Gly Ser Val Asn Ile Pro Phe Thr Asp Ile Ser Asp Glu His
185 190 195

```

ggt ttt gtc cgg cca gca gaa gaa ctg aag gaa ttg atc ttc agc cgc 739
 Gly Phe Val Arg Pro Ala Glu Glu Leu Lys Glu Leu Ile Phe Ser Arg
 200 205 210

aca aat gga gcg cag tcg ttg gtc ttt agc tgt ggc tcc gga gtc acg 787
 Thr Asn Gly Ala Gln Ser Leu Val Phe Ser Cys Gly Ser Gly Val Thr
 215 220 225

gca tgt gtt gat gcc tac gct gca gtt atc gca ggt tat gac gac gtt 835
 Ala Cys Val Asp Ala Tyr Ala Ala Val Ile Ala Gly Tyr Asp Asp Val
 230 235 240 245

gta gtg tat gaa ggc tct tgg gcg gag tgg ggc aac ccg gca aac caa 883
 Val Val Tyr Glu Gly Ser Trp Ala Glu Trp Gly Asn Pro Ala Asn Gln
 250 255 260

aag ccg att gct taacgccccgc tatgataacc act 918
 Lys Pro Ile Ala
 265

<210> 352

<211> 265

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Val Val Thr Val Asp Trp Leu Ser His Asn Leu Asp Arg Asp Asp Val
 1 5 10 15

Ile Val Leu Cys Ala Thr Met Glu Asp Asp Glu Ile Ala Arg Gln Ala
 20 25 30

Gly Ile Pro Gly Ala Phe Leu Ala Asp Leu Glu Gly Asp Phe Ser Asp
 35 40 45

Pro His Ser Glu Leu Pro His Thr Ala Pro Pro Asn Leu Val Gly Leu
 50 55 60

Leu Glu Ser Tyr Gly Ile Ser Thr Asp Ser Thr Val Val Val Tyr Asp
 65 70 75 80

Leu His Gly Leu Met Val Ala Pro Arg Val Trp Trp Leu Leu Arg Val
 85 90 95

Ala Gly Leu Ser Ser Ile Gly Val Leu Asp Gly Gly Leu Pro Ala Trp
 100 105 110

Val Asp Ala Gly Leu Pro Thr Glu Pro Leu Ser Leu Pro Thr Ser Gly
 115 120 125

Gly Arg Ile Ser Ala Glu Pro Gln Pro Asp Leu Leu Val Gly Ala Ser
 130 135 140

Gly Val Glu Arg Ala Ile Ala Arg Ser Ser Lys Ala Val Ile Asp Ala
 145 150 155 160

Arg Asn Ala Ser Arg Phe Ala Gly Val Glu Glu Glu Pro Arg Pro Gly
 165 170 175

Leu Arg Lys Gly Ser Ile Pro Gly Ser Val Asn Ile Pro Phe Thr Asp

	180		185		190
Ile Ser Asp Glu His Gly Phe Val Arg Pro Ala Glu Glu Leu Lys Glu					
195		200		205	
Leu Ile Phe Ser Arg Thr Asn Gly Ala Gln Ser Leu Val Phe Ser Cys					
210		215		220	
Gly Ser Gly Val Thr Ala Cys Val Asp Ala Tyr Ala Ala Val Ile Ala					
225		230		235	240
Gly Tyr Asp Asp Val Val Val Tyr Glu Gly Ser Trp Ala Glu Trp Gly					
	245		250		255
Asn Pro Ala Asn Gln Lys Pro Ile Ala					
	260		265		

<210> 353
 <211> 945
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(922)
 <223> RXA01664

<400> 353
 cggggttacca aagtgaatgg taggggaagt ttccgtgtct tataccggtt aggttttgcc 60
 cgcgctgcgc ttggtcacat taacgcctag gctcggggct atg acc gtg ttg att 115
 Met Thr Val Leu Ile
 1 5
 tct ccg tcc acc ctt gct gaa tca atc cac gct ggt aag aaa caa act 163
 Ser Pro Ser Thr Leu Ala Glu Ser Ile His Ala Gly Lys Lys Gln Thr
 10 15 20
 gtt ctc gct gct ttc tgg gct cca att gaa gga gca ggc cgc aca gtt 211
 Val Leu Ala Ala Phe Trp Ala Pro Ile Glu Gly Ala Gly Arg Thr Val
 25 30 35
 ttc tgc tct gag cac atc cca act tcc att ttc tgc gac cct gcc ctt 259
 Phe Cys Ser Glu His Ile Pro Thr Ser Ile Phe Cys Asp Pro Ala Leu
 40 45 50
 gag ctt tcc gga gtt cct tcc tct gaa gat ggc cgc aac cca ctg cca 307
 Glu Leu Ser Gly Val Pro Ser Ser Glu Asp Gly Arg Asn Pro Leu Pro
 55 60 65
 ccg ctg aat gtg ttg gca cgt tct ttc agg acc tgg ggt ttg aat acc 355
 Pro Leu Asn Val Leu Ala Arg Ser Phe Arg Thr Trp Gly Leu Asn Thr
 70 75 80 85
 gat cgt gaa atc gtg ttt tac gat cag gga cgt ggc ctt ttt gct gca 403
 Asp Arg Glu Ile Val Phe Tyr Asp Gln Gly Arg Gly Leu Phe Ala Ala
 90 95 100
 cgc gcc tgg tgg atc ctc cga tgg gcg ggc atg ccc aac gtt cgc atc 451
 Arg Ala Trp Trp Ile Leu Arg Trp Ala Gly Met Pro Asn Val Arg Ile

105	110	115	
ctt gac ggt ggt ttc cag aag tgg gaa gac cat gag ctg gga cac gct			499
Leu Asp Gly Gly Phe Gln Lys Trp Glu Asp His Glu Leu Gly His Ala			
120	125	130	
ggc ggg cct gga aac ttc ccg cac ttt tgc aat gtg cgt ccc aac cca			547
Gly Gly Pro Gly Asn Phe Pro His Phe Cys Asn Val Arg Pro Asn Pro			
135	140	145	
ggt cag ctg tcg gta gcg acc atc gaa gat gtc aag gca cat cag ggc			595
Gly Gln Leu Ser Val Ala Thr Ile Glu Asp Val Lys Ala His Gln Gly			
150	155	160	165
att ttg att gat tct cgc gat gaa caa cga ttt gcg ggt cgc agt gaa			643
Ile Leu Ile Asp Ser Arg Asp Glu Gln Arg Phe Ala Gly Arg Ser Glu			
170	175	180	
aag ctc gat ctg aaa gcc gga cac att cca ggc gct atc aac atc aac			691
Lys Leu Asp Leu Lys Ala Gly His Ile Pro Gly Ala Ile Asn Ile Asn			
185	190	195	
gct aaa tct ttg ctg gaa gat gat ttc acc ttc aaa tca cca gaa gaa			739
Ala Lys Ser Leu Leu Glu Asp Asp Phe Thr Phe Lys Ser Pro Glu Glu			
200	205	210	
atc cgc cag att ttt gcg gac aag ggg gta acc agc gga gag aac gtc			787
Ile Arg Gln Ile Phe Ala Asp Lys Gly Val Thr Ser Gly Glu Asn Val			
215	220	225	
atc gtt tat tcc ggt tcc ggt aac cac tcg tcc cag ttg ctg gct ggc			835
Ile Val Tyr Ser Gly Ser Gly Asn His Ser Ser Gln Leu Leu Ala Gly			
230	235	240	245
atg gag cac gcg ggg cta acc ggt gcg agc cat tat ttt gct ggt tgg			883
Met Glu His Ala Gly Leu Thr Gly Ala Ser His Tyr Phe Ala Gly Trp			
250	255	260	
tca cag tgg agc gct aac ccc gag aat cct atc gag gcc taaaatcgtg			932
Ser Gln Trp Ser Ala Asn Pro Glu Asn Pro Ile Glu Ala			
265	270		
gcttgagtac gca			945

<210> 354

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

Met	Thr	Val	Leu	Ile	Ser	Pro	Ser	Thr	Leu	Ala	Glu	Ser	Ile	His	Ala
1				5					10					15	

Gly	Lys	Lys	Gln	Thr	Val	Leu	Ala	Ala	Phe	Trp	Ala	Pro	Ile	Glu	Gly
			20					25					30		

Ala	Gly	Arg	Thr	Val	Phe	Cys	Ser	Glu	His	Ile	Pro	Thr	Ser	Ile	Phe
		35					40					45			

Cys	Asp	Pro	Ala	Leu	Glu	Leu	Ser	Gly	Val	Pro	Ser	Ser	Glu	Asp	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50 55 60
 Arg Asn Pro Leu Pro Pro Leu Asn Val Leu Ala Arg Ser Phe Arg Thr
 65 70 75 80
 Trp Gly Leu Asn Thr Asp Arg Glu Ile Val Phe Tyr Asp Gln Gly Arg
 85 90 95
 Gly Leu Phe Ala Ala Arg Ala Trp Trp Ile Leu Arg Trp Ala Gly Met
 100 105 110
 Pro Asn Val Arg Ile Leu Asp Gly Gly Phe Gln Lys Trp Glu Asp His
 115 120 125
 Glu Leu Gly His Ala Gly Gly Pro Gly Asn Phe Pro His Phe Cys Asn
 130 135 140
 Val Arg Pro Asn Pro Gly Gln Leu Ser Val Ala Thr Ile Glu Asp Val
 145 150 155 160
 Lys Ala His Gln Gly Ile Leu Ile Asp Ser Arg Asp Glu Gln Arg Phe
 165 170 175
 Ala Gly Arg Ser Glu Lys Leu Asp Leu Lys Ala Gly His Ile Pro Gly
 180 185 190
 Ala Ile Asn Ile Asn Ala Lys Ser Leu Leu Glu Asp Asp Phe Thr Phe
 195 200 205
 Lys Ser Pro Glu Glu Ile Arg Gln Ile Phe Ala Asp Lys Gly Val Thr
 210 215 220
 Ser Gly Glu Asn Val Ile Val Tyr Ser Gly Ser Gly Asn His Ser Ser
 225 230 235 240
 Gln Leu Leu Ala Gly Met Glu His Ala Gly Leu Thr Gly Ala Ser His
 245 250 255
 Tyr Phe Ala Gly Trp Ser Gln Trp Ser Ala Asn Pro Glu Asn Pro Ile
 260 265 270
 Glu Ala

<210> 355
 <211> 746
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(723)
 <223> RXN02334

<400> 355
 gtc aaa gac ctc aac gat ccc ctc acc cgc gat ttc att gac ggt gaa 48
 Val Lys Asp Leu Asn Asp Pro Leu Thr Arg Asp Phe Ile Asp Gly Glu
 1 5 10 15
 gct ttc gct gag ctg atg aac cgc aag ggc atc gct cgc gat gac acc 96

Ala	Phe	Ala	Glu	Leu	Met	Asn	Arg	Lys	Gly	Ile	Ala	Arg	Asp	Asp	Thr		
			20					25					30				
gtt	gtt	gtc	tac	ggg	gac	aag	tcc	aac	tgg	tgg	gct	gcg	ttc	acc	ctg	144	
Val	Val	Val	Tyr	Gly	Asp	Lys	Ser	Asn	Trp	Trp	Ala	Ala	Phe	Thr	Leu		
		35					40					45					
tgg	gtc	ttc	gaa	ctg	ttc	ggc	cac	tcc	gat	gtc	cgc	ctg	ctc	aac	ggc	192	
Trp	Val	Phe	Glu	Leu	Phe	Gly	His	Ser	Asp	Val	Arg	Leu	Leu	Asn	Gly		
	50					55					60						
ggc	cgc	gac	gcg	tgg	atg	gct	gaa	gag	cgc	gac	acc	tcc	tac	gtg	gtt	240	
Gly	Arg	Asp	Ala	Trp	Met	Ala	Glu	Glu	Arg	Asp	Thr	Ser	Tyr	Val	Val		
	65				70					75					80		
ccg	gag	tac	ccc	tcc	gcc	aac	tac	ccc	gtc	gtg	gag	cgt	gtc	gac	gaa	288	
Pro	Glu	Tyr	Pro	Ser	Ala	Asn	Tyr	Pro	Val	Val	Glu	Arg	Val	Asp	Glu		
				85					90					95			
aac	cag	cgc	gcg	ttc	gtg	gct	gag	gtg	ctc	ggg	tcg	ctc	acg	caa	tcc	336	
Asn	Gln	Arg	Ala	Phe	Val	Ala	Glu	Val	Leu	Gly	Ser	Leu	Thr	Gln	Ser		
			100					105						110			
ggg	ggc	atg	acg	ctt	gtc	gac	gtc	agg	acc	cct	tcg	gag	ttc	tcc	gga	384	
Gly	Gly	Met	Thr	Leu	Val	Asp	Val	Arg	Thr	Pro	Ser	Glu	Phe	Ser	Gly		
		115					120					125					
ttg	gat	gag	cac	ggc	aac	cca	acc	tca	aac	acc	ggc	gtg	ctt	cgt	ggg	432	
Leu	Asp	Glu	His	Gly	Asn	Pro	Thr	Ser	Asn	Thr	Gly	Val	Leu	Arg	Gly		
	130					135					140						
gga	cac	atc	cca	ggc	gcg	atc	aac	ctg	gat	tgg	tcg	gac	gct	gtt	ctt	480	
Gly	His	Ile	Pro	Gly	Ala	Ile	Asn	Leu	Asp	Trp	Ser	Asp	Ala	Val	Leu		
	145				150					155					160		
ccc	aac	gga	aac	ttc	cgc	acc	cgt	gca	gag	ttg	gac	aag	ctc	tac	gcc	528	
Pro	Asn	Gly	Asn	Phe	Arg	Thr	Arg	Ala	Glu	Leu	Asp	Lys	Leu	Tyr	Ala		
				165					170					175			
gat	ctc	aac	cca	gct	gac	gat	acc	gtt	gtc	tac	tgc	cag	gtt	ggc	gac	576	
Asp	Leu	Asn	Pro	Ala	Asp	Asp	Thr	Val	Val	Tyr	Cys	Gln	Val	Gly	Asp		
			180					185						190			
cgc	gcg	gcc	cac	acc	tgg	ttc	gtg	ctg	aag	tat	ctg	ctc	ggg	ttc	aac	624	
Arg	Ala	Ala	His	Thr	Trp	Phe	Val	Leu	Lys	Tyr	Leu	Leu	Gly	Phe	Asn		
		195					200					205					
aac	gtc	cga	aac	tat	gac	gga	tcg	tgg	gca	gaa	tgg	ggc	aat	atg	gtt	672	
Asn	Val	Arg	Asn	Tyr	Asp	Gly	Ser	Trp	Ala	Glu	Trp	Gly	Asn	Met	Val		
	210					215					220						
cgc	atg	ccg	atc	gaa	act	ggc	gaa	aac	acc	aaa	aat	aac	gtt	tcg	gtg	720	
Arg	Met	Pro	Ile	Glu	Thr	Gly	Glu	Asn	Thr	Lys	Asn	Asn	Val	Ser	Val		
	225				230					235					240		
tca	tagaataggc	gtatccccctt	ttt													746	
Ser																	

<210> 356

<211> 241

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 356

Val Lys Asp Leu Asn Asp Pro Leu Thr Arg Asp Phe Ile Asp Gly Glu
 1 5 10 15

Ala Phe Ala Glu Leu Met Asn Arg Lys Gly Ile Ala Arg Asp Asp Thr
 20 25 30

Val Val Val Tyr Gly Asp Lys Ser Asn Trp Trp Ala Ala Phe Thr Leu
 35 40 45

Trp Val Phe Glu Leu Phe Gly His Ser Asp Val Arg Leu Leu Asn Gly
 50 55 60

Gly Arg Asp Ala Trp Met Ala Glu Glu Arg Asp Thr Ser Tyr Val Val
 65 70 75 80

Pro Glu Tyr Pro Ser Ala Asn Tyr Pro Val Val Glu Arg Val Asp Glu
 85 90 95

Asn Gln Arg Ala Phe Val Ala Glu Val Leu Gly Ser Leu Thr Gln Ser
 100 105 110

Gly Gly Met Thr Leu Val Asp Val Arg Thr Pro Ser Glu Phe Ser Gly
 115 120 125

Leu Asp Glu His Gly Asn Pro Thr Ser Asn Thr Gly Val Leu Arg Gly
 130 135 140

Gly His Ile Pro Gly Ala Ile Asn Leu Asp Trp Ser Asp Ala Val Leu
 145 150 155 160

Pro Asn Gly Asn Phe Arg Thr Arg Ala Glu Leu Asp Lys Leu Tyr Ala
 165 170 175

Asp Leu Asn Pro Ala Asp Asp Thr Val Val Tyr Cys Gln Val Gly Asp
 180 185 190

Arg Ala Ala His Thr Trp Phe Val Leu Lys Tyr Leu Leu Gly Phe Asn
 195 200 205

Asn Val Arg Asn Tyr Asp Gly Ser Trp Ala Glu Trp Gly Asn Met Val
 210 215 220

Arg Met Pro Ile Glu Thr Gly Glu Asn Thr Lys Asn Asn Val Ser Val
 225 230 235 240

Ser

<210> 357

<211> 377

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(354)

<223> FRXA02334

<400> 357

```

gga gtt ctc ccg gat tgg atg agc acg gca acc caa ccc tca aac acc   48
Gly Val Leu Pro Asp Trp Met Ser Thr Ala Thr Gln Pro Ser Asn Thr
  1             5             10             15

ggc gtg ctt cgt ggt gaa cac atc cca ggc gcg atc aac ctg gat tgg   96
Gly Val Leu Arg Gly Glu His Ile Pro Gly Ala Ile Asn Leu Asp Trp
             20             25             30

tcg gac gct gtt ctt ccc aac gga aac ttc cgc acc cgt gca gag ttg  144
Ser Asp Ala Val Leu Pro Asn Gly Asn Phe Arg Thr Arg Ala Glu Leu
             35             40             45

gac aag ctc tac gcc gat ctc aac cca gct gac gat acc gtt gtc tac  192
Asp Lys Leu Tyr Ala Asp Leu Asn Pro Ala Asp Asp Thr Val Val Tyr
             50             55             60

tgc cag gtt ggc gac cgc gcg gcc cac acc tgg ttc gtg ctg aag tat  240
Cys Gln Val Gly Asp Arg Ala Ala His Thr Trp Phe Val Leu Lys Tyr
             65             70             75

ctg ctc ggt ttc aac aac gtc cga aac tat gac gga tcg tgg gca gaa  288
Leu Leu Gly Phe Asn Asn Val Arg Asn Tyr Asp Gly Ser Trp Ala Glu
             85             90             95

tgg ggc aat atg gtt cgc atg ccg atc gaa act ggc gaa aac acc aaa  336
Trp Gly Asn Met Val Arg Met Pro Ile Glu Thr Gly Glu Asn Thr Lys
             100            105            110

aat aac gtt tcg gtg tca tagaataggc gtatcccctt ttt   377
Asn Asn Val Ser Val Ser
             115

```

<210> 358

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

```

Gly Val Leu Pro Asp Trp Met Ser Thr Ala Thr Gln Pro Ser Asn Thr
  1             5             10             15

Gly Val Leu Arg Gly Glu His Ile Pro Gly Ala Ile Asn Leu Asp Trp
             20             25             30

Ser Asp Ala Val Leu Pro Asn Gly Asn Phe Arg Thr Arg Ala Glu Leu
             35             40             45

Asp Lys Leu Tyr Ala Asp Leu Asn Pro Ala Asp Asp Thr Val Val Tyr
             50             55             60

Cys Gln Val Gly Asp Arg Ala Ala His Thr Trp Phe Val Leu Lys Tyr
             65             70             75

Leu Leu Gly Phe Asn Asn Val Arg Asn Tyr Asp Gly Ser Trp Ala Glu
             85             90             95

```

Trp Gly Asn Met Val Arg Met Pro Ile Glu Thr Gly Glu Asn Thr Lys
 100 105 110

Asn Asn Val Ser Val Ser
 115

<210> 359
 <211> 3945
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(3922)
 <223> RXN01499

<400> 359
 gcagcaatta tctccaccga agaggactaa atataacgtg gcattgagca gtgttccagc 60

acagttcctg agatccgccc aggcgcctccc gaagcgtact ttg tgg gac gtc tta 115
 Leu Trp Asp Val Leu
 1 5

gaa tcc gtc gcc tct act tat cct gag gca gca gct att gac gat ggc 163
 Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala Ala Ile Asp Asp Gly
 10 15 20

cag gtg ttg acc tac gca gag ttg atg gaa gaa gtc acc gcg ttg gct 211
 Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu Val Thr Ala Leu Ala
 25 30 35

gat tcc att cat gca cag ggc att cgc cgt ggt gat cgc atc ggt att 259
 Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly Asp Arg Ile Gly Ile
 40 45 50

cgc atg ccg tct ggt acg cgt gac ctt tac atc gct att ttg gcc act 307
 Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile Ala Ile Leu Ala Thr
 55 60 65

ctc gct gct ggt gct gct tac gtg cca gtt gat gca gat gat cct gaa 355
 Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp Ala Asp Asp Pro Glu
 70 75 80 85

gag cgc gcc gag atg gtg ttt ggt gaa gca aat att aat gcg ctt ttc 403
 Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn Ile Asn Ala Leu Phe
 90 95 100

gac gcc acc ggc ttc cat atg ctt cgc ccg acc gcg ggc ggc gat acc 451
 Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr Ala Gly Gly Asp Thr
 105 110 115

cgt aga cca cgc ttg gat gat acg gcg tgg att atc ttt act tcc ggt 499
 Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile Ile Phe Thr Ser Gly
 120 125 130

tcc acc ggc aag cct aag ggt gtg gct gtg tcc cac cgt tca gct gcg 547
 Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser His Arg Ser Ala Ala
 135 140 145

gct ttc gtg gat gcc gaa gca caa atg ttc ctt gtc gat cac cct tcc 595

Ala 150	Phe	Val	Asp	Ala 155	Glu	Ala	Gln	Met	Phe	Leu 160	Val	Asp	His	Pro	Ser 165	
ggc	ccc	ctt	ggc	cca	gaa	gac	cga	gtc	ctt	gcg	gga	ttg	tct	gta	gcc	643
Gly	Pro	Leu	Gly	Pro	Glu	Asp	Arg	Val	Leu	Ala	Gly	Leu	Ser	Val	Ala	
				170					175					180		
ttt	gac	gca	tct	tgt	gag	gaa	atg	tgg	ttg	gcc	tgg	ggc	cac	ggc	gcc	691
Phe	Asp	Ala	Ser	Cys	Glu	Glu	Met	Trp	Leu	Ala	Trp	Gly	His	Gly	Ala	
			185					190					195			
tgc	ttg	gtg	cca	gca	cca	cgc	tcc	cta	gtc	cgt	tcc	ggt	atg	gac	ttg	739
Cys	Leu	Val	Pro	Ala	Pro	Arg	Ser	Leu	Val	Arg	Ser	Gly	Met	Asp	Leu	
		200					205					210				
ggc	cca	tgg	ctg	att	cgc	cgc	gac	atc	agt	gtc	gtc	tcc	acc	gtc	cca	787
Gly	Pro	Trp	Leu	Ile	Arg	Arg	Asp	Ile	Ser	Val	Val	Ser	Thr	Val	Pro	
	215					220					225					
act	ctg	gct	ggc	ctg	tgg	cca	gca	gaa	gca	ttg	tca	cag	gtc	cgc	ttg	835
Thr	Leu	Ala	Gly	Leu	Trp	Pro	Ala	Glu	Ala	Leu	Ser	Gln	Val	Arg	Leu	
230					235					240					245	
ctc	atc	gtc	ggc	ggc	gag	gct	tgc	tgc	cag	gag	ctc	ggt	gaa	cgc	tta	883
Leu	Ile	Val	Gly	Gly	Glu	Ala	Cys	Ser	Gln	Glu	Leu	Val	Glu	Arg	Leu	
				250					255					260		
tgc	acg	cct	gac	cgc	gag	gtg	tgg	aac	act	tac	ggc	ccc	acc	gaa	gca	931
Ser	Thr	Pro	Asp	Arg	Glu	Val	Trp	Asn	Thr	Tyr	Gly	Pro	Thr	Glu	Ala	
			265					270					275			
acg	gtg	gtt	gcc	tgt	ggc	act	caa	ctc	tat	gct	ggt	cag	cca	gtg	ggc	979
Thr	Val	Val	Ala	Cys	Gly	Thr	Gln	Leu	Tyr	Ala	Gly	Gln	Pro	Val	Gly	
		280					285					290				
att	ggt	ttg	cca	ctt	gct	ggt	tgg	gat	ctt	gtt	gtt	gtc	gac	gat	gcc	1027
Ile	Gly	Leu	Pro	Leu	Ala	Gly	Trp	Asp	Leu	Val	Val	Val	Asp	Asp	Ala	
	295					300					305					
ggc	gaa	cct	gtc	gga	atc	ggc	gag	gtc	ggc	gaa	ttg	gtc	atc	ggt	ggt	1075
Gly	Glu	Pro	Val	Gly	Ile	Gly	Glu	Val	Gly	Glu	Leu	Val	Ile	Gly	Gly	
310					315					320					325	
gtg	ggt	ctt	gca	cgc	tac	ctt	gat	cca	gaa	aaa	gac	cgc	gag	aag	tat	1123
Val	Gly	Leu	Ala	Arg	Tyr	Leu	Asp	Pro	Glu	Lys	Asp	Arg	Glu	Lys	Tyr	
				330					335					340		
gcg	cca	ctg	aag	tct	gtt	ggt	tgg	acc	cgc	gct	tat	cgt	tcc	ggt	gac	1171
Ala	Pro	Leu	Lys	Ser	Val	Gly	Trp	Thr	Arg	Ala	Tyr	Arg	Ser	Gly	Asp	
			345					350					355			
cac	gtt	cgt	ctg	gaa	gaa	gat	ggc	ctc	tac	ttt	gtg	ggc	cgc	gtt	gat	1219
His	Val	Arg	Leu	Glu	Glu	Asp	Gly	Leu	Tyr	Phe	Val	Gly	Arg	Val	Asp	
		360					365					370				
gat	cag	gtg	aaa	atc	ggc	ggt	cga	cgc	atc	gag	ctc	ggt	gaa	gtt	gat	1267
Asp	Gln	Val	Lys	Ile	Gly	Gly	Arg	Arg	Ile	Glu	Leu	Gly	Glu	Val	Asp	
	375					380					385					
gcc	aat	gtg	gca	gcg	ctt	tcc	aac	gtt	cgt	tcc	tcc	gca	gtg	gtt	gtt	1315
Ala	Asn	Val	Ala	Ala	Leu	Ser	Asn	Val	Arg	Ser	Ser	Ala	Val	Val	Val	

390	395	400	405	
cag acc act ggt gcg gat caa aaa gtt ctg gtt gca tac gtt tct ttg	1363			
Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val Ala Tyr Val Ser Leu				
410 415 420				
gaa gat gct gca gct gga ttt gat cac aac gtc gcg act gcc cga ctc	1411			
Glu Asp Ala Ala Ala Gly Phe Asp His Asn Val Ala Thr Ala Arg Leu				
425 430 435				
acc gaa acc atg cct gct gct ttg gtt ccg cgc att cac gtg atg gat	1459			
Thr Glu Thr Met Pro Ala Ala Leu Val Pro Arg Ile His Val Met Asp				
440 445 450				
gat ctg cct gtc acc acc tcc ggc aag gtt gat aag aag tct ttg ccg	1507			
Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp Lys Lys Ser Leu Pro				
455 460 465				
tgg cct ctt cct ggc acc gtg gtg gaa gct aat gac ctc agc gca acg	1555			
Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn Asp Leu Ser Ala Thr				
470 475 480 485				
gaa gcg tgg att gct cag gaa tgg gtc gat atc ctc ggc act tct gtg	1603			
Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile Leu Gly Thr Ser Val				
490 495 500				
agc agc aaa gac gcc gac ttc ttc tcc ctt ggc ggt acc tct ctc gcg	1651			
Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly Gly Thr Ser Leu Ala				
505 510 515				
gct gcg act ttg gtt ggc cgg gta cgc gca aag gtt ccc acc gct gcg	1699			
Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys Val Pro Thr Ala Ala				
520 525 530				
gtg cgt gat ctt tac gat cac cct cgc ttg gag aaa ttc gcc gag cgt	1747			
Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu Lys Phe Ala Glu Arg				
535 540 545				
gtc gag gct atc gcc gcc gac act ggc att tct ttg gag gcg cca aac	1795			
Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser Leu Glu Ala Pro Asn				
550 555 560 565				
cag gtg gag gag cgc gtc gtc aag cct gtt tct ttt ggc act cgt gtg	1843			
Gln Val Glu Glu Arg Val Val Lys Pro Val Ser Phe Gly Thr Arg Val				
570 575 580				
atg cag acc ctc atc cag att ccg atc atg acg ctg caa gca gca cag	1891			
Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr Leu Gln Ala Ala Gln				
585 590 595				
tgg att gca tgg ttg ctg ttg ggc aac aac atc atg gca gcg ctt gat	1939			
Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile Met Ala Ala Leu Asp				
600 605 610				
ttc gat tgg gct gtt cat gtc tcc tgg tgg ctt gtc atc ggc atg att	1987			
Phe Asp Trp Ala Val His Val Ser Trp Trp Leu Val Ile Gly Met Ile				
615 620 625				
ttg gtg ttc gct acc ccg att ggt cgc ttg ccg atc ggc ggt tgg ggc	2035			
Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro Ile Gly Gly Trp Gly				
630 635 640 645				

gcc cgc atc atc acc cgt ggc ata act cct ggc tcc tac cct cgt ggc	2083
Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly Ser Tyr Pro Arg Gly	
650 655 660	
ggt tcc act cac ctg cgc att tgg tcc gcc gag cgc ctt gct gat gcc	2131
Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu Arg Leu Ala Asp Ala	
665 670 675	
tct ggc tct cgc aat att tct ggc gca acc tgg gtg aac tac ttc gcg	2179
Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp Val Asn Tyr Phe Ala	
680 685 690	
cgt tcc ctg ggt gtg aag atg ggc aag ggc gtg gat ctt cac tcc ctg	2227
Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val Asp Leu His Ser Leu	
695 700 705	
cca cca atc act ggc ctt ttg acc ttg ggc aac aat gtt tcc atc gag	2275
Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn Asn Val Ser Ile Glu	
710 715 720 725	
caa gaa gtt gac ctt cgt ggc tac tgg ctc gac ggc gat atc ctg cgt	2323
Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp Gly Asp Ile Leu Arg	
730 735 740	
gta ggc acc att gag gtc cat gac aac gct cgc atc ggc gct cgt tcc	2371
Val Gly Thr Ile Glu Val His Asp Asn Ala Arg Ile Gly Ala Arg Ser	
745 750 755	
acc ctg ctt ccc ggc acc gtg gtg ggc acc ggc gct cac ctg ctg cct	2419
Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly Ala His Leu Leu Pro	
760 765 770	
ggt tca aca gtg act ggt gat aag acc atc aag cct ggt tct cgt tgg	2467
Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys Pro Gly Ser Arg Trp	
775 780 785	
gct ggc tcc cct gca caa aag gtg ggt cgt gca aag cac cgg ttc cca	2515
Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala Lys His Arg Phe Pro	
790 795 800 805	
acc tcc cat cct cca cgc agg tcc cgg tgg gtt ccg gtg ttc ggc gcg	2563
Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val Pro Val Phe Gly Ala	
810 815 820	
acc tcc atc gtg ttg tcg ctg ctg cca ctt cag gct ctc gct att ggc	2611
Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln Ala Leu Ala Ile Gly	
825 830 835	
gct gct atc acc ttg tgg ctg gcc acg att agc ccg ctt cca ctg atc	2659
Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser Pro Leu Pro Leu Ile	
840 845 850	
tgg ggt gtg ctg gtt ttt gct acc gtc ggc gcg ttg gct gcg ttc ttt	2707
Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala Leu Ala Ala Phe Phe	
855 860 865	
gct tac acc gtg acc atc tgg gtg ctt gtc cgt ttg atc cag atc ggc	2755
Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg Leu Ile Gln Ile Gly	
870 875 880 885	

atc aag ggc ggc acc gca cca gtg agg tcc cgt ctt ggt tgg cag gtc	2803
Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg Leu Gly Trp Gln Val	
890 895 900	
tgg gca gtt caa cgc ctc atg gac gat gcc cgc acc tat ctc ttc ccg	2851
Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg Thr Tyr Leu Phe Pro	
905 910 915	
ctc tac gca tcc caa ctg acc cca ctg tgg ttc cgc agc ttg ggc gcg	2899
Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe Arg Ser Leu Gly Ala	
920 925 930	
aag atc ggc aag gat gtt gag atc tcc acc gcg gtg atg gtt cct aaa	2947
Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala Val Met Val Pro Lys	
935 940 945	
ctg gct gat atc cgc gaa ggc gca ttc ctg gcc gat gac acc ctc atc	2995
Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala Asp Asp Thr Leu Ile	
950 955 960 965	
ggg ggc tat gag ctg ggt aat ggt tgg ctg ctc agt ggt gaa acc cgc	3043
Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu Ser Gly Glu Thr Arg	
970 975 980	
gtg ggt aag cgt tcc ttc att ggt aac tct ggc atc gca gga cct gag	3091
Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly Ile Ala Gly Pro Glu	
985 990 995	
cgc aag ctc gct aag aac tcc ctg gtt gca gtg ctc tcc tcc acc ccg	3139
Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val Leu Ser Ser Thr Pro	
1000 1005 1010	
aag aag gct aag gcc aac tcc aac tgg tgg ggt tcc cct cca gag cgc	3187
Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly Ser Pro Pro Glu Arg	
1015 1020 1025	
atg cgt cgt gtc act gtc gaa gtt gat gag ggc gaa gca aag acc tac	3235
Met Arg Arg Val Thr Val Glu Val Asp Glu Gly Glu Ala Lys Thr Tyr	
1030 1035 1040 1045	
agc cct ggc ttt ggt gtg aag ttt gca cgt ggc gcg gtg gaa acc gca	3283
Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly Ala Val Glu Thr Ala	
1050 1055 1060	
cgt ctg ctt gct cca ata acc tct ggt gtg ttg gct gcg ctg tca ctg	3331
Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu Ala Ala Leu Ser Leu	
1065 1070 1075	
ctg ctc atg cag tac ctg ctc act gag ttc aac atg tgg atc acc tgg	3379
Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn Met Trp Ile Thr Trp	
1080 1085 1090	
ttg ctt ggc gga ctg atc ctc atg acg gtt ggt gtg ctc gcc atg ggc	3427
Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly Val Leu Ala Met Gly	
1095 1100 1105	
att acg gtt gtg atg aag tgg gtt tgc gtc ggc aag cat aag ccg tct	3475
Ile Thr Val Val Met Lys Trp Val Cys Val Gly Lys His Lys Pro Ser	
1110 1115 1120 1125	
gag cac cct ctc ttc agc cgc ttt gtg tgg ctg aat gag ctg caa gat	3523

Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu Asn Glu Leu Gln Asp
 1130 1135 1140
 gcg ttc gtg gaa tcc gtg gct ggc cca tgg ttc ctc gtg ccc aac ctg 3571
 Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe Leu Val Pro Asn Leu
 1145 1150 1155
 ggc acc ggc gcg ctg aac gcc ggc atg agc gcg ctt ggc gca cac atc 3619
 Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala Leu Gly Ala His Ile
 1160 1165 1170
 ggc cgt ggc gca tgg atc gaa tcc tac tgg ctg ccg gaa acc gac ctc 3667
 Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu Pro Glu Thr Asp Leu
 1175 1180 1185
 tgc tac atc ggc aag ggc gca acc gtg ggc cct ggc gtg gtc gtg cag 3715
 Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro Gly Val Val Val Gln
 1190 1195 1200 1205
 acc cac ctc ttc cag gac cgc gtg atg agc cta gat acg gtg acc gtc 3763
 Thr His Leu Phe Gln Asp Arg Val Met Ser Leu Asp Thr Val Thr Val
 1210 1215 1220
 gct gac ggc gcc acc cta gcg gac cac tcc gtt gcc ctt cct gct tcg 3811
 Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val Ala Leu Pro Ala Ser
 1225 1230 1235
 ctt atc gac gcc tcc gcc acc atc ggc cca ggc tcg ctg gtg atg cgc 3859
 Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly Ser Leu Val Met Arg
 1240 1245 1250
 ggc gac aag gta cca gcg cat acc cgc tgg caa ggc aac cca att gag 3907
 Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln Gly Asn Pro Ile Glu
 1255 1260 1265
 ccg tgg agc aac tct taaataacaa caatcagccg gat 3945
 Pro Trp Ser Asn Ser
 1270

<210> 360

<211> 1274

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Leu Trp Asp Val Leu Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala
 1 5 10 15
 Ala Ile Asp Asp Gly Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu
 20 25 30
 Val Thr Ala Leu Ala Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly
 35 40 45
 Asp Arg Ile Gly Ile Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile
 50 55 60
 Ala Ile Leu Ala Thr Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp
 65 70 75 80

481

405										410					415				
Ala	Tyr	Val	Ser	Leu	Glu	Asp	Ala	Ala	Ala	Gly	Phe	Asp	His	Asn	Val				
			420					425					430						
Ala	Thr	Ala	Arg	Leu	Thr	Glu	Thr	Met	Pro	Ala	Ala	Leu	Val	Pro	Arg				
		435					440					445							
Ile	His	Val	Met	Asp	Asp	Leu	Pro	Val	Thr	Thr	Ser	Gly	Lys	Val	Asp				
	450					455					460								
Lys	Lys	Ser	Leu	Pro	Trp	Pro	Leu	Pro	Gly	Thr	Val	Val	Glu	Ala	Asn				
465					470					475					480				
Asp	Leu	Ser	Ala	Thr	Glu	Ala	Trp	Ile	Ala	Gln	Glu	Trp	Val	Asp	Ile				
				485					490					495					
Leu	Gly	Thr	Ser	Val	Ser	Ser	Lys	Asp	Ala	Asp	Phe	Phe	Ser	Leu	Gly				
			500					505					510						
Gly	Thr	Ser	Leu	Ala	Ala	Ala	Thr	Leu	Val	Gly	Arg	Val	Arg	Ala	Lys				
		515					520					525							
Val	Pro	Thr	Ala	Ala	Val	Arg	Asp	Leu	Tyr	Asp	His	Pro	Arg	Leu	Glu				
	530					535					540								
Lys	Phe	Ala	Glu	Arg	Val	Glu	Ala	Ile	Ala	Ala	Asp	Thr	Gly	Ile	Ser				
545					550					555					560				
Leu	Glu	Ala	Pro	Asn	Gln	Val	Glu	Glu	Arg	Val	Val	Lys	Pro	Val	Ser				
				565					570					575					
Phe	Gly	Thr	Arg	Val	Met	Gln	Thr	Leu	Ile	Gln	Ile	Pro	Ile	Met	Thr				
			580					585					590						
Leu	Gln	Ala	Ala	Gln	Trp	Ile	Ala	Trp	Leu	Leu	Leu	Gly	Asn	Asn	Ile				
		595					600					605							
Met	Ala	Ala	Leu	Asp	Phe	Asp	Trp	Ala	Val	His	Val	Ser	Trp	Trp	Leu				
	610					615					620								
Val	Ile	Gly	Met	Ile	Leu	Val	Phe	Ala	Thr	Pro	Ile	Gly	Arg	Leu	Pro				
625					630					635				640					
Ile	Gly	Gly	Trp	Gly	Ala	Arg	Ile	Ile	Thr	Arg	Gly	Ile	Thr	Pro	Gly				
				645					650					655					
Ser	Tyr	Pro	Arg	Gly	Gly	Ser	Thr	His	Leu	Arg	Ile	Trp	Ser	Ala	Glu				
			660					665					670						
Arg	Leu	Ala	Asp	Ala	Ser	Gly	Ser	Arg	Asn	Ile	Ser	Gly	Ala	Thr	Trp				
		675					680					685							
Val	Asn	Tyr	Phe	Ala	Arg	Ser	Leu	Gly	Val	Lys	Met	Gly	Lys	Gly	Val				
	690					695					700								
Asp	Leu	His	Ser	Leu	Pro	Pro	Ile	Thr	Gly	Leu	Leu	Thr	Leu	Gly	Asn				
705					710					715					720				
Asn	Val	Ser	Ile	Glu	Gln	Glu	Val	Asp	Leu	Arg	Gly	Tyr	Trp	Leu	Asp				
				725					730					735					

Gly Asp Ile Leu Arg Val Gly Thr Ile Glu Val His Asp Asn Ala Arg
 740 745 750
 Ile Gly Ala Arg Ser Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly
 755 760 765
 Ala His Leu Leu Pro Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys
 770 775 780
 Pro Gly Ser Arg Trp Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala
 785 790 795 800
 Lys His Arg Phe Pro Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val
 805 810 815
 Pro Val Phe Gly Ala Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln
 820 825 830
 Ala Leu Ala Ile Gly Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser
 835 840 845
 Pro Leu Pro Leu Ile Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala
 850 855 860
 Leu Ala Ala Phe Phe Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg
 865 870 875 880
 Leu Ile Gln Ile Gly Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg
 885 890 895
 Leu Gly Trp Gln Val Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg
 900 905 910
 Thr Tyr Leu Phe Pro Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe
 915 920 925
 Arg Ser Leu Gly Ala Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala
 930 935 940
 Val Met Val Pro Lys Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala
 945 950 955 960
 Asp Asp Thr Leu Ile Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu
 965 970 975
 Ser Gly Glu Thr Arg Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly
 980 985 990
 Ile Ala Gly Pro Glu Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val
 995 1000 1005
 Leu Ser Ser Thr Pro Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly
 1010 1015 1020
 Ser Pro Pro Glu Arg Met Arg Arg Val Thr Val Glu Val Asp Glu Gly
 1025 1030 1035 1040
 Glu Ala Lys Thr Tyr Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly
 1045 1050 1055

Ala Val Glu Thr Ala Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu
 1060 1065 1070

Ala Ala Leu Ser Leu Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn
 1075 1080 1085

Met Trp Ile Thr Trp Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly
 1090 1095 1100

Val Leu Ala Met Gly Ile Thr Val Val Met Lys Trp Val Cys Val Gly
 1105 1110 1115 1120

Lys His Lys Pro Ser Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu
 1125 1130 1135

Asn Glu Leu Gln Asp Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe
 1140 1145 1150

Leu Val Pro Asn Leu Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala
 1155 1160 1165

Leu Gly Ala His Ile Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu
 1170 1175 1180

Pro Glu Thr Asp Leu Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro
 1185 1190 1195 1200

Gly Val Val Val Gln Thr His Leu Phe Gln Asp Arg Val Met Ser Leu
 1205 1210 1215

Asp Thr Val Thr Val Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val
 1220 1225 1230

Ala Leu Pro Ala Ser Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly
 1235 1240 1245

Ser Leu Val Met Arg Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln
 1250 1255 1260

Gly Asn Pro Ile Glu Pro Trp Ser Asn Ser
 1265 1270

<210> 361
 <211> 609
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(586)
 <223> RXN01997

<400> 361
 aaaaggtgg gaaacttagc caatccaaag cccaaaaatg cgggttatgc tgcgctaacc 60
 tatgctgaca gccttgcgga agttgtgtac gttaggggcc atg aca atc aac gag 115
 Met Thr Ile Asn Glu
 1 5
 aag atc gca tca gct ttc aac aac caa gtg act gca gag ctt gaa gct 163

Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr Ala Glu Leu Glu Ala
 10 15 20
 tca atg gtg tac ctt cag ctc tcc tac gtt cta gac gat ctg ggc ctc 211
 Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu Asp Asp Leu Gly Leu
 25 30 35
 acc ggc atg cgc gac tgg atg aag gca cag agc aaa gaa gag ctc gaa 259
 Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser Lys Glu Glu Leu Glu
 40 45 50
 cac gca cag aag ttc gct cag cac ctt ctt gac cgt gac tac acc cca 307
 His Ala Gln Lys Phe Ala Gln His Leu Leu Asp Arg Asp Tyr Thr Pro
 55 60 65
 cag atc ggt gac att gca cca cca aag ctt gat gtc acc tcc gct atc 355
 Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp Val Thr Ser Ala Ile
 70 75 80 85
 gag gct ttc gag gct tcc ctg gca cac gag cag aag atc tcc ggc ctg 403
 Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln Lys Ile Ser Gly Leu
 90 95 100
 atc cgc gag ctc gct gcc atc cag gac gct gag aag gac tac gat tcc 451
 Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu Lys Asp Tyr Asp Ser
 105 110 115
 cgc gca ctg atc gac tgg ttc ctc aac gag cag atc gaa gaa gaa gca 499
 Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln Ile Glu Glu Glu Ala
 120 125 130
 acc gtc ggc gag atc atc gac cgc ctc cgt atc gct ggt gat tcc ggt 547
 Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile Ala Gly Asp Ser Gly
 135 140 145
 tcc gga atc ctg cgc atc gac ggc gaa ctc ggc tcc cgc taaattcccc 596
 Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Ser Arg
 150 155 160
 gcagtttttta atg 609

<210> 362

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Met Thr Ile Asn Glu Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr
 1 5 10 15
 Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu
 20 25 30
 Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser
 35 40 45
 Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp
 50 55 60
 Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp

65	70	75	80
Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln			
	85	90	95
Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu			
	100	105	110
Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln			
	115	120	125
Ile Glu Glu Glu Ala Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile			
	130	135	140
Ala Gly Asp Ser Gly Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Gly			
	145	150	155
			160
Ser Arg			

<210> 363
 <211> 867
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(844)
 <223> RXA01848

<400> 363
 ctgcaaggaa ctgcgaggc gaaggcgag actactggaa aggtaggtac tgccggatcc 60
 ggcgacccct ttcgctccta ggcatttgcg cctggcggtcc atg ggg gag gag gac 115
 Met Gly Glu Glu Asp
 1 5
 tcc acc cca ggt agg cgt tcc aag gcg tat tcg cgc cag ggc gct gat 163
 Ser Thr Pro Gly Arg Arg Ser Lys Ala Tyr Ser Arg Gln Gly Ala Asp
 10 15 20
 gtc cgc ccc atg aag ggt gga cac ggc atc aac tta gtg ggc acg ctc 211
 Val Arg Pro Met Lys Gly Gly His Gly Ile Asn Leu Val Gly Thr Leu
 25 30 35
 atg gcg gct acg gaa cgc ggc gcc aac att gtt gaa ggc gtg gtc gat 259
 Met Ala Ala Thr Glu Arg Gly Ala Asn Ile Val Glu Gly Val Val Asp
 40 45 50
 ttc cgg ccc acg gac ctg cgg ggt tcg ctg cgc cgt ggg cgc gaa gcc 307
 Phe Arg Pro Thr Asp Leu Arg Gly Ser Leu Arg Arg Gly Arg Glu Ala
 55 60 65
 aac ctc atc gtg ttc gtc gtc gac aca tcg ggg tcg atg gct gcg cgt 355
 Asn Leu Ile Val Phe Val Val Asp Thr Ser Gly Ser Met Ala Ala Arg
 70 75 80 85
 tcc agg gtg cgt gcg gtc acc ggg act att acc tct atg ctt aac gac 403
 Ser Arg Val Arg Ala Val Thr Gly Thr Ile Thr Ser Met Leu Asn Asp
 90 95 100

gcc tac cag cgc cgc gac aag gtt gcg gtt atc gcg gtc aac ggc aac 451
 Ala Tyr Gln Arg Arg Asp Lys Val Ala Val Ile Ala Val Asn Gly Asn
 105 110 115
 aag ccg aca ctg gtg ttg aat cca aca aat tct gtg gag caa gct cag 499
 Lys Pro Thr Leu Val Leu Asn Pro Thr Asn Ser Val Glu Gln Ala Gln
 120 125 130
 cag aaa tta aag gat atg ccg atg ggt ggt cgc act cca ctg gca gag 547
 Gln Lys Leu Lys Asp Met Pro Met Gly Gly Arg Thr Pro Leu Ala Glu
 135 140 145
 ggg ctg ctc atg gcc aag gat ctc atg gca agg gaa ctc cga aag gaa 595
 Gly Leu Leu Met Ala Lys Asp Leu Met Ala Arg Glu Leu Arg Lys Glu
 150 155 160 165
 ccc ggc cga cgc gcg atc ctc atg gtg atg acc gat ggc caa gac acc 643
 Pro Gly Arg Arg Ala Ile Leu Met Val Met Thr Asp Gly Gln Asp Thr
 170 175 180
 tcc gat gcc ggc gaa gca ggc att gcc acc gcg gcg gaa aca gtg gtg 691
 Ser Asp Ala Gly Glu Ala Gly Ile Ala Thr Ala Ala Glu Thr Val Val
 185 190 195
 aaa tca cga ctg tcc ggc aac gtg gtc atc gac tgc gaa ggc cga ctc 739
 Lys Ser Arg Leu Ser Gly Asn Val Val Ile Asp Cys Glu Gly Arg Leu
 200 205 210
 aaa gtg cgc aaa gag cgc gcc ggg gtg ttg gct gaa atg ctc ggt ggt 787
 Lys Val Arg Lys Glu Arg Ala Gly Val Leu Ala Glu Met Leu Gly Gly
 215 220 225
 gtg tgc gtg aga ttg cgt gat ctt aac tcc gag cac atc aaa atg gtg 835
 Val Cys Val Arg Leu Arg Asp Leu Asn Ser Glu His Ile Lys Met Val
 230 235 240 245
 att aac gcc tagacaacca gagtgaggggt ttc 867
 Ile Asn Ala

<210> 364

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Met Gly Glu Glu Asp Ser Thr Pro Gly Arg Arg Ser Lys Ala Tyr Ser
 1 5 10 15
 Arg Gln Gly Ala Asp Val Arg Pro Met Lys Gly Gly His Gly Ile Asn
 20 25 30
 Leu Val Gly Thr Leu Met Ala Ala Thr Glu Arg Gly Ala Asn Ile Val
 35 40 45
 Glu Gly Val Val Asp Phe Arg Pro Thr Asp Leu Arg Gly Ser Leu Arg
 50 55 60
 Arg Gly Arg Glu Ala Asn Leu Ile Val Phe Val Val Asp Thr Ser Gly

65	70	75	80
Ser Met Ala Ala Arg	Ser Arg Val Arg	Ala Val Thr Gly Thr	Ile Thr
85	90	95	
Ser Met Leu Asn Asp	Ala Tyr Gln Arg	Arg Asp Lys Val	Ala Val Ile
100	105	110	
Ala Val Asn Gly Asn	Lys Pro Thr Leu	Val Leu Asn Pro	Thr Asn Ser
115	120	125	
Val Glu Gln Ala Gln	Gln Lys Leu Lys	Asp Met Pro Met	Gly Gly Arg
130	135	140	
Thr Pro Leu Ala Glu	Gly Leu Leu Met	Ala Lys Asp Leu	Met Ala Arg
145	150	155	160
Glu Leu Arg Lys Glu	Pro Gly Arg Arg	Ala Ile Leu Met	Val Met Thr
165	170	175	
Asp Gly Gln Asp Thr	Ser Asp Ala Gly	Glu Ala Gly Ile	Ala Thr Ala
180	185	190	
Ala Glu Thr Val Val	Lys Ser Arg Leu	Ser Gly Asn Val	Val Ile Asp
195	200	205	
Cys Glu Gly Arg Leu	Lys Val Arg Lys	Glu Arg Ala Gly	Val Leu Ala
210	215	220	
Glu Met Leu Gly Gly	Val Cys Val Arg	Leu Arg Asp Leu	Asn Ser Glu
225	230	235	240
His Ile Lys Met Val	Ile Asn Ala		
245			

<210> 365
 <211> 1224
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1201)
 <223> RXN01849

<400> 365
 aaaaccttaa gttgggtggt taaaccact aaggtctcac tttatggatg tgccagggtca 60
 caccaaaaaa tctcaagaaa actcacatta aaggacagta atg gcg tca caa cag 115
 Met Ala Ser Gln Gln
 1 5
 atc cgc tat cca ttc tcc gcg gtt gtg gga caa gac gag ctt cgg ctt 163
 Ile Arg Tyr Pro Phe Ser Ala Val Val Gly Gln Asp Glu Leu Arg Leu
 10 15 20
 gcg ttg atc ctc act gcg att tcc cca cgc att ggt ggc gtg gtg att 211
 Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile Gly Gly Val Val Ile
 25 30 35

cga ggt gag aag ggt aca gcg aaa act acc act gtg cgt gct ttt gct	259
Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr Val Arg Ala Phe Ala	
40 45 50	
ggt ctt tta ggt gat gcc cct ttg gtg aac ttg cct ctc gga tcc acg	307
Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu Pro Leu Gly Ser Thr	
55 60 65	
gag gat cgt gtg gtg ggt tcc ctc aac atg gaa act gtg ttg acc acc	355
Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu Thr Val Leu Thr Thr	
70 75 80 85	
ggc cgt gcg gaa tat cag cca ggt ttg ctc gcg cag gct gat ggc ggt	403
Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala Gln Ala Asp Gly Gly	
90 95 100	
gtg ctg tat gtc gat gag gtc aac ctc ttg gcg gat cac ctg gtg gat	451
Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala Asp His Leu Val Asp	
105 110 115	
gct ctg ctc gat gca gct gca agc ggt cgc gtc agc att gag cgt gac	499
Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val Ser Ile Glu Arg Asp	
120 125 130	
ggt att tcg cat tct tca cca gca aac ttt gtg ttg gtg ggc acc atg	547
Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val Leu Val Gly Thr Met	
135 140 145	
aat ccg gag gaa ggc gag ctg cgc ccg cag ctg ctg gac cgt ttc ggt	595
Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu Leu Asp Arg Phe Gly	
150 155 160 165	
ttg gct gtg gac gtt gct gcg tct acg aac cct gag gtg cgc gtg gag	643
Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro Glu Val Arg Val Glu	
170 175 180	
atc att cgc cgc cgg ctt gat ttt gaa aac gct cct gag cag ttc atg	691
Ile Ile Arg Arg Arg Leu Asp Phe Glu Asn Ala Pro Glu Gln Phe Met	
185 190 195	
gct aag tgg gct gag caa gat gcg gac acc tcc aac cgt att ttg gcg	739
Ala Lys Trp Ala Glu Gln Asp Ala Asp Thr Ser Asn Arg Ile Leu Ala	
200 205 210	
gct aag gat ttg ctg cct ggt gtg gag ctg ccg gat ctg atc ttg tcg	787
Ala Lys Asp Leu Leu Pro Gly Val Glu Leu Pro Asp Leu Ile Leu Ser	
215 220 225	
cag att gcg tgg ttg tgt gca cgt att gaa gtc gac ggt atg cgc gct	835
Gln Ile Ala Trp Leu Cys Ala Arg Ile Glu Val Asp Gly Met Arg Ala	
230 235 240 245	
gac ctg gtg atc acg cgt acc gca ctt gct cac gcc gcg tgg gct gga	883
Asp Leu Val Ile Thr Arg Thr Ala Leu Ala His Ala Ala Trp Ala Gly	
250 255 260	
cgc act gtg gtt acg gaa gaa gac gtg gag atc gca gct cgc cta gcg	931
Arg Thr Val Val Thr Glu Glu Asp Val Glu Ile Ala Ala Arg Leu Ala	
265 270 275	
ttg ccg cac cgc cgt cgc cgt aat cct ttc gat gct cca gaa atg gag	979

Leu Pro His Arg Arg Arg Arg Asn Pro Phe Asp Ala Pro Glu Met Glu
 280 285 290
 gag cgc aag ctt cag gaa acc ctg cag gaa gct cgg gac ttc ttc aaa 1027
 Glu Arg Lys Leu Gln Glu Thr Leu Gln Glu Ala Arg Asp Phe Phe Lys
 295 300 305
 gac aat gaa gat aaa gga cct gcc gcc aag atc acc gat gag gaa acc 1075
 Asp Asn Glu Asp Lys Gly Pro Ala Ala Lys Ile Thr Asp Glu Glu Thr
 310 315 320 325
 ggt gca gag gcc ttt acc gat acc gac aat ccc acc gag gaa gac ggt 1123
 Gly Ala Glu Ala Phe Thr Asp Thr Asp Asn Pro Thr Glu Glu Asp Gly
 330 335 340
 ctg caa gga act gcg cag gcg aag gcg cag act act gga aag gta ggt 1171
 Leu Gln Gly Thr Ala Gln Ala Lys Ala Gln Thr Thr Gly Lys Val Gly
 345 350 355
 act gcc gga tcc ggc gac ccc ttt cgc tcc taggcatttg cgcctggcgt 1221
 Thr Ala Gly Ser Gly Asp Pro Phe Arg Ser
 360 365
 cca 1224

 <210> 366
 <211> 367
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 366
 Met Ala Ser Gln Gln Ile Arg Tyr Pro Phe Ser Ala Val Val Gly Gln
 1 5 10 15
 Asp Glu Leu Arg Leu Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile
 20 25 30
 Gly Gly Val Val Ile Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr
 35 40 45
 Val Arg Ala Phe Ala Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu
 50 55 60
 Pro Leu Gly Ser Thr Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu
 65 70 75 80
 Thr Val Leu Thr Thr Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala
 85 90 95
 Gln Ala Asp Gly Gly Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala
 100 105 110
 Asp His Leu Val Asp Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val
 115 120 125
 Ser Ile Glu Arg Asp Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val
 130 135 140
 Leu Val Gly Thr Met Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu
 145 150 155 160

Leu Asp Arg Phe Gly Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro
 165 170 175
 Glu Val Arg Val Glu Ile Ile Arg Arg Arg Leu Asp Phe Glu Asn Ala
 180 185 190
 Pro Glu Gln Phe Met Ala Lys Trp Ala Glu Gln Asp Ala Asp Thr Ser
 195 200 205
 Asn Arg Ile Leu Ala Ala Lys Asp Leu Leu Pro Gly Val Glu Leu Pro
 210 215 220
 Asp Leu Ile Leu Ser Gln Ile Ala Trp Leu Cys Ala Arg Ile Glu Val
 225 230 235 240
 Asp Gly Met Arg Ala Asp Leu Val Ile Thr Arg Thr Ala Leu Ala His
 245 250 255
 Ala Ala Trp Ala Gly Arg Thr Val Val Thr Glu Glu Asp Val Glu Ile
 260 265 270
 Ala Ala Arg Leu Ala Leu Pro His Arg Arg Arg Arg Asn Pro Phe Asp
 275 280 285
 Ala Pro Glu Met Glu Glu Arg Lys Leu Gln Glu Thr Leu Gln Glu Ala
 290 295 300
 Arg Asp Phe Phe Lys Asp Asn Glu Asp Lys Gly Pro Ala Ala Lys Ile
 305 310 315 320
 Thr Asp Glu Glu Thr Gly Ala Glu Ala Phe Thr Asp Thr Asp Asn Pro
 325 330 335
 Thr Glu Glu Asp Gly Leu Gln Gly Thr Ala Gln Ala Lys Ala Gln Thr
 340 345 350
 Thr Gly Lys Val Gly Thr Ala Gly Ser Gly Asp Pro Phe Arg Ser
 355 360 365

<210> 367
 <211> 473
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(450)
 <223> FRXA01849

<400> 367
 ctg cct ggt gtg gag ctg ccg gat ctg atc ttg tcg cag att gcg tgg 48
 Leu Pro Gly Val Glu Leu Pro Asp Leu Ile Leu Ser Gln Ile Ala Trp
 1 5 10 15
 ttg tgt gca cgt att gaa gtc gac ggt atg cgc gct gac ctg gtg atc 96
 Leu Cys Ala Arg Ile Glu Val Asp Gly Met Arg Ala Asp Leu Val Ile
 20 25 30
 acg cgt acc gca ctt gct cac gcc gcg tgg gct gga cgc act gtg gtt 144

Thr Arg Thr Ala Leu Ala His Ala Ala Trp Ala Gly Arg Thr Val Val
 35 40 45
 acg gaa gaa gac gtg gag atc gca gct cgc cta gcg ttg ccg cac cgc 192
 Thr Glu Glu Asp Val Glu Ile Ala Ala Arg Leu Ala Leu Pro His Arg
 50 55 60
 cgt cgc cgt aat cct ttc gat gct cca gaa atg gag gag cgc aag ctt 240
 Arg Arg Arg Asn Pro Phe Asp Ala Pro Glu Met Glu Glu Arg Lys Leu
 65 70 75 80
 cag gaa acc ctg cag gaa gct cgg gac ttc ttc aaa gac aat gaa gat 288
 Gln Glu Thr Leu Gln Glu Ala Arg Asp Phe Phe Lys Asp Asn Glu Asp
 85 90 95
 aaa gga cct gcc gcc aag atc acc gat gag gaa acc ggt gca gag gcc 336
 Lys Gly Pro Ala Ala Lys Ile Thr Asp Glu Glu Thr Gly Ala Glu Ala
 100 105 110
 ttt acc gat acc gac aat ccc acc gag gaa gac ggt ctg caa gga act 384
 Phe Thr Asp Thr Asp Asn Pro Thr Glu Glu Asp Gly Leu Gln Gly Thr
 115 120 125
 gcg cag gcg aag gcg cag act act gga aag gta ggt act gcc gga tcc 432
 Ala Gln Ala Lys Ala Gln Thr Thr Gly Lys Val Gly Thr Ala Gly Ser
 130 135 140
 ggc gac ccc ttt cgc tcc taggcatttg cgcctggcgt cca 473
 Gly Asp Pro Phe Arg Ser
 145 150

<210> 368

<211> 150

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Leu Pro Gly Val Glu Leu Pro Asp Leu Ile Leu Ser Gln Ile Ala Trp
 1 5 10 15
 Leu Cys Ala Arg Ile Glu Val Asp Gly Met Arg Ala Asp Leu Val Ile
 20 25 30
 Thr Arg Thr Ala Leu Ala His Ala Ala Trp Ala Gly Arg Thr Val Val
 35 40 45
 Thr Glu Glu Asp Val Glu Ile Ala Ala Arg Leu Ala Leu Pro His Arg
 50 55 60
 Arg Arg Arg Asn Pro Phe Asp Ala Pro Glu Met Glu Glu Arg Lys Leu
 65 70 75 80
 Gln Glu Thr Leu Gln Glu Ala Arg Asp Phe Phe Lys Asp Asn Glu Asp
 85 90 95
 Lys Gly Pro Ala Ala Lys Ile Thr Asp Glu Glu Thr Gly Ala Glu Ala
 100 105 110
 Phe Thr Asp Thr Asp Asn Pro Thr Glu Glu Asp Gly Leu Gln Gly Thr
 115 120 125

Ala Gln Ala Lys Ala Gln Thr Thr Gly Lys Val Gly Thr Ala Gly Ser
 130 135 140

Gly Asp Pro Phe Arg Ser
 145 150

<210> 369
 <211> 667
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(667)
 <223> FRXA01691

<400> 369

aaaaccttaa gttgggtggt taaaccact aaggtctcac tttatggatg tgccagggtca 60
 caccaaaaaa tctcaagaaa actcacatta aaggacagta atg gcg tca caa cag 115
 Met Ala Ser Gln Gln
 1 5
 atc cgc tat cca ttc tcc gcg gtt gtg gga caa gac gag ctt cgg ctt 163
 Ile Arg Tyr Pro Phe Ser Ala Val Val Gly Gln Asp Glu Leu Arg Leu
 10 15 20
 gcg ttg atc ctc act gcg att tcc cca cgc att ggt ggc gtg gtg att 211
 Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile Gly Gly Val Val Ile
 25 30 35
 cga ggt gag aag ggt aca gcg aaa act acc act gtg cgt gct ttt gct 259
 Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr Val Arg Ala Phe Ala
 40 45 50
 ggt ctt tta ggt gat gcc cct ttg gtg aac ttg cct ctc gga tcc acg 307
 Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu Pro Leu Gly Ser Thr
 55 60 65
 gag gat cgt gtg gtg ggt tcc ctc aac atg gaa act gtg ttg acc acc 355
 Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu Thr Val Leu Thr Thr
 70 75 80 85
 ggc cgt gcg gaa tat cag cca ggt ttg ctc gcg cag gct gat ggc ggt 403
 Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala Gln Ala Asp Gly Gly
 90 95 100
 gtg ctg tat gtc gat gag gtc aac ctc ttg gcg gat cac ctg gtg gat 451
 Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala Asp His Leu Val Asp
 105 110 115
 gct ctg ctc gat gca gct gca agc ggt cgc gtc agc att gag cgt gac 499
 Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val Ser Ile Glu Arg Asp
 120 125 130
 ggt att tcg cat tct tca cca gca aac ttt gtg ttg gtg ggc acc atg 547
 Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val Leu Val Gly Thr Met
 135 140 145

aat ccg gag gaa ggc gag ctg cgc ccg cag ctg ctg gac cgt ttc ggt 595
 Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu Leu Asp Arg Phe Gly
 150 155 160 165

ttg gct gtg gac gtt gct gcg tct acg aac cct gag gtg cgc gtg gag 643
 Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro Glu Val Arg Val Glu
 170 175 180

atc att cgc cgc cgg ctt gat ttt 667
 Ile Ile Arg Arg Arg Leu Asp Phe
 185

<210> 370

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Met Ala Ser Gln Gln Ile Arg Tyr Pro Phe Ser Ala Val Val Gly Gln
 1 5 10 15

Asp Glu Leu Arg Leu Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile
 20 25 30

Gly Gly Val Val Ile Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr
 35 40 45

Val Arg Ala Phe Ala Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu
 50 55 60

Pro Leu Gly Ser Thr Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu
 65 70 75 80

Thr Val Leu Thr Thr Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala
 85 90 95

Gln Ala Asp Gly Gly Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala
 100 105 110

Asp His Leu Val Asp Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val
 115 120 125

Ser Ile Glu Arg Asp Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val
 130 135 140

Leu Val Gly Thr Met Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu
 145 150 155 160

Leu Asp Arg Phe Gly Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro
 165 170 175

Glu Val Arg Val Glu Ile Ile Arg Arg Arg Leu Asp Phe
 180 185

<210> 371

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN00665

<400> 371

```

accaaact tctgtgctg acacgcgcca cttatactc ccacaagcaa cacagaacac 60

tcgggatctc aaagtttcga gaaacacaga aagggcagca atg agc agc tca aca 115
Met Ser Ser Ser Thr
1 5

ctt ctc ctg gct tca gga caa gtc acg gca tta gcc gct gac tac acg 163
Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu Ala Ala Asp Tyr Thr
10 15 20

ctc agc cac acc ccc tca gat ggc atc ctg gta gtc ctt ggc ttc gcc 211
Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val Val Leu Gly Phe Ala
25 30 35

atg atc ctc acc ttc atg acc ctg atc atg ctg ggt cga ctc acc cca 259
Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu Gly Arg Leu Thr Pro
40 45 50

atg gtg gcc atg ctg ttg gtc ccc acc atc ttc ggt ctc atc gcc ggc 307
Met Val Ala Met Leu Leu Val Pro Thr Ile Phe Gly Leu Ile Ala Gly
55 60 65

gca gga ctc ggc ctt ggt gac atg gcg ctt gac gcc atc aag gac atg 355
Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp Ala Ile Lys Asp Met
70 75 80 85

gcg cct acc gcg gca ctc ctg atg ttc gcg att atg ttc ttc gga atc 403
Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile Met Phe Phe Gly Ile
90 95 100

atg atc gac gtc gga ctc ttc gac ccc ctg atc cgc gtg atc acc cgc 451
Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile Arg Val Ile Thr Arg
105 110 115

gtt ctt cac gat gac ccc gca aag gtc gtc atc ggc acc gca gta ctt 499
Val Leu His Asp Asp Pro Ala Lys Val Val Ile Gly Thr Ala Val Leu
120 125 130

gca ggt gtt gtc tcc ctc gac ggc gac ggc tcc acc acc ttc atc att 547
Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser Thr Thr Phe Ile Ile
135 140 145

acc acc ttc cgc gat gct gcc cat cta cct gcg cct tgg cat gag ccc 595
Thr Thr Phe Arg Asp Ala Ala His Leu Pro Ala Pro Trp His Glu Pro
150 155 160 165

tgt ggt
Cys Gly 601

```

<210> 372

<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

Met Ser Ser Ser Thr Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu
 1 5 10 15
 Ala Ala Asp Tyr Thr Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val
 20 25 30
 Val Leu Gly Phe Ala Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu
 35 40 45
 Gly Arg Leu Thr Pro Met Val Ala Met Leu Leu Val Pro Thr Ile Phe
 50 55 60
 Gly Leu Ile Ala Gly Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp
 65 70 75 80
 Ala Ile Lys Asp Met Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile
 85 90 95
 Met Phe Phe Gly Ile Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile
 100 105 110
 Arg Val Ile Thr Arg Val Leu His Asp Asp Pro Ala Lys Val Val Ile
 115 120 125
 Gly Thr Ala Val Leu Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser
 130 135 140
 Thr Thr Phe Ile Ile Thr Thr Phe Arg Asp Ala Ala His Leu Pro Ala
 145 150 155 160
 Pro Trp His Glu Pro Cys Gly
 165

<210> 373

<211> 390

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(367)

<223> RXN03026

<400> 373

gttggcggcg cagtatcgtg aggtgcggga cctcgagcgg ggaatcccaa actagcatcc 60
 cgaactagcc ccccaacaac aattagaaat ggaacctaaa atg cct gga aaa att 115
 Met Pro Gly Lys Ile
 1 5
 ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
 Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
 10 15 20
 gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
 Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
 25 30 35

gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
 Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
 40 45 50

cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307
 His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His
 55 60 65

atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85

ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 374
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 374
 Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu
 1 5 10 15

Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val
 20 25 30

Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
 35 40 45

Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
 50 55 60

Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
 65 70 75 80

Thr Leu Arg Trp Arg Phe Trp Met Leu
 85

<210> 375
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> RXN02908

<400> 375
 gccaacgagg gttggtttac cacctctgat tcaggtgaac tccacgacgg gattctcacc 60

gtgactggtc gogtggatac ccgtcattga ttccggtgga ttg aag ttg cac cca 115
 Leu Lys Leu His Pro
 1 5

gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala

	10	15	20	
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc				211
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala				
	25	30	35	
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac				259
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp				
	40	45	50	
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct				307
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser				
	55	60	65	
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag				355
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys				
	70	75	80	85
ctg ttt tagtcttcat tcttgctggc tgc				384
Leu Phe				

<210> 376
 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 376
 Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
 1 5 10 15
 Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
 20 25 30
 Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
 35 40 45
 Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
 50 55 60
 Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
 65 70 75 80
 Arg Ala Ile Ala Lys Leu Phe
 85

<210> 377
 <211> 667
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(667)
 <223> RXN03000

<400> 377
 cagcgtgttg ctgcgcctgc agaaaacctc cagcgtcacc cacaaagtcg aaatccaagg 60

ctaaccacct ttttcaactc acagtttagga aacttcacccc atg tct ctt cca cat 115
Met Ser Leu Pro His
1 5

tct gat gaa ctc cgc ggc caa aag atc att att tcc ggt ggc gga att 163
Ser Asp Glu Leu Arg Gly Gln Lys Ile Ile Ile Ser Gly Gly Gly Ile
10 15 20

ggt ggc gca gca ggt gca ctt gcg ctt gct ttg cgc ggt gcc gat gtc 211
Gly Gly Ala Ala Gly Ala Leu Ala Leu Ala Leu Arg Gly Ala Asp Val
25 30 35

act ttg tac gaa cgc gca gct gag ttc aag gag gtc ggc gct ggc ctc 259
Thr Leu Tyr Glu Arg Ala Ala Glu Phe Lys Glu Val Gly Ala Gly Leu
40 45 50

cag atc ggt ccg cac ggc tgg cga atg ctg gaa tcc tgg ggt ctg ctc 307
Gln Ile Gly Pro His Gly Trp Arg Met Leu Glu Ser Trp Gly Leu Leu
55 60 65

gac caa att gtc gtg gcc ggc tac ctc cca gaa gac atg cag ttc cgc 355
Asp Gln Ile Val Val Ala Gly Tyr Leu Pro Glu Asp Met Gln Phe Arg
70 75 80 85

gac gct gtc aac cgc gaa acc atc ctg acc atg cgt ttc gat gaa gaa 403
Asp Ala Val Asn Arg Glu Thr Ile Leu Thr Met Arg Phe Asp Glu Glu
90 95 100

ttc cag cag cac tac ggc ggt cgc tac ctg gtg att cac cgc tct gac 451
Phe Gln Gln His Tyr Gly Gly Arg Tyr Leu Val Ile His Arg Ser Asp
105 110 115

ctg ctc aac atc ctg gtc acc aac gcc gaa gca gcg ggc gcg aag ctc 499
Leu Leu Asn Ile Leu Val Thr Asn Ala Glu Ala Ala Gly Ala Lys Leu
120 125 130

cac aat ggc gtc ctg gtc acc gat tcc cgc acc gtc gac ggc ggt atc 547
His Asn Gly Val Leu Val Thr Asp Ser Arg Thr Val Asp Gly Gly Ile
135 140 145

gag gtg gac atc gaa tcc tcc atc aac aag ggc gaa gat aac aag act 595
Glu Val Asp Ile Glu Ser Ser Ile Asn Lys Gly Glu Asp Asn Lys Thr
150 155 160 165

ttg ctt gtc gac gcc ttc ctc gcc ttc gac ggc atc cac tcg gtc atg 643
Leu Leu Val Asp Ala Phe Leu Ala Phe Asp Gly Ile His Ser Val Met
170 175 180

cgc aaa aag ctt gtc gac gac gcc 667
Arg Lys Lys Leu Val Asp Asp Ala
185

<210> 378

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

Met Ser Leu Pro His Ser Asp Glu Leu Arg Gly Gln Lys Ile Ile Ile
1 5 10 15

Ser Gly Gly Gly Ile Gly Gly Ala Ala Gly Ala Leu Ala Leu Ala Leu
 20 25 30
 Arg Gly Ala Asp Val Thr Leu Tyr Glu Arg Ala Ala Glu Phe Lys Glu
 35 40 45
 Val Gly Ala Gly Leu Gln Ile Gly Pro His Gly Trp Arg Met Leu Glu
 50 55 60
 Ser Trp Gly Leu Leu Asp Gln Ile Val Val Ala Gly Tyr Leu Pro Glu
 65 70 75 80
 Asp Met Gln Phe Arg Asp Ala Val Asn Arg Glu Thr Ile Leu Thr Met
 85 90 95
 Arg Phe Asp Glu Glu Phe Gln Gln His Tyr Gly Gly Arg Tyr Leu Val
 100 105 110
 Ile His Arg Ser Asp Leu Leu Asn Ile Leu Val Thr Asn Ala Glu Ala
 115 120 125
 Ala Gly Ala Lys Leu His Asn Gly Val Leu Val Thr Asp Ser Arg Thr
 130 135 140
 Val Asp Gly Gly Ile Glu Val Asp Ile Glu Ser Ser Ile Asn Lys Gly
 145 150 155 160
 Glu Asp Asn Lys Thr Leu Leu Val Asp Ala Phe Leu Ala Phe Asp Gly
 165 170 175
 Ile His Ser Val Met Arg Lys Lys Leu Val Asp Asp Ala
 180 185

<210> 379
 <211> 766
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXN03036

<400> 379
 tagaaaaatc taccagtaa gcattcagga accattcaga atcttttctt agcatgtctc 60
 tatcagcgta aacgtccgaa catgaaaggc tagaaaagcc atg gct gag cag ttg 115
 Met Ala Glu Gln Leu
 1 5
 cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa 163
 Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln Ser Glu Asp Leu Glu
 10 15 20
 gat cag ggt ttg gga ttt gac ctg gga acc gtt ttc tcc cgc agg aag 211
 Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val Phe Ser Arg Arg Lys
 25 30 35
 gtt ttg gga ttc atc ggt gtt ggt gga gca ggt gtg gca ctt gct gct 259

Val	Leu	Gly	Phe	Ile	Gly	Val	Gly	Gly	Ala	Gly	Val	Ala	Leu	Ala	Ala		
		40					45					50					
tgt	tca	cct	tct	ggc	tct	tcc	gcg	gca	tcg	agc	acc	tca	agc	gcg	tcc	307	
Cys	Ser	Pro	Ser	Gly	Ser	Ser	Ala	Ala	Ser	Ser	Thr	Ser	Ser	Ala	Ser		
	55					60					65						
agc	agc	gca	gct	gca	acc	acc	agt	gca	gca	gca	gag	act	ttg	act	gag	355	
Ser	Ser	Ala	Ala	Ala	Thr	Thr	Ser	Ala	Ala	Ala	Glu	Thr	Leu	Thr	Glu		
70					75					80					85		
atg	aag	tcg	gag	act	gct	ggc	ccg	tac	ccg	ggc	gat	ggc	tcg	aat	ggc	403	
Met	Lys	Ser	Glu	Thr	Ala	Gly	Pro	Tyr	Pro	Gly	Asp	Gly	Ser	Asn	Gly		
				90					95					100			
ccg	gat	gtg	ttg	gag	gtc	tcc	ggc	gtg	gag	cgc	cag	gac	atc	acc	aag	451	
Pro	Asp	Val	Leu	Glu	Val	Ser	Gly	Val	Glu	Arg	Gln	Asp	Ile	Thr	Lys		
		105					110						115				
tcg	att	gat	tct	gac	acc	gtg	gca	gag	ggc	gta	cct	ctg	acg	ttg	act	499	
Ser	Ile	Asp	Ser	Asp	Thr	Val	Ala	Glu	Gly	Val	Pro	Leu	Thr	Leu	Thr		
	120						125					130					
atg	acc	att	ttg	gac	atg	aac	aac	aac	aat	cag	cca	atg	gag	ggc	gct	547	
Met	Thr	Ile	Leu	Asp	Met	Asn	Asn	Asn	Asn	Gln	Pro	Met	Glu	Gly	Ala		
	135					140					145						
gcg	gtg	tac	gtg	tgg	cac	tgt	gat	gcg	ccg	ggc	cga	tat	tcg	atg	tac	595	
Ala	Val	Tyr	Val	Trp	His	Cys	Asp	Ala	Pro	Gly	Arg	Tyr	Ser	Met	Tyr		
150					155				160						165		
gac	tct	gag	ctg	gaa	gat	gag	acc	tat	tta	cgc	ggc	gtg	cag	att	acc	643	
Asp	Ser	Glu	Leu	Glu	Asp	Glu	Thr	Tyr	Leu	Arg	Gly	Val	Gln	Ile	Thr		
				170					175					180			
gat	aag	tat	ggc	cag	gtc	acg	ttc	gat	acc	att	ttc	cct	ggc	tgt	tat	691	
Asp	Lys	Tyr	Gly	Gln	Val	Thr	Phe	Asp	Thr	Ile	Phe	Pro	Gly	Cys	Tyr		
		185					190						195				
gcg	ggc	cgt	tgg	gtg	cat	att	cat	ttc	gag	gtg	ttc	ccg	gat	cga	gac	739	
Ala	Gly	Arg	Trp	Val	His	Ile	His	Phe	Glu	Val	Phe	Pro	Asp	Arg	Asp		
		200				205						210					
agc	atc	acg	gat	tcc	acg	aac	aac	att								766	
Ser	Ile	Thr	Asp	Ser	Thr	Asn	Asn	Ile									
	215					220											

<210> 380

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met	Ala	Glu	Gln	Leu	Arg	Gln	Phe	Glu	Gly	Arg	Val	Leu	Pro	Asn	Gln		
1				5					10					15			

Ser	Glu	Asp	Leu	Glu	Asp	Gln	Gly	Leu	Gly	Phe	Asp	Leu	Gly	Thr	Val		
	20						25						30				

Phe	Ser	Arg	Arg	Lys	Val	Leu	Gly	Phe	Ile	Gly	Val	Gly	Gly	Ala	Gly		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

```
<210> 381
<211> 318
<212> DNA
<213> Corynebacterium glutamicum
```

```

<400> 381
gcaggcatgg acacattcca ggtcctgacc ggcgtcagcg gctactacga tttggtgcgc 60

gccattccca gagcagcgcc ccacctatat cgccacctcg atg cag gat ctc tac 115
                                         Met Gln Asp Leu Tyr
                                         1                               5

agc gat ccg ggc gag ctc aag cca ggt gcc cag ggc ggt ttt tca gcg 163
Ser Asp Pro Gly Glu Leu Lys Pro Gly Ala Gln Gly Gly Phe Ser Ala
                        10                        15                        20

ctt atc gac ggc gac acc ctg gtc att tcc ggc ggc gat gcc ggc gca 211
Leu Ile Asp Gly Asp Thr Leu Val Ile Ser Gly Gly Asp Ala Gly Ala
                        25                        30                        35

```

act ccg gtt gca gca ctc cgc act gcg ttg gat gtg gcc tgg gcg gcc 259
 Thr Pro Val Ala Ala Leu Arg Thr Ala Leu Asp Val Ala Trp Ala Ala
 40 45 50

aca gag cag tca ccg agg tac gcg ctg att cag agg tagctgctac 305
 Thr Glu Gln Ser Pro Arg Tyr Ala Leu Ile Gln Arg
 55 60 65

tgcattgcag agc 318

<210> 382

<211> 65

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Met Gln Asp Leu Tyr Ser Asp Pro Gly Glu Leu Lys Pro Gly Ala Gln
 1 5 10 15

Gly Gly Phe Ser Ala Leu Ile Asp Gly Asp Thr Leu Val Ile Ser Gly
 20 25 30

Gly Asp Ala Gly Ala Thr Pro Val Ala Ala Leu Arg Thr Ala Leu Asp
 35 40 45

Val Ala Trp Ala Ala Thr Glu Gln Ser Pro Arg Tyr Ala Leu Ile Gln
 50 55 60

Arg
 65

<210> 383

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXN00393

<400> 383

tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tattttcaagc 60

aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20

cgc cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 Ala Leu Ala Phe Ser
 295.

1017

<210> 384
 <211> 298
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 384

Met	Ser	His	Thr	Glu	Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp
1				5				10						15	
Ile	Gln	Gly	Ala	Arg	Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val
			20					25					30		
Ile	Ala	Gly	Ser	Gly	Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp
		35					40					45			
Lys	Ala	Leu	Leu	Ala	Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val
	50					55					60				
Asn	Tyr	Ala	Asn	Asp	Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp
	65				70					75					80
Arg	Thr	Gly	Pro	Leu	Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys
				85					90					95	
Lys	Val	Lys	Ala	Ala	Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala
			100					105					110		
Gly	Thr	Ala	Leu	Ser	Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly
		115					120					125			
Ile	Leu	Cys	Val	Leu	Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro
	130					135					140				
Tyr	Gly	Tyr	Arg	Gly	Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly
	145				150					155					160
Leu	Val	Ala	Val	Met	Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser
				165					170					175	
Trp	Ala	Gly	Leu	Ala	Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly
			180					185					190		
Val	Asn	Leu	Ala	Asn	Asn	Ile	Arg	Asp	Ile	Pro	Thr	Asp	Ser	Lys	Thr
		195					200					205			
Gly	Lys	Ile	Thr	Leu	Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys
	210					215					220				
Leu	Phe	Leu	Ala	Leu	Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu
	225				230					235					240
Ala	Phe	Val	Ala	Trp	Pro	Ala	Leu	Ile	Ala	Ile	Ile	Val	Phe	Pro	Leu
			245						250					255	
Ala	Leu	Lys	Ala	Ala	Gly	Pro	Ile	Arg	Asn	Asn	Ala	Thr	Gly	Lys	Asp
		260						265					270		

Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala
 275 280 285

Val Leu Thr Gly Leu Ala Leu Ala Phe Ser
 290 295

<210> 385

<211> 1242

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1219)

<223> RXN00948

<400> 385

acaccctcca aatgatctcg taaaacagta ttgaatttag gtacgactct aatcgtaacct 60

tgccctcaag ccaagctagt tgtacgatca aactcgttgt atg gca aac gtc gta 115
 Met Ala Asn Val Val
 1 5

cta gtc gat cga atg gag cct ttg gtg tcc aag ctg ttt acc cca att 163
 Leu Val Asp Arg Met Glu Pro Leu Val Ser Lys Leu Phe Thr Pro Ile
 10 15 20

caa atc cgc gac atc acc atc ccc aac cgc gtg tgg atg tca ccg atg 211
 Gln Ile Arg Asp Ile Thr Ile Pro Asn Arg Val Trp Met Ser Pro Met
 25 30 35

tgc acc tac tct gca gcc acc ggt tca ggt ctt ccc acc gat ttt cac 259
 Cys Thr Tyr Ser Ala Ala Thr Gly Ser Gly Leu Pro Thr Asp Phe His
 40 45 50

cag gct cat tac gca gct cgc gca gca ggt ggt gtc gga tta gtc atg 307
 Gln Ala His Tyr Ala Ala Arg Ala Ala Gly Gly Val Gly Leu Val Met
 55 60 65

gtt gaa gca act gga gtg aac ccc gta gct ccc atc tcc cca gtc gac 355
 Val Glu Ala Thr Gly Val Asn Pro Val Ala Pro Ile Ser Pro Val Asp
 70 75 80 85

ctt gga ctt tgg agc cat gac caa att gaa cca ttc tcc cga gtg aca 403
 Leu Gly Leu Trp Ser His Asp Gln Ile Glu Pro Phe Ser Arg Val Thr
 90 95 100

gca gct att cgc gcc ggt ggg gca gta ccg gcc gtt caa tta gcc cat 451
 Ala Ala Ile Arg Ala Gly Gly Ala Val Pro Ala Val Gln Leu Ala His
 105 110 115

gct ggc cgc aag gca tcc acc gat gct ccg tgg aat ggt ggc gga tat 499
 Ala Gly Arg Lys Ala Ser Thr Asp Ala Pro Trp Asn Gly Gly Gly Tyr
 120 125 130

gtt gga cca gaa acc aat gga tgg gag act gtc ggc ccc agc cct ctg 547
 Val Gly Pro Glu Thr Asn Gly Trp Glu Thr Val Gly Pro Ser Pro Leu
 135 140 145

gca ttc cca ggt ttg cct gct ccg cgc gag ctg acg gtt tca gaa atc	595
Ala Phe Pro Gly Leu Pro Ala Pro Arg Glu Leu Thr Val Ser Glu Ile	
150 155 160 165	
caa gag gtt gtg cag cag ttc gct ggc gcc gcc gtt cgt gcc gat cag	643
Gln Glu Val Val Gln Gln Phe Ala Gly Ala Ala Val Arg Ala Asp Gln	
170 175 180	
gct ggt ttt gat gtc gtg gaa att cac gca gca cac ggc tac ctt ttg	691
Ala Gly Phe Asp Val Val Glu Ile His Ala Ala His Gly Tyr Leu Leu	
185 190 195	
cat aac ttc ctt tct ccg atc tcc aac aag cgc acc gat tca tac ggc	739
His Asn Phe Leu Ser Pro Ile Ser Asn Lys Arg Thr Asp Ser Tyr Gly	
200 205 210	
gga tct tta gaa aac cgc gct cgc atc gtg ctc gaa gtc att gat gca	787
Gly Ser Leu Glu Asn Arg Ala Arg Ile Val Leu Glu Val Ile Asp Ala	
215 220 225	
atc cgc gca gtg tgg cca gag gaa aag cct gta ttc atg cgc att tcc	835
Ile Arg Ala Val Trp Pro Glu Glu Lys Pro Val Phe Met Arg Ile Ser	
230 235 240 245	
acc acc gac tgg gtg gag gaa aac cca cag gat gat cgc gag tcc tgg	883
Thr Thr Asp Trp Val Glu Glu Asn Pro Gln Asp Asp Arg Glu Ser Trp	
250 255 260	
acg ctg agc caa agc agg cag ctg gct ttg tgg gca tcc gag cac gga	931
Thr Leu Ser Gln Ser Arg Gln Leu Ala Leu Trp Ala Ser Glu His Gly	
265 270 275	
gtt gat ttg atc gat gcc tct tct ggt ggc ctc gac atc gtc ccc att	979
Val Asp Leu Ile Asp Ala Ser Ser Gly Gly Leu Asp Ile Val Pro Ile	
280 285 290	
ccg cat gac cgc gat tac caa acc gcg aag gcc gca gat ctt cac gca	1027
Pro His Asp Arg Asp Tyr Gln Thr Ala Lys Ala Ala Asp Leu His Ala	
295 300 305	
agt acc gga gtg aca gtc gct gct gtg ggg cgc att gat gac gcc caa	1075
Ser Thr Gly Val Thr Val Ala Ala Val Gly Arg Ile Asp Asp Ala Gln	
310 315 320 325	
act gcg cac aat ttg gtt gat tct ggc gat gtc aat gca gtt ttc ctc	1123
Thr Ala His Asn Leu Val Asp Ser Gly Asp Val Asn Ala Val Phe Leu	
330 335 340	
ggc cgt cca ctg ctc aag gat cct tcc tgg gca aac caa gca gcc ctc	1171
Gly Arg Pro Leu Leu Lys Asp Pro Ser Trp Ala Asn Gln Ala Ala Leu	
345 350 355	
gca cta ggt gcg gaa ccc agg tat gtt cac caa tac gac tac gta ctt	1219
Ala Leu Gly Ala Glu Pro Arg Tyr Val His Gln Tyr Asp Tyr Val Leu	
360 365 370	
taaaggagag ttgacatgaa ggt	1242

<210> 386

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

```

Met Ala Asn Val Val Leu Val Asp Arg Met Glu Pro Leu Val Ser Lys
 1           5           10           15

Leu Phe Thr Pro Ile Gln Ile Arg Asp Ile Thr Ile Pro Asn Arg Val
      20           25           30

Trp Met Ser Pro Met Cys Thr Tyr Ser Ala Ala Thr Gly Ser Gly Leu
      35           40           45

Pro Thr Asp Phe His Gln Ala His Tyr Ala Ala Arg Ala Ala Gly Gly
      50           55           60

Val Gly Leu Val Met Val Glu Ala Thr Gly Val Asn Pro Val Ala Pro
      65           70           75           80

Ile Ser Pro Val Asp Leu Gly Leu Trp Ser His Asp Gln Ile Glu Pro
      85           90           95

Phe Ser Arg Val Thr Ala Ala Ile Arg Ala Gly Gly Ala Val Pro Ala
      100          105          110

Val Gln Leu Ala His Ala Gly Arg Lys Ala Ser Thr Asp Ala Pro Trp
      115          120          125

Asn Gly Gly Gly Tyr Val Gly Pro Glu Thr Asn Gly Trp Glu Thr Val
      130          135          140

Gly Pro Ser Pro Leu Ala Phe Pro Gly Leu Pro Ala Pro Arg Glu Leu
      145          150          155          160

Thr Val Ser Glu Ile Gln Glu Val Val Gln Gln Phe Ala Gly Ala Ala
      165          170          175

Val Arg Ala Asp Gln Ala Gly Phe Asp Val Val Glu Ile His Ala Ala
      180          185          190

His Gly Tyr Leu Leu His Asn Phe Leu Ser Pro Ile Ser Asn Lys Arg
      195          200          205

Thr Asp Ser Tyr Gly Gly Ser Leu Glu Asn Arg Ala Arg Ile Val Leu
      210          215          220

Glu Val Ile Asp Ala Ile Arg Ala Val Trp Pro Glu Glu Lys Pro Val
      225          230          235          240

Phe Met Arg Ile Ser Thr Thr Asp Trp Val Glu Glu Asn Pro Gln Asp
      245          250          255

Asp Arg Glu Ser Trp Thr Leu Ser Gln Ser Arg Gln Leu Ala Leu Trp
      260          265          270

Ala Ser Glu His Gly Val Asp Leu Ile Asp Ala Ser Ser Gly Gly Leu
      275          280          285

Asp Ile Val Pro Ile Pro His Asp Arg Asp Tyr Gln Thr Ala Lys Ala
      290          295          300

```


Ala Asp Leu His Ala Ser Thr Gly Val Thr Val Ala Ala Val Gly Arg
 305 310 315 320

Ile Asp Asp Ala Gln Thr Ala His Asn Leu Val Asp Ser Gly Asp Val
 325 330 335

Asn Ala Val Phe Leu Gly Arg Pro Leu Leu Lys Asp Pro Ser Trp Ala
 340 345 350

Asn Gln Ala Ala Leu Ala Leu Gly Ala Glu Pro Arg Tyr Val His Gln
 355 360 365

Tyr Asp Tyr Val Leu
 370

<210> 387
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(850)
 <223> RXN01923

<400> 387
 ccaaagtgaat taccgagact gcagcagcgc aaaagttcaa gtactttggg atgcaaattct 60

agtagcacgt cccatgtttc tcacactctc aggagctgac atg tct gca ctt att 115
 Met Ser Ala Leu Ile
 1 5

aaa ggt tca gga cct cat cat gtg gtt gtc tta aat ggt tgg ttt ggt 163
 Lys Gly Ser Gly Pro His His Val Val Leu Asn Gly Trp Phe Gly
 10 15 20

cat gct gcg ggc tgg gga gct ttc gct gac tat ctt gac ctc ggc aac 211
 His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr Leu Asp Leu Gly Asn
 25 30 35

tac acc tgg cac ttt tgg gat tac cga ggt tac ggc aac aga aaa gac 259
 Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr Gly Asn Arg Lys Asp
 40 45 50

gac gca gga gaa ttt act ctg gag gaa att tca gcg gat atc gtt gca 307
 Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser Ala Asp Ile Val Ala
 55 60 65

tac atc gac tcg att gag gca gaa aag gtt tcc atc ctg ggc cat tcc 355
 Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser Ile Leu Gly His Ser
 70 75 80 85

atg ggt gga gtg ttc atg cag aaa gtc ctt gca gac agc gcc acc ccc 403
 Met Gly Gly Val Phe Met Gln Lys Val Leu Ala Asp Ser Ala Thr Pro
 90 95 100

atc gct tca ctg gtt gga att tct gcc gtt gct gca gct gga aca cca 451
 Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala Ala Ala Gly Thr Pro
 105 110 115

ttc gat gag gat tct cgg aag ctt ttc acc tca gca ggg cac aac ccg 499
 Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser Ala Gly His Asn Pro
 120 125 130

 gac tcg agg cga gcc atc atc gat ttc acc tca gga tct cgc caa cct 547
 Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr Ser Gly Ser Arg Gln Pro
 135 140 145

 gcc gcg tgg ttg gat gat ctc acc gac tcg gcg gtg cag aat tcc act 595
 Ala Ala Trp Leu Asp Asp Leu Thr Asp Ser Ala Val Gln Asn Ser Thr
 150 155 160 165

 cca gag gcc gtt gaa aag tac ttt ttt gcg tgg gct gat tgt aat ttc 643
 Pro Glu Ala Val Glu Lys Tyr Phe Phe Ala Trp Ala Asp Cys Asn Phe
 170 175 180

 gca gcg gat tta ggc acc caa gat ttg ccc gtg gac att ctc acc ggc 691
 Ala Ala Asp Leu Gly Thr Gln Asp Leu Pro Val Asp Ile Leu Thr Gly
 185 190 195

 gat ctc gac ccc gcg gtc act aaa act gcc gtg gaa tcc gca ttc ggc 739
 Asp Leu Asp Pro Ala Val Thr Lys Thr Ala Val Glu Ser Ala Phe Gly
 200 205 210

 ccg atc tat caa aat ctg acc gtt gaa gaa ctc cac gat gtc gga cac 787
 Pro Ile Tyr Gln Asn Leu Thr Val Glu Glu Leu His Asp Val Gly His
 215 220 225

 tac gca att ttc gag cac ccc tta ggc ctt gcc gcc agg gtg ctt cga 835
 Tyr Ala Ile Phe Glu His Pro Leu Gly Leu Ala Ala Arg Val Leu Arg
 230 235 240 245

 ttt ctc gac gcc gtc tagtacttcc gcaaattcac cgg 873
 Phe Leu Asp Ala Val
 250

<210> 388

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Met Ser Ala Leu Ile Lys Gly Ser Gly Pro His His Val Val Val Leu
 1 5 10 15

 Asn Gly Trp Phe Gly His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr
 20 25 30

 Leu Asp Leu Gly Asn Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr
 35 40 45

 Gly Asn Arg Lys Asp Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser
 50 55 60

 Ala Asp Ile Val Ala Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser
 65 70 75 80

 Ile Leu Gly His Ser Met Gly Gly Val Phe Met Gln Lys Val Leu Ala
 85 90 95

Asp Ser Ala Thr Pro Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala
 100 105 110
 Ala Ala Gly Thr Pro Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser
 115 120 125
 Ala Gly His Asn Pro Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr Ser
 130 135 140
 Gly Ser Arg Gln Pro Ala Ala Trp Leu Asp Asp Leu Thr Asp Ser Ala
 145 150 155 160
 Val Gln Asn Ser Thr Pro Glu Ala Val Glu Lys Tyr Phe Phe Ala Trp
 165 170 175
 Ala Asp Cys Asn Phe Ala Ala Asp Leu Gly Thr Gln Asp Leu Pro Val
 180 185 190
 Asp Ile Leu Thr Gly Asp Leu Asp Pro Ala Val Thr Lys Thr Ala Val
 195 200 205
 Glu Ser Ala Phe Gly Pro Ile Tyr Gln Asn Leu Thr Val Glu Glu Leu
 210 215 220
 His Asp Val Gly His Tyr Ala Ile Phe Glu His Pro Leu Gly Leu Ala
 225 230 235 240
 Ala Arg Val Leu Arg Phe Leu Asp Ala Val
 245 250

<210> 389
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(850)
 <223> RXN00398

<400> 389
 tgagttcgc accatcagca ccggcacc caagcgcggt gtggttaacc gtgagaagtt 60
 tgtctcccggt ctgcctgaag cacctaagga aaactaaatc atg gcc aag ttg ttt 115
 Met Ala Lys Leu Phe
 1 5
 gat tcc cat ttc cat atc atc gat ccc cag cac cca ctg atc gaa aac 163
 Asp Ser His Phe His Ile Ile Asp Pro Gln His Pro Leu Ile Glu Asn
 10 15 20
 aac ggc tac ctc ccc gag cct ttc acc gtg gag gat tac act gcg cgt 211
 Asn Gly Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg
 25 30 35
 gtt gaa ggc ctc gaa gtt gct gcc gga gcg att gtt tcc ggt tct ttc 259
 Val Glu Gly Leu Glu Val Ala Ala Gly Ala Ile Val Ser Gly Ser Phe
 40 45 50
 cag gct ttc gac cag ggc tac ctc aaa gat gct ctc gca gtg ctt ggc 307

Gln Ala Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly
 55 60 65

cca ggc tat gtc ggt gtc act cag atc ccc gca gat acc tct gat cag 355
 Pro Gly Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln
 70 75 80 85

gag att ctt gat ctg gac aaa gct ggc gtg aag gct gtg cgt tta aac 403
 Glu Ile Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn
 90 95 100

ttg aag cgc ggt ggt tcg gca ggt ctt gac gat ctc gag acc ttg gca 451
 Leu Lys Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala
 105 110 115

cgc cga gtc cac gac cta gcc ggt tgg cac acc gaa ctc tat gtg gat 499
 Arg Arg Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp
 120 125 130

gct cgc gaa cta gac gag ttg gaa tca acc ttg gcc tcc ctc cct gct 547
 Ala Arg Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala
 135 140 145

gtc agc att gat cac tta ggg ctc cac cgc gat gga ctt ccc gca ctt 595
 Val Ser Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu
 150 155 160 165

ctt cgc ttg gta gaa aat ggc att aaa gtc aaa gca acc gga ttc gga 643
 Leu Arg Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly
 170 175 180

cgg gta gaa cta gat cca act gaa gtc atc cag gca atc atg gct gtc 691
 Arg Val Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val
 185 190 195

gat ccc act gct ttg atg atc gga act gat ctt cca tcc acc cgc act 739
 Asp Pro Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr
 200 205 210

aag cga cct ttc gaa gac gct gac cta gat ttg atc gct gaa acg gtt 787
 Lys Arg Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val
 215 220 225

ggc gaa gat cat gtc gac aac gtc ttc tgg aac aac gct gca gcg ttc 835
 Gly Glu Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe
 230 235 240 245

tac ctc gga gac cag tagttttaag acccgaaatg tct 873
 Tyr Leu Gly Asp Gln
 250

<210> 390

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

Met Ala Lys Leu Phe Asp Ser His Phe His Ile Ile Asp Pro Gln His
 1 5 10 15

```
<210> 391
<211> 1108
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 391
ggactctaaa ttgaccgat ctttatactc cgaccttgct ggtagtggag aacacctcag 60
cagcctttcc gacgagactt tcctaaagaa tcttcttgct gtg gag gcc gct ttg 115
Val Glu Ala Ala Leu

																1	5
gcg gtt gca gct gcc ccc gag cac gca gca atg gcg aag gcc acc att	163																
Ala Val Ala Ala Ala Pro Glu His Ala Ala Met Ala Lys Ala Thr Ile																	
				10					15						20		
gat tct tat cag ttg gat gtg gag gag ctt tcc cgt cgc gca gcc gag	211																
Asp Ser Tyr Gln Leu Asp Val Glu Glu Leu Ser Arg Arg Ala Ala Glu				25					30					35			
ggc ggt aat ccg ctc att ccg ctg gtc act gac ctc aag gcc atc aat	259																
Gly Gly Asn Pro Leu Ile Pro Leu Val Thr Asp Leu Lys Ala Ile Asn				40					45					50			
ccg gca ggc atc cac att ggc gca acg agc cag gac atc att gat tct	307																
Pro Ala Gly Ile His Ile Gly Ala Thr Ser Gln Asp Ile Ile Asp Ser				55					60					65			
gcg tta atg ctg tgc atg aag gaa ggg gtg ggg gag gtc gtc gac aag	355																
Ala Leu Met Leu Cys Met Lys Glu Gly Val Gly Glu Val Val Asp Lys									70					80			85
ctt aaa aag ctt gcg cga gat ttg gcc gag ctc acc gcg gag cat aaa	403																
Leu Lys Lys Leu Ala Arg Asp Leu Ala Glu Leu Thr Ala Glu His Lys									90					95			100
gca acc ccg atc atg ggg cgc acg ttg ggg cag atc gcg acg ccg acg	451																
Ala Thr Pro Ile Met Gly Arg Thr Leu Gly Gln Ile Ala Thr Pro Thr									105					110			115
acg ttc ggc gcg ctg acc ggc ggc tgg ctg gtt gcg gtg gac aat gcg	499																
Thr Phe Gly Ala Leu Thr Gly Gly Trp Leu Val Ala Val Asp Asn Ala									120					125			130
gca cgc gcc ctg gag gcg ctg gag ttt ccg gtg tcg tat ggc ggt gcc	547																
Ala Arg Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala									135					140			145
agc gga aat atg acg gcg gtg cac ccg cgt ggc ttc gag att cag gcg	595																
Ser Gly Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala									150					155			160
aag ctg gcc gag gag ttg ggc ctt ttt gat ccg cag tgg gtg tgg cat	643																
Lys Leu Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His									170					175			180
tcc gat cgc acg ccg atc act gcg atc gcg tcg gcg ctg gca acg gcc	691																
Ser Asp Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala									185					190			195
gct ggt gtg gta cgc aaa att gct ggt gac gtg gtg ttt tac tca caa	739																
Ala Gly Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln									200					205			210
acc gag gtc ggc gag ttg cgg gag aaa tcc ccc ggc ggc agc tcc gcg	787																
Thr Glu Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala									215					220			225
atg ccc cac aaa gcc aat ccg gcc gct gcg att gcg tgc gac ggt tac	835																
Met Pro His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr									230					235			240
																	245

gcg cgc cgg gca cct ggc ctt ctt gca acg ctt ttc gac gcc ctc gac 883
 Ala Arg Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp
 250 255 260

tgc cgt ttg cag cgc ggc acc ggc agc tgg cac gcg gag tgg gca acg 931
 Cys Arg Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr
 265 270 275

ctg cgc gag ttg gct gct gtc act cac tca gca gtg agc agg gct gca 979
 Leu Arg Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala
 280 285 290

acc agc atc gat ggc atc acc gtc aac gtt gat gtg atg gca agt cgc 1027
 Thr Ser Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg
 295 300 305

gtc aat gga cca acc ggg cac gcc gaa gat ttg gcg gag cgg gca cta 1075
 Val Asn Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu
 310 315 320 325

gaa att tat gga aaa gga cgc agt taatggatc 1108
 Glu Ile Tyr Gly Lys Gly Arg Ser
 330

<210> 392
 <211> 333
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 392
 Val Glu Ala Ala Leu Ala Val Ala Ala Ala Pro Glu His Ala Ala Met
 1 5 10 15

Ala Lys Ala Thr Ile Asp Ser Tyr Gln Leu Asp Val Glu Glu Leu Ser
 20 25 30

Arg Arg Ala Ala Glu Gly Gly Asn Pro Leu Ile Pro Leu Val Thr Asp
 35 40 45

Leu Lys Ala Ile Asn Pro Ala Gly Ile His Ile Gly Ala Thr Ser Gln
 50 55 60

Asp Ile Ile Asp Ser Ala Leu Met Leu Cys Met Lys Glu Gly Val Gly
 65 70 75 80

Glu Val Val Asp Lys Leu Lys Lys Leu Ala Arg Asp Leu Ala Glu Leu
 85 90 95

Thr Ala Glu His Lys Ala Thr Pro Ile Met Gly Arg Thr Leu Gly Gln
 100 105 110

Ile Ala Thr Pro Thr Thr Phe Gly Ala Leu Thr Gly Gly Trp Leu Val
 115 120 125

Ala Val Asp Asn Ala Ala Arg Ala Leu Glu Ala Leu Glu Phe Pro Val
 130 135 140

Ser Tyr Gly Gly Ala Ser Gly Asn Met Thr Ala Val His Pro Arg Gly
 145 150 155 160

```
<210> 393
<211> 1218
<212> DNA
<213> Corynebacterium glutamicum
```

```

<400> 393
cagtggttgca tcatctagaa atcgattaat taaaccgggc acctgattaa cattggggctg 60

cccggtttct tcctattaca agcgaaaggc aacgtgcccc atg agc gca gtg cag 115
Met Ser Ala Val Gln
1 5

att ttc aac acc gtc cac gtc aat gga tct tcc ccc tat gat gtc cac 163
Ile Phe Asn Thr Val His Val Asn Gly Ser Ser Pro Tyr Asp Val His
10 15 20

att ggt tcc ggc ctc aac gag ctc att gtt cag cgc gca gcg gaa tca 211
Ile Gly Ser Gly Leu Asn Glu Leu Ile Val Gln Arg Ala Ala Glu Ser
25 30 35

ggc gcg gag cag gta gcg att ttg cac cag ccc agc atg gat gac att 259

```


Gly	Ala	Glu	Gln	Val	Ala	Ile	Leu	His	Gln	Pro	Ser	Met	Asp	Asp	Ile		
	40						45					50					
gca	tcc	gag	ttg	gat	gca	gca	cta	gtc	gct	gct	ggg	ttg	aag	gtc	ctg	307	
Ala	Ser	Glu	Leu	Asp	Ala	Ala	Leu	Val	Ala	Ala	Gly	Leu	Lys	Val	Leu		
	55					60					65						
cac	ctt	aat	gtt	ccc	gat	gcg	gaa	aac	ggc	aag	tcc	ttg	gaa	gta	gcg	355	
His	Leu	Asn	Val	Pro	Asp	Ala	Glu	Asn	Gly	Lys	Ser	Leu	Glu	Val	Ala		
	70				75				80						85		
ggg	cag	tgc	tgg	gat	gaa	ttg	ggg	ggc	gca	gca	ttc	ggc	cgc	cgc	gat	403	
Gly	Gln	Cys	Trp	Asp	Glu	Leu	Gly	Gly	Ala	Ala	Phe	Gly	Arg	Arg	Asp		
				90					95					100			
atc	gtc	atc	gga	ctt	ggg	ggc	ggg	gct	gcc	aca	gat	ctc	gcg	gga	ttc	451	
Ile	Val	Ile	Gly	Leu	Gly	Gly	Gly	Ala	Ala	Thr	Asp	Leu	Ala	Gly	Phe		
			105					110						115			
gtc	gct	gct	gca	tgg	atg	cgt	ggc	gtg	cgc	gtc	att	cag	gtt	cca	acc	499	
Val	Ala	Ala	Ala	Trp	Met	Arg	Gly	Val	Arg	Val	Ile	Gln	Val	Pro	Thr		
		120					125					130					
acc	ttg	ttg	gcc	atg	gtg	gac	gct	gcg	gtg	ggc	ggc	aag	act	ggc	atc	547	
Thr	Leu	Leu	Ala	Met	Val	Asp	Ala	Ala	Val	Gly	Gly	Lys	Thr	Gly	Ile		
	135					140					145						
aat	acc	gcc	gca	ggc	aag	aac	ctt	gtg	ggc	gcg	ttc	cac	gag	cct	gac	595	
Asn	Thr	Ala	Ala	Gly	Lys	Asn	Leu	Val	Gly	Ala	Phe	His	Glu	Pro	Asp		
	150				155					160					165		
gca	gta	ttc	att	gac	acc	gat	cgc	cta	gcc	acc	ctg	cct	gac	gcg	gaa	643	
Ala	Val	Phe	Ile	Asp	Thr	Asp	Arg	Leu	Ala	Thr	Leu	Pro	Asp	Ala	Glu		
				170					175					180			
atc	atc	gcg	gga	tcc	gcc	gaa	atc	atc	aaa	act	ggg	ttc	atc	gcc	gac	691	
Ile	Ile	Ala	Gly	Ser	Ala	Glu	Ile	Ile	Lys	Thr	Gly	Phe	Ile	Ala	Asp		
		185					190						195				
cca	gaa	atc	ctg	cgc	ctt	tac	gaa	act	gat	ccc	gca	gcc	tgc	ctg	aag	739	
Pro	Glu	Ile	Leu	Arg	Leu	Tyr	Glu	Thr	Asp	Pro	Ala	Ala	Cys	Leu	Lys		
		200					205					210					
aaa	gaa	gtc	gaa	ggc	tcc	cac	cta	cct	gaa	ctg	att	tgg	cgc	tcc	gtc	787	
Lys	Glu	Val	Glu	Gly	Ser	His	Leu	Pro	Glu	Leu	Ile	Trp	Arg	Ser	Val		
	215					220					225						
acc	gtc	aag	ggc	tcc	gtg	gtc	ggc	caa	gac	ctc	aaa	gaa	tct	agc	ctg	835	
Thr	Val	Lys	Gly	Ser	Val	Val	Gly	Gln	Asp	Leu	Lys	Glu	Ser	Ser	Leu		
	230				235					240					245		
cgc	gaa	atc	ctc	aac	tac	gga	cac	acc	ttt	gcc	cac	gcc	gtc	gaa	ctc	883	
Arg	Glu	Ile	Leu	Asn	Tyr	Gly	His	Thr	Phe	Ala	His	Ala	Val	Glu	Leu		
				250					255					260			
cgc	gaa	aac	ttc	cgc	tgg	cgc	cac	ggc	aat	gcc	gtt	gca	gtg	ggc	atg	931	
Arg	Glu	Asn	Phe	Arg	Trp	Arg	His	Gly	Asn	Ala	Val	Ala	Val	Gly	Met		
		265						270				275					
atg	ttc	atc	gcc	aac	ctc	tcc	cac	aag	ctc	ggg	ctt	atc	gac	gcg	ccc	979	
Met	Phe	Ile	Ala	Asn	Leu	Ser	His	Lys	Leu	Gly	Leu	Ile	Asp	Ala	Pro		

280	285	290	
ctc ctc gag cgc cac cgc tca atc ctg gcg gcc atc ggt ctg ccc act			1027
Leu Leu Glu Arg His Arg Ser Ile Leu Ala Ala Ile Gly Leu Pro Thr			
295	300	305	
tcc tac gaa ggc gga gcc ttc gac gag ctt tac gac ggt atg acc cgc			1075
Ser Tyr Glu Gly Gly Ala Phe Asp Glu Leu Tyr Asp Gly Met Thr Arg			
310	315	320	325
gac aag aaa aac cgc gac ggc aac atc cgc ttc gtc gca ctg acc gcc			1123
Asp Lys Lys Asn Arg Asp Gly Asn Ile Arg Phe Val Ala Leu Thr Ala			
	330	335	340
gtg ggc gag gtt acc cgc att gag ggg ccc tca aaa caa gat tta cag			1171
Val Gly Glu Val Thr Arg Ile Glu Gly Pro Ser Lys Gln Asp Leu Gln			
	345	350	355
agt gct tat gag gca atc agc cac taagtgttga gtaatctact agt			1218
Ser Ala Tyr Glu Ala Ile Ser His			
	360	365	

<210> 394

<211> 365

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met Ser Ala Val Gln Ile Phe Asn Thr Val His Val Asn Gly Ser Ser			
1	5	10	15
Pro Tyr Asp Val His Ile Gly Ser Gly Leu Asn Glu Leu Ile Val Gln			
	20	25	30
Arg Ala Ala Glu Ser Gly Ala Glu Gln Val Ala Ile Leu His Gln Pro			
	35	40	45
Ser Met Asp Asp Ile Ala Ser Glu Leu Asp Ala Ala Leu Val Ala Ala			
	50	55	60
Gly Leu Lys Val Leu His Leu Asn Val Pro Asp Ala Glu Asn Gly Lys			
	65	70	75
Ser Leu Glu Val Ala Gly Gln Cys Trp Asp Glu Leu Gly Gly Ala Ala			
	85	90	95
Phe Gly Arg Arg Asp Ile Val Ile Gly Leu Gly Gly Gly Ala Ala Thr			
	100	105	110
Asp Leu Ala Gly Phe Val Ala Ala Ala Trp Met Arg Gly Val Arg Val			
	115	120	125
Ile Gln Val Pro Thr Thr Leu Leu Ala Met Val Asp Ala Ala Val Gly			
	130	135	140
Gly Lys Thr Gly Ile Asn Thr Ala Ala Gly Lys Asn Leu Val Gly Ala			
	145	150	155
Phe His Glu Pro Asp Ala Val Phe Ile Asp Thr Asp Arg Leu Ala Thr			
	165	170	175

Leu Pro Asp Ala Glu Ile Ile Ala Gly Ser Ala Glu Ile Ile Lys Thr
 180 185 190
 Gly Phe Ile Ala Asp Pro Glu Ile Leu Arg Leu Tyr Glu Thr Asp Pro
 195 200 205
 Ala Ala Cys Leu Lys Lys Glu Val Glu Gly Ser His Leu Pro Glu Leu
 210 215 220
 Ile Trp Arg Ser Val Thr Val Lys Gly Ser Val Val Gly Gln Asp Leu
 225 230 235 240
 Lys Glu Ser Ser Leu Arg Glu Ile Leu Asn Tyr Gly His Thr Phe Ala
 245 250 255
 His Ala Val Glu Leu Arg Glu Asn Phe Arg Trp Arg His Gly Asn Ala
 260 265 270
 Val Ala Val Gly Met Met Phe Ile Ala Asn Leu Ser His Lys Leu Gly
 275 280 285
 Leu Ile Asp Ala Pro Leu Leu Glu Arg His Arg Ser Ile Leu Ala Ala
 290 295 300
 Ile Gly Leu Pro Thr Ser Tyr Glu Gly Gly Ala Phe Asp Glu Leu Tyr
 305 310 315 320
 Asp Gly Met Thr Arg Asp Lys Lys Asn Arg Asp Gly Asn Ile Arg Phe
 325 330 335
 Val Ala Leu Thr Ala Val Gly Glu Val Thr Arg Ile Glu Gly Pro Ser
 340 345 350
 Lys Gln Asp Leu Gln Ser Ala Tyr Glu Ala Ile Ser His
 355 360 365

<210> 395
 <211> 1977
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1954)
 <223> RXN02508

<400> 395
 tgcacactgc tgggtggtgag gccgcagacc tggcagccgc aagcaaagcc tccgaggccc 60
 aactcgcggc tcagtaaaac caaaaggaat ctttgaccac atg cgt aca tcc att 115
 Met Arg Thr Ser Ile
 1 5
 gcc act gtt tgt ttg tcc gga act ctt gct gaa aag ctg cgc gca gct 163
 Ala Thr Val Cys Leu Ser Gly Thr Leu Ala Glu Lys Leu Arg Ala Ala
 10 15 20
 gca gat gct gga ttt gat ggt gtg gaa atc ttc gag cag gac ttg gtg 211
 Ala Asp Ala Gly Phe Asp Gly Val Glu Ile Phe Glu Gln Asp Leu Val

520

cca agc gct ctt gaa ctg cgt gca ctt cct gag gtc gcg gaa cct gag	979
Pro Ser Ala Leu Glu Leu Arg Ala Leu Pro Glu Val Ala Glu Pro Glu	
280 285 290	
ggt gtt gat ttc att gag atc gcc act gga cgt ttg ggt gag acc att	1027
Gly Val Asp Phe Ile Glu Ile Ala Thr Gly Arg Leu Gly Glu Thr Ile	
295 300 305	
cgg gtt ctt cat caa ttg ggt ttc cgc ttg ggt ggt cat cac tgc agt	1075
Arg Val Leu His Gln Leu Gly Phe Arg Leu Gly Gly His His Cys Ser	
310 315 320 325	
aag cag gat tac cag gta tgg acc cag ggc gat gtg cgc att gtg gtg	1123
Lys Gln Asp Tyr Gln Val Trp Thr Gln Gly Asp Val Arg Ile Val Val	
330 335 340	
tgt gat cgt ggg gtc acc ggg gct cca acc acg atc tct gcg atg ggc	1171
Cys Asp Arg Gly Val Thr Gly Ala Pro Thr Thr Ile Ser Ala Met Gly	
345 350 355	
ttt gac acc ccc gat cca gaa gct gct cat gcc cgt gcg gaa ttg ctg	1219
Phe Asp Thr Pro Asp Pro Glu Ala Ala His Ala Arg Ala Glu Leu Leu	
360 365 370	
cgg gct cag aca att gat cgt ccc cac atc gag ggc gaa gtt gac cta	1267
Arg Ala Gln Thr Ile Asp Arg Pro His Ile Glu Gly Glu Val Asp Leu	
375 380 385	
aaa ggt gtg tac gca ccg gat ggg gtg gag ctg ttt ttc gcg ggg ccg	1315
Lys Gly Val Tyr Ala Pro Asp Gly Val Glu Leu Phe Phe Ala Gly Pro	
390 395 400 405	
agc ccc gat gga atg ccc gag tgg ctg ccg gaa ttc ggc gtc gaa aag	1363
Ser Pro Asp Gly Met Pro Glu Trp Leu Pro Glu Phe Gly Val Glu Lys	
410 415 420	
caa gaa gct ggt ctc att gaa gcc atc gac cac gtc aat ttc gcc cag	1411
Gln Glu Ala Gly Leu Ile Glu Ala Ile Asp His Val Asn Phe Ala Gln	
425 430 435	
ccg tgg caa cat ttt gat gag gca gtg ctg ttt tac acc gcg ctg atg	1459
Pro Trp Gln His Phe Asp Glu Ala Val Leu Phe Tyr Thr Ala Leu Met	
440 445 450	
gcg ttg gag act gtg cgt gag gat gag ttc ccg agc cca att ggt ttg	1507
Ala Leu Glu Thr Val Arg Glu Asp Glu Phe Pro Ser Pro Ile Gly Leu	
455 460 465	
gtg cgc aat cag gtg atg cgt tgc ccg aat gat gcg gtg cgg ttg ctg	1555
Val Arg Asn Gln Val Met Arg Ser Pro Asn Asp Ala Val Arg Leu Leu	
470 475 480 485	
ctc agc gtg gcg ccc gag gac ggt gag cag gga gat ttc ctc aac gcg	1603
Leu Ser Val Ala Pro Glu Asp Gly Glu Gln Gly Asp Phe Leu Asn Ala	
490 495 500	
gcc tac ccg gag cac att gcg ttg gcc acg gcg gac atc gtg gcg gtg	1651
Ala Tyr Pro Glu His Ile Ala Leu Ala Thr Ala Asp Ile Val Ala Val	
505 510 515	

gct gaa cgt gcg cgc aaa cga ggc ctg gat ttc ttg ccc gtc cca gag 1699
 Ala Glu Arg Ala Arg Lys Arg Gly Leu Asp Phe Leu Pro Val Pro Glu
 520 525 530

aat tac tac gac gat gtg cag gcg cgt ttt gat ttg ccg cag gaa ttc 1747
 Asn Tyr Tyr Asp Asp Val Gln Ala Arg Phe Asp Leu Pro Gln Glu Phe
 535 540 545

ttg gac aca ctc aag gaa aac cac ctg ctt tac gac cgc gac gag aac 1795
 Leu Asp Thr Leu Lys Glu Asn His Leu Leu Tyr Asp Arg Asp Glu Asn
 550 555 560 565

ggc gaa ttc ctc cac ttt tac acc cgc acg ttg ggc acg ctg ttc ttc 1843
 Gly Glu Phe Leu His Phe Tyr Thr Arg Thr Leu Gly Thr Leu Phe Phe
 570 575 580

gaa gtg gtg gaa cgc cgc ggc ggt ttt gca ggt tgg ggc gaa aca aac 1891
 Glu Val Val Glu Arg Arg Gly Gly Phe Ala Gly Trp Gly Glu Thr Asn
 585 590 595

gct ccg gtg cgg ttg gcg gcg cag tat cgt gag gtg cgg gac ctc gag 1939
 Ala Pro Val Arg Leu Ala Ala Gln Tyr Arg Glu Val Arg Asp Leu Glu
 600 605 610

cgg gga atc cca aac tagcatcccg aactagcccc cca 1977
 Arg Gly Ile Pro Asn
 615

<210> 396

<211> 618

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Arg Thr Ser Ile Ala Thr Val Cys Leu Ser Gly Thr Leu Ala Glu
 1 5 10 15

Lys Leu Arg Ala Ala Ala Asp Ala Gly Phe Asp Gly Val Glu Ile Phe
 20 25 30

Glu Gln Asp Leu Val Val Ser Pro His Ser Ala Glu Gln Ile Arg Gln
 35 40 45

Arg Ala Gln Asp Leu Gly Leu Thr Leu Asp Leu Phe Gln Pro Phe Arg
 50 55 60

Asp Phe Glu Gly Val Glu Glu Gln Phe Leu Lys Asn Leu His Arg
 65 70 75 80

Leu Glu Glu Lys Phe Lys Leu Met Asn Arg Leu Gly Ile Glu Met Ile
 85 90 95

Leu Leu Cys Ser Asn Val Gly Thr Ala Thr Ile Asn Asp Asp Asp Leu
 100 105 110

Phe Val Glu Gln Leu His Arg Ala Ala Asp Leu Ala Glu Lys Tyr Asn
 115 120 125

Val Lys Ile Ala Tyr Glu Ala Leu Ala Trp Gly Lys Phe Val Asn Asp
 130 135 140

Phe Glu His Ala His Ala Leu Val Glu Lys Val Asn His Lys Ala Leu
 145 150 155 160
 Gly Thr Cys Leu Asp Thr Phe His Ile Leu Ser Arg Gly Trp Glu Thr
 165 170 175
 Asp Glu Val Glu Asn Ile Pro Ala Glu Lys Ile Phe Phe Val Gln Leu
 180 185 190
 Ala Asp Ala Pro Lys Leu Ser Met Asp Ile Leu Ser Trp Ser Arg His
 195 200 205
 His Arg Val Phe Pro Gly Glu Gly Asp Phe Asp Leu Val Lys Phe Met
 210 215 220
 Val His Leu Ala Lys Thr Gly Tyr Asp Gly Pro Ile Ser Leu Glu Ile
 225 230 235 240
 Phe Asn Asp Ser Phe Arg Lys Ala Glu Val Gly Arg Thr Ala Ile Asp
 245 250 255
 Gly Leu Arg Ser Leu Arg Trp Leu Glu Asp Gln Thr Trp His Ala Leu
 260 265 270
 Asn Ala Glu Asp Arg Pro Ser Ala Leu Glu Leu Arg Ala Leu Pro Glu
 275 280 285
 Val Ala Glu Pro Glu Gly Val Asp Phe Ile Glu Ile Ala Thr Gly Arg
 290 295 300
 Leu Gly Glu Thr Ile Arg Val Leu His Gln Leu Gly Phe Arg Leu Gly
 305 310 315 320
 Gly His His Cys Ser Lys Gln Asp Tyr Gln Val Trp Thr Gln Gly Asp
 325 330 335
 Val Arg Ile Val Val Cys Asp Arg Gly Val Thr Gly Ala Pro Thr Thr
 340 345 350
 Ile Ser Ala Met Gly Phe Asp Thr Pro Asp Pro Glu Ala Ala His Ala
 355 360 365
 Arg Ala Glu Leu Leu Arg Ala Gln Thr Ile Asp Arg Pro His Ile Glu
 370 375 380
 Gly Glu Val Asp Leu Lys Gly Val Tyr Ala Pro Asp Gly Val Glu Leu
 385 390 395 400
 Phe Phe Ala Gly Pro Ser Pro Asp Gly Met Pro Glu Trp Leu Pro Glu
 405 410 415
 Phe Gly Val Glu Lys Gln Glu Ala Gly Leu Ile Glu Ala Ile Asp His
 420 425 430
 Val Asn Phe Ala Gln Pro Trp Gln His Phe Asp Glu Ala Val Leu Phe
 435 440 445
 Tyr Thr Ala Leu Met Ala Leu Glu Thr Val Arg Glu Asp Glu Phe Pro
 450 455 460

Ser Pro Ile Gly Leu Val Arg Asn Gln Val Met Arg Ser Pro Asn Asp
 465 470 475 480

Ala Val Arg Leu Leu Leu Ser Val Ala Pro Glu Asp Gly Glu Gln Gly
 485 490 495

Asp Phe Leu Asn Ala Ala Tyr Pro Glu His Ile Ala Leu Ala Thr Ala
 500 505 510

Asp Ile Val Ala Val Ala Glu Arg Ala Arg Lys Arg Gly Leu Asp Phe
 515 520 525

Leu Pro Val Pro Glu Asn Tyr Tyr Asp Asp Val Gln Ala Arg Phe Asp
 530 535 540

Leu Pro Gln Glu Phe Leu Asp Thr Leu Lys Glu Asn His Leu Leu Tyr
 545 550 555 560

Asp Arg Asp Glu Asn Gly Glu Phe Leu His Phe Tyr Thr Arg Thr Leu
 565 570 575

Gly Thr Leu Phe Phe Glu Val Val Glu Arg Arg Gly Gly Phe Ala Gly
 580 585 590

Trp Gly Glu Thr Asn Ala Pro Val Arg Leu Ala Ala Gln Tyr Arg Glu
 595 600 605

Val Arg Asp Leu Glu Arg Gly Ile Pro Asn
 610 615

<210> 397
 <211> 470
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(447)
 <223> RXN02839

<400> 397
 tgt gtg gtg aat gat tat gct gac cgc aag ttt gat ggt cat gtt aag 48
 Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
 1 5 10 15

cgc acg gcg aac cga cca ctt ccc agc ggc gcg gta aca gag aaa gag 96
 Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30

gcg cgc gcg ctg ttt gtc gtg ctg gta ctg att tcg ttt tta ctg gtg 144
 Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45

ctg acg ctg aat acg atg acc att ctg ttg tcg att gcc gcg cta gcg 192
 Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60

ctg gcg tgg gtg tac ccg ttt atg aag cgg tat acc cat cta ccg caa 240
 Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80

gtg gtg ctg ggc gcg gcg ttt ggc tgg tgc att cca atg gct ttt gcc 288
 Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

gct gtg agt gag tgc gtg cca ttg agt tgc tgg tta atg ttc ctc gcc 336
 Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac 384
 Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

cgc gat gat gat gtg aag att ggc att aaa tcc acg gca atc ctg ttg 432
 Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
 130 135 140

gcc aat acg ata aat tgatattggg attttgcaga ttg 470
 Ala Asn Thr Ile Asn
 145

<210> 398

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
 1 5 10 15

Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30

Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45

Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60

Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80

Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
 130 135 140

Ala Asn Thr Ile Asn
 145

<210> 399

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXN00639

<400> 399

```

agtgttggtta tcgagttcag ccgatcacaa agatTTTTcc gctaggcagt gatccgactc 60
gcaccccccta cttcaccccc aaagtctcta ggagtatgac atg act tca gct gaa 115
                                         Met Thr Ser Ala Glu
                                         1                               5

cag atc gtt gat cca aca gcc cac gat tcg ggc aac aag gca act gac 163
Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp
                        10                        15                        20

aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca 211
Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala
                        25                        30                        35

aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac 259
Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His
                        40                        45                        50

aag cac gaa gtc acc tac gaa gag tac gca gtg ctc aag cag tgg atg 307
Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val Leu Lys Gln Trp Met
                        55                        60                        65

atc gac gtt gga gaa tac ggc gag tgg cca ctg tgg ttg gac gtt ttc 355
Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu Trp Leu Asp Val Phe
                        70                        75                        80                        85

gtt gag cat gag atc gaa gag atc aac tac aac cgc cac gac tac acc 403
Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn Arg His Asp Tyr Thr
                        90                        95                        100

gga acc aag ggt tcc atc gaa ggc cct tat tac gta gag aac tct ccg 451
Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr Val Glu Asn Ser Pro
                        105                        110                        115

aag ctc cct tgg gat gct gaa atg cca atg cgt gac aag gac cgc gca 499
Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg Asp Lys Asp Arg Ala
                        120                        125                        130

tgc acc cca ctg atc ttc gag ggg cag gtt act gac ctc gac ggc aac 547
Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr Asp Leu Asp Gly Asn
                        135                        140                        145

ggt ctt gat gga gca gaa gtt gag ctc tgg cac gca gat gag gac gga 595
Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His Ala Asp Glu Asp Gly
                        150                        155                        160                        165

tac tac tcc cag ttc gcg cct gga atc cca gag tgg aac ctg cgt ggc 643
Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu Trp Asn Leu Arg Gly
                        170                        175                        180

acc atc gtt acc gat gag gaa ggc cgc tac aag atc aag acc ctg cag 691
Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys Ile Lys Thr Leu Gln

```

```
<210> 400
<211> 285
<212> PRT
<213> Corynebacterium glutamicum
```

527

145				150				155				160			
Ala	Asp	Glu	Asp	Gly 165	Tyr	Tyr	Ser	Gln	Phe 170	Ala	Pro	Gly	Ile	Pro 175	Glu
Trp	Asn	Leu	Arg 180	Gly	Thr	Ile	Val	Thr 185	Asp	Glu	Glu	Gly	Arg 190	Tyr	Lys
Ile	Lys	Thr 195	Leu	Gln	Pro	Ala	Pro 200	Tyr	Gln	Ile	Pro	His 205	Asp	Gly	Pro
Thr	Gly 210	Trp	Phe	Ile	Glu	Ser 215	Tyr	Gly	Gly	His	Pro 220	Trp	Arg	Pro	Ala
His 225	Leu	His	Leu	Arg 230	Val	Ser	His	Pro	Gly	Tyr 235	Arg	Thr	Ile	Thr	Thr 240
Gln	Leu	Tyr	Phe	Glu 245	Gly	Gly	Glu	Trp	Val 250	Glu	Asn	Asp	Val	Ala 255	Thr
Ala	Val	Lys	Pro 260	Glu	Leu	Val	Leu	His 265	Pro	Glu	Thr	Gly	Glu 270	Asp	Gly
Asn	His	Val 275	His	Tyr	Pro	Phe	Val 280	Leu	Asp	Lys	Glu	Asp 285			

```
<210> 401
<211> 780
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(757)
<223> RXN02530
```

<400> 401																	
gaggctgagc tttccgtcaa acaacatctt cccaatgtgg atgaaatgac tgtgaccatc																60	
accccttcca aaccttgagt cccgtgatac aattgttgat																	115
												atg	tca	aca	aat	tat	
												Met	Ser	Thr	Asn	Tyr	
												1				5	
gaa gca atc atc att gga gca ggt cag gct gga ctc gcg gcg gcg cat																163	
Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly Leu Ala Ala Ala His																	
										10		15		20			
gaa ctt tcc cgc cgc ggt ttc act ccc gga aaa gat ttt ctc gtc ctc																211	
Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys Asp Phe Leu Val Leu																	
										25		30		35			
gat tcc aac gac ggg ccc ggt ggc gcc tgg cgg cat agg tgg gat tca																259	
Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg His Arg Trp Asp Ser																	
										40		45		50			
ctc aca tta ggt aaa gcc cac gga atc gcc gat ctc cca ggg ctt ccc																307	
Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp Leu Pro Gly Leu Pro																	
					55		60		65								
atg aat cgc ccc gat ccg aaa act ccg gct tcc aca ttg qtt qct qgt																355	

```

Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser Thr Leu Val Ala Gly
 70                75                80                85
tat tac ggc gct tac gag aac gag ttc tcc ttc gca gtt gtg cgc cca 403
Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe Ala Val Val Arg Pro
                90                95                100

gtc aaa gtc tca cga gtt gag ccc act tcc gag gat cct tcg agc cca 451
Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu Asp Pro Ser Ser Pro
                105                110                115

ttg cgc gtg agc agc gac gat ggt cga gag tgg att acc cgc atg gtt 499
Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp Ile Thr Arg Met Val
                120                125                130

ctt aat gca aca ggt acg tgg aca aac cct tat gtt ccg tac att cct 547
Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr Val Pro Tyr Ile Pro
                135                140                145

ggc atc gat aaa ttc cag ggc aag cag ctc cac acc gtt aat tac cgc 595
Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His Thr Val Asn Tyr Arg
150                155                160                165

aag gcc gag gat ttc aaa ggt aag aaa gtc ctg gtc gtc ggc ggt ggt 643
Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
                170                175                180

ttg agt gct gtg caa ttt ctg ctg gag ttg gaa ggc ttg gcg gaa acc 691
Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu Gly Leu Ala Glu Thr
                185                190                195

acc tgg gcg acg cgt cgt ccg cga act tac gca gcg cga gtt cga cgc 739
Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala Ala Arg Val Arg Arg
                200                205                210

cgg ctg ggg cat tgc ggt tgagcgcgcc gtccgcgaac gca 780
Arg Leu Gly His Cys Gly
215

```

<210> 402

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

```

Met Ser Thr Asn Tyr Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly
 1                5                10                15

Leu Ala Ala Ala His Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys
                20                25                30

Asp Phe Leu Val Leu Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg
                35                40                45

His Arg Trp Asp Ser Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp
                50                55                60

Leu Pro Gly Leu Pro Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser
65                70                75                80

```

Thr Leu Val Ala Gly Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe
85 90 95

Ala Val Val Arg Pro Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu
100 105 110

Asp Pro Ser Ser Pro Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp
115 120 125

Ile Thr Arg Met Val Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr
130 135 140

Val Pro Tyr Ile Pro Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His
145 150 155 160

Thr Val Asn Tyr Arg Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu
165 170 175

Val Val Gly Gly Gly Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu
180 185 190

Gly Leu Ala Glu Thr Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala
195 200 205

Ala Arg Val Arg Arg Arg Leu Gly His Cys Gly
210 215

<210> 403

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXN00434

<400> 403

ccacgcgcca aaccatgcaa gccatcggtcc aaactgagga gaaggctcact gcttctctctgg 60

aattacagga agtccccgtc cgcaccctga agccaggtag gtg ctg gtg aag gtg 115
Val Leu Val Lys Val
1 5

aag cct gcg ggc gtt aac cgt gcg gat ctt ttg cag acg cag gga aat 163
Lys Pro Ala Gly Val Asn Arg Ala Asp Leu Leu Gln Thr Gln Gly Asn
10 15 20

tat cct gtg ccg gcg ggg gct tcg gag att ctc ggg ctg gaa tgt gcg 211
Tyr Pro Val Pro Ala Gly Ala Ser Glu Ile Leu Gly Leu Glu Cys Ala
25 30 35

ggg gtg atc gtg aat gcc ggc gac act ggg caa aca gtg ggt cag gaa 259
Gly Val Ile Val Asn Ala Gly Asp Thr Gly Gln Thr Val Gly Gln Glu
40 45 50

gtc gct tgc ctt ctc act ggc ggt gga tat gcg caa tat gtg gcg gtt 307
Val Ala Cys Leu Leu Thr Gly Gly Gly Tyr Ala Gln Tyr Val Ala Val
55 60 65

ccg gaa ggt cag ttg atg cca att cca gag ggt tac agc ttt gtg gaa	355
Pro Glu Gly Gln Leu Met Pro Ile Pro Glu Gly Tyr Ser Phe Val Glu	
70 75 80 85	
gcg gcc tcg atc gtg gag gtt gcg tgc acg gtg tgg tcg aat atc ggc	403
Ala Ala Ser Ile Val Glu Val Ala Cys Thr Val Trp Ser Asn Ile Gly	
90 95 100	
atg ctg gcg ggc ttg cag aag gag gat act ttc ctt att cat ggt ggc	451
Met Leu Ala Gly Leu Gln Lys Glu Asp Thr Phe Leu Ile His Gly Gly	
105 110 115	
gcg ggc ggt atc gga acg ttt gcc att cag atg ggc aag gct ctg ggt	499
Ala Gly Gly Ile Gly Thr Phe Ala Ile Gln Met Gly Lys Ala Leu Gly	
120 125 130	
gtg acg gtt gcg gtg act gcc ggt tca act gaa aag tta aaa acc tgt	547
Val Thr Val Ala Val Thr Ala Gly Ser Thr Glu Lys Leu Lys Thr Cys	
135 140 145	
aag aac tta ggg gcc gat atc ctc atc aat tac aag gag gaa gat ttc	595
Lys Asn Leu Gly Ala Asp Ile Leu Ile Asn Tyr Lys Glu Glu Asp Phe	
150 155 160 165	
gcc gag gtt ttg aag aac aag gcg gat gtc att ctc gat att att ggt	643
Ala Glu Val Leu Lys Asn Lys Ala Asp Val Ile Leu Asp Ile Ile Gly	
170 175 180	
gcg aag tat ttg tca cag aat gtg aag gcg atg gcc aag gac gcg cac	691
Ala Lys Tyr Leu Ser Gln Asn Val Lys Ala Met Ala Lys Asp Ala His	
185 190 195	
atg gta gtc atc ggg atg cag ggt ggc gtg aaa ggg gag ctg aat ttg	739
Met Val Val Ile Gly Met Gln Gly Gly Val Lys Gly Glu Leu Asn Leu	
200 205 210	
ggt cat ctt ttg gcc aag cga ggc acg att tct gcc act gcg ctg cgt	787
Gly His Leu Leu Ala Lys Arg Gly Thr Ile Ser Ala Thr Ala Leu Arg	
215 220 225	
ggt cgc gat gag gcg gat aag gct cgg att gtc agc agc act gtc gaa	835
Gly Arg Asp Glu Ala Asp Lys Ala Arg Ile Val Ser Ser Thr Val Glu	
230 235 240 245	
aat att tgg ccg ctg ctg caa tcg aag gaa att acc cct cac atc gac	883
Asn Ile Trp Pro Leu Leu Gln Ser Lys Glu Ile Thr Pro His Ile Asp	
250 255 260	
cac acc ttg ccg cta gcc gaa gca gcc gcc gcc ttg cag aaa att caa	931
His Thr Leu Pro Leu Ala Glu Ala Ala Ala Leu Gln Lys Ile Gln	
265 270 275	
gac ggc acc atc acc ggc aag ctc gtg ctt gcg gtt taggcaagcg	977
Asp Gly Thr Ile Thr Gly Lys Leu Val Leu Ala Val	
280 285	
atgccagcac cct	990

<210> 404

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

Val Leu Val Lys Val Lys Pro Ala Gly Val Asn Arg Ala Asp Leu Leu
 1 5 10 15
 Gln Thr Gln Gly Asn Tyr Pro Val Pro Ala Gly Ala Ser Glu Ile Leu
 20 25 30
 Gly Leu Glu Cys Ala Gly Val Ile Val Asn Ala Gly Asp Thr Gly Gln
 35 40 45
 Thr Val Gly Gln Glu Val Ala Cys Leu Leu Thr Gly Gly Gly Tyr Ala
 50 55 60
 Gln Tyr Val Ala Val Pro Glu Gly Gln Leu Met Pro Ile Pro Glu Gly
 65 70 75 80
 Tyr Ser Phe Val Glu Ala Ala Ser Ile Val Glu Val Ala Cys Thr Val
 85 90 95
 Trp Ser Asn Ile Gly Met Leu Ala Gly Leu Gln Lys Glu Asp Thr Phe
 100 105 110
 Leu Ile His Gly Gly Ala Gly Gly Ile Gly Thr Phe Ala Ile Gln Met
 115 120 125
 Gly Lys Ala Leu Gly Val Thr Val Ala Val Thr Ala Gly Ser Thr Glu
 130 135 140
 Lys Leu Lys Thr Cys Lys Asn Leu Gly Ala Asp Ile Leu Ile Asn Tyr
 145 150 155 160
 Lys Glu Glu Asp Phe Ala Glu Val Leu Lys Asn Lys Ala Asp Val Ile
 165 170 175
 Leu Asp Ile Ile Gly Ala Lys Tyr Leu Ser Gln Asn Val Lys Ala Met
 180 185 190
 Ala Lys Asp Ala His Met Val Val Ile Gly Met Gln Gly Gly Val Lys
 195 200 205
 Gly Glu Leu Asn Leu Gly His Leu Leu Ala Lys Arg Gly Thr Ile Ser
 210 215 220
 Ala Thr Ala Leu Arg Gly Arg Asp Glu Ala Asp Lys Ala Arg Ile Val
 225 230 235 240
 Ser Ser Thr Val Glu Asn Ile Trp Pro Leu Leu Gln Ser Lys Glu Ile
 245 250 255
 Thr Pro His Ile Asp His Thr Leu Pro Leu Ala Glu Ala Ala Ala Ala
 260 265 270
 Leu Gln Lys Ile Gln Asp Gly Thr Ile Thr Gly Lys Leu Val Leu Ala
 275 280 285
 Val

gct caa aac atc agc ggc gtc gtt tcc act gag acc cca ggc tgg gaa 691
 Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu Thr Pro Gly Trp Glu
 185 190 195

 aag cag gtc gaa gac atc acc ggt ggc gca agc atc gcc gtc gca ctt 739
 Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser Ile Ala Val Ala Leu
 200 205 210

 gat tcc gtc ggt gga tcc tcc gca gct gac ctg gtg aaa ctg ctt ggc 787
 Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu Val Lys Leu Leu Gly
 215 220 225

 gaa ggc ggc acc ctc gtc tcc ttc ggc gcc atg ggc aac cca atc atg 835
 Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met Gly Asn Pro Ile Met
 230 235 240 245

 gaa atc cca tcc ggc ccc gtc atc ttc aag cac atc acc gtc aag ggc 883
 Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His Ile Thr Val Lys Gly
 250 255 260

 ttc tgg gga agc aaa gtc agc cgc gaa atg cca gca gag aag aaa acc 931
 Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro Ala Glu Lys Lys Thr
 265 270 275

 cag ttg ttc ggc gag ctc att gcg cgc ata ctt gat gga aca ttg acc 979
 Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu Asp Gly Thr Leu Thr
 280 285 290

 ctt cca gtt gat tcc acc ttt gat gcc gct gac atc gtc tcg gcc gtg 1027
 Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp Ile Val Ser Ala Val
 295 300 305

 cgc gcc tcc agc gag cct ggc cgt gcc gga aaa gtg ctc att cgt ttc 1075
 Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys Val Leu Ile Arg Phe
 310 315 320 325

 taaacgttta aggcccatta gac 1098

<210> 406

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

Met Arg Ala Ile Thr His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu
 1 5 10 15

 Gln Ile Thr Glu Lys Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg
 20 25 30

 Ile Gln Val Thr Leu Ala Thr Ile His Asn His Asp Leu Trp Thr Val
 35 40 45

 Lys Gly Ser Tyr Gly Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr
 50 55 60

 Glu Ala Val Gly Ile Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu
 65 70 75 80

Gln Val Gly Gln Arg Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala
 85 90 95
 Glu Tyr Ala Leu Val Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln
 100 105 110
 Leu Ser Asp Glu Ser Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala
 115 120 125
 Ile Ser Leu Leu Asp Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile
 130 135 140
 Gln Asn Ser Ala Asn Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala
 145 150 155 160
 Glu Ser Arg Gly Ile His Val Val Gly Leu Val Arg Arg Asp Ala Gly
 165 170 175
 Val Gln Glu Leu Ala Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu
 180 185 190
 Thr Pro Gly Trp Glu Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser
 195 200 205
 Ile Ala Val Ala Leu Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu
 210 215 220
 Val Lys Leu Leu Gly Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met
 225 230 235 240
 Gly Asn Pro Ile Met Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His
 245 250 255
 Ile Thr Val Lys Gly Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro
 260 265 270
 Ala Glu Lys Lys Thr Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu
 275 280 285
 Asp Gly Thr Leu Thr Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp
 290 295 300
 Ile Val Ser Ala Val Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys
 305 310 315 320
 Val Leu Ile Arg Phe
 325

<210> 407

<211> 1041

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1018)

<223> RXN01842

<400> 407

cacgtcatgg tctcgcggtg atcatcttcc taccgtgaca ggcaaggccg caaacggccg 60

tgaccacagg aaagaaattc acgaggagag gaagcacacg atg tcg aag gta tac	115
Met Ser Lys Val Tyr	5
1	
gtg tcc aac gag tac ggc ggc ccg gaa aac cag gaa ctg atc acc cgc	163
Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln Glu Leu Ile Thr Arg	20
10	15
aac acc ccc cag cca ggc ccg gga gaa ctc ggg gtc aag gtc cac gcg	211
Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly Val Lys Val His Ala	35
25	30
gcc ggg gtc aac ccg ctt gat tgg aag gtc cgt tcc ggg gtt gcc gga	259
Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg Ser Gly Val Ala Gly	50
40	45
acc ccg cga gag ctt ccg gca ccc ctg ggc gag gag gcc tcc ggg atc	307
Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu Ala Ser Gly Ile	65
55	60
gtc acc gcc gtt gga gac ggt gtg gag ggc ttc gcg gtc ggc gat ccg	355
Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe Ala Val Gly Asp Pro	85
70	75
gtg ctc ggc ctg gtg gcc ccc ggc gtc ggc gga tat gcc gag gac acc	403
Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly Tyr Ala Glu Asp Thr	100
90	95
ctg ctg gtg gca gag agt acc gtg cta aag ccg gag gag atc tcg ttc	451
Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro Glu Glu Ile Ser Phe	115
105	110
acc gac gcc gcc gcg atc ccg gtc gct ggg gcg agc gcc tac gcc ggc	499
Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala Ser Ala Tyr Ala Gly	130
120	125
act cac cag gtc gag ctt gaa cca ggc cag tcg ttg ctg atc aat ggg	547
Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser Leu Leu Ile Asn Gly	145
135	140
gcc ggt ggt ggg gtc ggg ctg atg gcc gcg cag atc gga cgg gtc cac	595
Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln Ile Gly Arg Val His	165
150	155
aag ttc cag gtc gtc ggc gtt gac cac gag gac aag cgc gag ctc atc	643
Lys Phe Gln Val Val Gly Val Asp His Glu Asp Lys Arg Glu Leu Ile	180
170	175
gaa tcc acc ggt gct atc ttc gtc gcc acc ggc gac gcc gtc gcg gag	691
Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly Asp Ala Val Ala Glu	195
185	190
cag gtg cgt gcg ctg ctc cct gac ggt gtg gac gta gtc ttc gac cta	739
Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp Val Val Phe Asp Leu	210
200	205
gtc ggc ggg gag gcg ttg cgg gtg gtt gct ccc tta gcg aag aat ccg	787
Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro Leu Ala Lys Asn Pro	225
215	220

gcg cac gtg atc tcg gcg gct gat gct gcc acc gtg gga gaa ctc ggt 835
 Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr Val Gly Glu Leu Gly
 230 235 240 245

gga cag gtg ctg cgc cgc acc ccg gaa atg gtc gga cag atc acc ggg 883
 Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val Gly Gln Ile Thr Gly
 250 255 260

gtg gtc cag tac ggg ctg gtc gac ccg aag gtc gat acg acc tac ccg 931
 Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val Asp Thr Thr Tyr Pro
 265 270 275

ctg gaa cag gcc ggt aag gcc ctg gcc cac gtt gag cag ggc cac gcc 979
 Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val Glu Gln Gly His Ala
 280 285 290

cgc ggc aag atc gtc ctc gag ctc atc acc tcc cag gac taaccagaca 1028
 Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser Gln Asp
 295 300 305

acgcggtgac ctc 1041

<210> 408
 <211> 306
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 408
 Met Ser Lys Val Tyr Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln
 1 5 10 15

Glu Leu Ile Thr Arg Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly
 20 25 30

Val Lys Val His Ala Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg
 35 40 45

Ser Gly Val Ala Gly Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu
 50 55 60

Glu Ala Ser Gly Ile Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe
 65 70 75 80

Ala Val Gly Asp Pro Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly
 85 90 95

Tyr Ala Glu Asp Thr Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro
 100 105 110

Glu Glu Ile Ser Phe Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala
 115 120 125

Ser Ala Tyr Ala Gly Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser
 130 135 140

Leu Leu Ile Asn Gly Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln
 145 150 155 160

Ile Gly Arg Val His Lys Phe Gln Val Val Gly Val Asp His Glu Asp
 165 170 175

Lys Arg Glu Leu Ile Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly
 180 185 190
 Asp Ala Val Ala Glu Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp
 195 200 205
 Val Val Phe Asp Leu Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro
 210 215 220
 Leu Ala Lys Asn Pro Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr
 225 230 235 240
 Val Gly Glu Leu Gly Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val
 245 250 255
 Gly Gln Ile Thr Gly Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val
 260 265 270
 Asp Thr Thr Tyr Pro Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val
 275 280 285
 Glu Gln Gly His Ala Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser
 290 295 300
 Gln Asp
 305

<210> 409
 <211> 1614
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1591)
 <223> RXN00641

<400> 409
 tgcggaattg ctcgcaaattg tcacacaccg cttcaaagca aaaacgaaaa cgacatcgcg 60

gtggcaatac caacttcttt tcactctctt ggaggttcac atg tcc aca cca gtt 115
 Met Ser Thr Pro Val
 1 5

tca aat ttg gca agc gtt cag aaa act ctg gac cat gcg ctt gag gac 163
 Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp His Ala Leu Glu Asp
 10 15 20

cgc cct gaa gag gga atc gtc cgc gtc aac cgc aac atc ttc act gac 211
 Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg Asn Ile Phe Thr Asp
 25 30 35

cct gag atc ttc gag ctg gag atg cgc cac atc ttc gaa ggc atc tgg 259
 Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile Phe Glu Gly Ile Trp
 40 45 50

atg gac atg gct cac gag tcc cag atc cct aac ggt gga gac tac ttc 307
 Met Asp Met Ala His Glu Ser Gln Ile Pro Asn Gly Gly Asp Tyr Phe
 55 60 65

acc	acc	tac	att	ggc	tgc	cag	cgg	atc	atg	atc	acc	cgt	tcc	aag	gaa	355
Thr	Thr	Tyr	Ile	Gly	Cys	Gln	Arg	Ile	Met	Ile	Thr	Arg	Ser	Lys	Glu	
70					75					80					85	
ggc	aca	ctc	aac	ggc	ctg	atc	aac	gcg	tgt	tct	cac	cgt	ggc	gcc	atg	403
Gly	Thr	Leu	Asn	Gly	Leu	Ile	Asn	Ala	Cys	Ser	His	Arg	Gly	Ala	Met	
				90					95					100		
ctc	tgc	cgt	ggc	aag	agt	gac	aac	cgc	acc	tcc	ttg	acc	tgc	cca	ttc	451
Leu	Cys	Arg	Gly	Lys	Ser	Asp	Asn	Arg	Thr	Ser	Leu	Thr	Cys	Pro	Phe	
			105					110					115			
cac	ggc	tgg	cca	ttc	tgc	aac	ggc	ggc	gca	ctg	ctc	aag	gtc	aag	ggc	499
His	Gly	Trp	Pro	Phe	Cys	Asn	Gly	Gly	Ala	Leu	Leu	Lys	Val	Lys	Gly	
		120					125					130				
gaa	aaa	gaa	ggc	gcc	tac	cca	gag	aat	ttc	cgc	acc	gac	ggc	tcc	cac	547
Glu	Lys	Glu	Gly	Ala	Tyr	Pro	Glu	Asn	Phe	Arg	Thr	Asp	Gly	Ser	His	
	135					140					145					
gat	gtg	cgt	cgc	gtt	cct	aag	tta	gag	tcc	tac	cgt	ggc	ttc	ctc	ttc	595
Asp	Val	Arg	Arg	Val	Pro	Lys	Leu	Glu	Ser	Tyr	Arg	Gly	Phe	Leu	Phe	
150					155					160					165	
ggc	tcc	ctc	aac	gat	gat	gtc	gtt	tct	ttg	gaa	gag	cac	ctc	ggc	gac	643
Gly	Ser	Leu	Asn	Asp	Asp	Val	Val	Ser	Leu	Glu	Glu	His	Leu	Gly	Asp	
				170				175						180		
acc	cgt	acc	gtc	att	gac	atg	ctg	gtt	gac	caa	tcc	cca	gaa	ggc	ctc	691
Thr	Arg	Thr	Val	Ile	Asp	Met	Leu	Val	Asp	Gln	Ser	Pro	Glu	Gly	Leu	
			185					190					195			
gaa	gta	ctg	cgc	gga	tcc	tcc	acc	tac	acc	tac	gac	ggc	aac	tgg	aag	739
Glu	Val	Leu	Arg	Gly	Ser	Ser	Thr	Tyr	Thr	Tyr	Asp	Gly	Asn	Trp	Lys	
		200					205					210				
ctc	cag	acc	gaa	aac	ggt	gca	gac	ggc	tac	cac	gtt	tcc	tcc	acc	cac	787
Leu	Gln	Thr	Glu	Asn	Gly	Ala	Asp	Gly	Tyr	His	Val	Ser	Ser	Thr	His	
	215					220					225					
tgg	aac	tac	gct	gca	acc	acc	tcc	cgc	cgt	ggc	act	ggt	gaa	tcc	gcg	835
Trp	Asn	Tyr	Ala	Ala	Thr	Thr	Ser	Arg	Arg	Gly	Thr	Gly	Glu	Ser	Ala	
230					235					240					245	
aac	gaa	acc	aag	gca	atg	gac	gct	ggt	acc	tgg	ggc	aag	cag	ggt	ggc	883
Asn	Glu	Thr	Lys	Ala	Met	Asp	Ala	Gly	Thr	Trp	Gly	Lys	Gln	Gly	Gly	
				250				255						260		
gga	tac	ttc	tcc	tac	cct	tac	ggc	cac	atg	ctg	ctg	tgg	atg	tgg	tgg	931
Gly	Tyr	Phe	Ser	Tyr	Pro	Tyr	Gly	His	Met	Leu	Leu	Trp	Met	Trp	Trp	
			265					270					275			
ggc	aac	cca	gaa	gac	cgc	cca	ctg	ttc	gag	cgc	cgc	gac	gag	ttc	aag	979
Gly	Asn	Pro	Glu	Asp	Arg	Pro	Leu	Phe	Glu	Arg	Arg	Asp	Glu	Phe	Lys	
		280					285					290				
aag	gaa	ttc	ggc	gaa	gaa	aag	ggc	gag	ttc	atg	gtt	ggt	gct	tcc	cgc	1027
Lys	Glu	Phe	Gly	Glu	Glu	Lys	Gly	Glu	Phe	Met	Val	Gly	Ala	Ser	Arg	
	295					300					305					

aat ctg tgc ctc tac ccc aat gtt tac ctg atg gat cag ttc tcc tca	1075
Asn Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met Asp Gln Phe Ser Ser	
310 315 320 325	
cag atc cgc cac atc cgc cca atc tca gtt gat cag acc gaa gtc acc	1123
Gln Ile Arg His Ile Arg Pro Ile Ser Val Asp Gln Thr Glu Val Thr	
330 335 340	
atc tac tgc atc gca cct aag ggc gag tcc gcg gaa gca cgt gca aac	1171
Ile Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn	
345 350 355	
cgc atc cgc cag tac gaa gac ttc ttc aac gca acg ggc atg gca acc	1219
Arg Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala Thr Gly Met Ala Thr	
360 365 370	
cca gat gac ctg gag gaa ttc cgc tcc tgc cag aag acc tac cag gca	1267
Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala	
375 380 385	
tct gcc ttc cca tgg aat gac atg acc cgc ggt ttg ggc cac cag gta	1315
Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly Leu Gly His Gln Val	
390 395 400 405	
cag gga cca aac gag gtt gcc aag ggc cta ggc atg aac gaa gtt ctt	1363
Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu	
410 415 420	
tcc tcc gga gca cgc acc gaa gat gaa ggc ctc tac cca atc cag cac	1411
Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His	
425 430 435	
ggc ttc tgg cat gaa ctc atg cag gag gct gtg aat aag cag agc atc	1459
Gly Phe Trp His Glu Leu Met Gln Glu Ala Val Asn Lys Gln Ser Ile	
440 445 450	
aag gaa aag gaa ttg gct gac gat acc gct tct tcc ctt gcc acc gta	1507
Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser Ser Leu Ala Thr Val	
455 460 465	
gct gca gcc aaa atc cgt gag gaa gca aag gca gcc gcg aag tcc gac	1555
Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp	
470 475 480 485	
gct gga gag cct cgc cgc cgt cgt cgc acc cgc ggt tagtcgtcga	1601
Ala Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg Gly	
490 495	
aaagcaaaaa atc	1614

<210> 410

<211> 497

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

Met	Ser	Thr	Pro	Val	Ser	Asn	Leu	Ala	Ser	Val	Gln	Lys	Thr	Leu	Asp
1				5					10					15	

His Ala Leu Glu Asp Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg

20					25					30					
Asn	Ile	Phe	Thr	Asp	Pro	Glu	Ile	Phe	Glu	Leu	Glu	Met	Arg	His	Ile
	35						40					45			
Phe	Glu	Gly	Ile	Trp	Met	Asp	Met	Ala	His	Glu	Ser	Gln	Ile	Pro	Asn
	50					55					60				
Gly	Gly	Asp	Tyr	Phe	Thr	Thr	Tyr	Ile	Gly	Cys	Gln	Arg	Ile	Met	Ile
	65					70					75				80
Thr	Arg	Ser	Lys	Glu	Gly	Thr	Leu	Asn	Gly	Leu	Ile	Asn	Ala	Cys	Ser
				85					90					95	
His	Arg	Gly	Ala	Met	Leu	Cys	Arg	Gly	Lys	Ser	Asp	Asn	Arg	Thr	Ser
			100					105					110		
Leu	Thr	Cys	Pro	Phe	His	Gly	Trp	Pro	Phe	Cys	Asn	Gly	Gly	Ala	Leu
			115				120					125			
Leu	Lys	Val	Lys	Gly	Glu	Lys	Glu	Gly	Ala	Tyr	Pro	Glu	Asn	Phe	Arg
	130					135					140				
Thr	Asp	Gly	Ser	His	Asp	Val	Arg	Arg	Val	Pro	Lys	Leu	Glu	Ser	Tyr
	145					150					155				160
Arg	Gly	Phe	Leu	Phe	Gly	Ser	Leu	Asn	Asp	Asp	Val	Val	Ser	Leu	Glu
				165					170					175	
Glu	His	Leu	Gly	Asp	Thr	Arg	Thr	Val	Ile	Asp	Met	Leu	Val	Asp	Gln
			180					185					190		
Ser	Pro	Glu	Gly	Leu	Glu	Val	Leu	Arg	Gly	Ser	Ser	Thr	Tyr	Thr	Tyr
		195					200					205			
Asp	Gly	Asn	Trp	Lys	Leu	Gln	Thr	Glu	Asn	Gly	Ala	Asp	Gly	Tyr	His
	210					215					220				
Val	Ser	Ser	Thr	His	Trp	Asn	Tyr	Ala	Ala	Thr	Thr	Ser	Arg	Arg	Gly
	225					230					235				240
Thr	Gly	Glu	Ser	Ala	Asn	Glu	Thr	Lys	Ala	Met	Asp	Ala	Gly	Thr	Trp
				245					250					255	
Gly	Lys	Gln	Gly	Gly	Gly	Tyr	Phe	Ser	Tyr	Pro	Tyr	Gly	His	Met	Leu
		260						265					270		
Leu	Trp	Met	Trp	Trp	Gly	Asn	Pro	Glu	Asp	Arg	Pro	Leu	Phe	Glu	Arg
		275					280					285			
Arg	Asp	Glu	Phe	Lys	Lys	Glu	Phe	Gly	Glu	Glu	Lys	Gly	Glu	Phe	Met
	290					295					300				
Val	Gly	Ala	Ser	Arg	Asn	Leu	Cys	Leu	Tyr	Pro	Asn	Val	Tyr	Leu	Met
	305					310					315				320
Asp	Gln	Phe	Ser	Ser	Gln	Ile	Arg	His	Ile	Arg	Pro	Ile	Ser	Val	Asp
				325					330					335	
Gln	Thr	Glu	Val	Thr	Ile	Tyr	Cys	Ile	Ala	Pro	Lys	Gly	Glu	Ser	Ala
			340					345					350		

Glu Ala Arg Ala Asn Arg Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala
 355 360 365

Thr Gly Met Ala Thr Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln
 370 375 380

Lys Thr Tyr Gln Ala Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly
 385 390 395 400

Leu Gly His Gln Val Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly
 405 410 415

Met Asn Glu Val Leu Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu
 420 425 430

Tyr Pro Ile Gln His Gly Phe Trp His Glu Leu Met Gln Glu Ala Val
 435 440 445

Asn Lys Gln Ser Ile Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser
 450 455 460

Ser Leu Ala Thr Val Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala
 465 470 475 480

Ala Ala Lys Ser Asp Ala Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg
 485 490 495

Gly

<210> 411
 <211> 1166
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (16)..(1143)
 <223> RXN01993

<400> 411
 ctttaggagt tcaccatg aca ctg tcc gaa cgc aag ctc acc acc acc gcc 51
 Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala
 1 5 10

aag att ctt ccc cac cca ctc aac gcc tgg tac gtc gcc gct tgg gat 99
 Lys Ile Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp
 15 20 25

tat gaa gtc aca tct aaa aag ccc atg gcc agg aca atc gcc aac aaa 147
 Tyr Glu Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys
 30 35 40

cca ctc gct ttg tac cgc acc aaa gat ggc cga gcc gtt gcc ctt gca 195
 Pro Leu Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala
 45 50 55 60

gac gcc tgc tgg cac cgc ctc gca ccg cta tcc aag gga aaa ctc gtg 243
 Asp Ala Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val

65					70					75						
ggc	aca	gac	gga	atc	caa	tgc	cct	tat	cac	ggc	ttg	gag	tac	aac	tcc	291
Gly	Thr	Asp	Gly	Ile	Gln	Cys	Pro	Tyr	His	Gly	Leu	Glu	Tyr	Asn	Ser	
80					85					90						
gcg	ggc	cgc	tgc	atg	aaa	atg	ccc	gcg	cag	gaa	acc	ctc	aac	ccg	tca	339
Ala	Gly	Arg	Cys	Met	Lys	Met	Pro	Ala	Gln	Glu	Thr	Leu	Asn	Pro	Ser	
95					100					105						
gca	gcc	gtc	aac	tcc	tac	ccc	gtg	gtg	gaa	gcc	cac	cgc	ttt	gtg	tgg	387
Ala	Ala	Val	Asn	Ser	Tyr	Pro	Val	Val	Glu	Ala	His	Arg	Phe	Val	Trp	
110					115					120						
gtg	tgg	ctg	ggc	gat	ccc	aca	ttg	gca	gat	ccc	acc	caa	gta	ccc	gat	435
Val	Trp	Leu	Gly	Asp	Pro	Thr	Leu	Ala	Asp	Pro	Thr	Gln	Val	Pro	Asp	
125					130					135					140	
atg	cac	cag	atg	agc	cac	ccc	gaa	tgg	gca	ggc	gat	gga	cgc	acc	atc	483
Met	His	Gln	Met	Ser	His	Pro	Glu	Trp	Ala	Gly	Asp	Gly	Arg	Thr	Ile	
145					150					155						
tcc	gct	gac	tgc	aac	tac	caa	tta	gtg	ctg	gac	aac	ttg	atg	gac	ctc	531
Ser	Ala	Asp	Cys	Asn	Tyr	Gln	Leu	Val	Leu	Asp	Asn	Leu	Met	Asp	Leu	
160					165					170						
acc	cac	gaa	gag	ttc	gtg	cac	tcc	tcc	agc	atc	gga	caa	gac	gaa	ctt	579
Thr	His	Glu	Glu	Phe	Val	His	Ser	Ser	Ser	Ile	Gly	Gln	Asp	Glu	Leu	
175					180					185						
agt	gaa	tca	gag	ttc	gtg	gtc	acc	cac	act	gaa	gat	tcc	gtg	acg	gtc	627
Ser	Glu	Ser	Glu	Phe	Val	Val	Thr	His	Thr	Glu	Asp	Ser	Val	Thr	Val	
190					195					200						
acc	cgc	tgg	atg	cat	gac	ata	gat	gca	cca	ccg	ttt	tgg	caa	aag	aac	675
Thr	Arg	Trp	Met	His	Asp	Ile	Asp	Ala	Pro	Pro	Phe	Trp	Gln	Lys	Asn	
205					210					215					220	
atg	aat	gat	aag	ttc	cca	gga	ttt	gaa	ggc	aag	gtg	gat	cgt	tgg	cag	723
Met	Asn	Asp	Lys	Phe	Pro	Gly	Phe	Glu	Gly	Lys	Val	Asp	Arg	Trp	Gln	
225					230					235						
atc	atc	cac	tac	tac	tac	cct	tcc	acc	atc	tgc	att	gat	gtt	ggc	gta	771
Ile	Ile	His	Tyr	Tyr	Tyr	Pro	Ser	Thr	Ile	Cys	Ile	Asp	Val	Gly	Val	
240					245					250						
gca	aag	gct	gga	act	ggc	gcg	cag	gaa	ggc	gac	cgc	agc	cag	ggc	gtt	819
Ala	Lys	Ala	Gly	Thr	Gly	Ala	Gln	Glu	Gly	Asp	Arg	Ser	Gln	Gly	Val	
255					260					265						
aat	ggg	tat	gtc	atg	aac	acc	att	acc	cca	gat	tca	gat	cgt	tcc	tct	867
Asn	Gly	Tyr	Val	Met	Asn	Thr	Ile	Thr	Pro	Asp	Ser	Asp	Arg	Ser	Ser	
270					275					280						
cat	tac	ttc	tgg	gca	ttc	atg	cgc	aac	tac	cgc	ctg	gaa	agc	caa	acc	915
His	Tyr	Phe	Trp	Ala	Phe	Met	Arg	Asn	Tyr	Arg	Leu	Glu	Ser	Gln	Thr	
285					290					295					300	
atc	acc	acc	cag	ctg	cgc	gac	ggc	gta	tcc	ggc	gta	ttc	aaa	gaa	gac	963
Ile	Thr	Thr	Gln	Leu	Arg	Asp	Gly	Val	Ser	Gly	Val	Phe	Lys	Glu	Asp	
305					310					315						

gaa gac atg ctg acc gct cag caa gat gcc atc gac gcc aac acc gac 1011
 Glu Asp Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp
 320 325 330
 tac gag ttt tac agc ctc aac att gat gcc ggt ggc atg tgg gtg cgc 1059
 Tyr Glu Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg
 335 340 345
 cga atc ctc gag gaa gca ctc tcc aag gaa ggc cga ctg gat atc ccc 1107
 Arg Ile Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro
 350 355 360
 acc aca ttc ccc cgc gca aca ccg aag ccg gag gca taaaccatga 1153
 Thr Thr Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
 365 370 375
 actcgcaatg gca 1166

<210> 412
 <211> 376
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 412
 Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile Leu Pro
 1 5 10 15
 His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu Val Thr
 20 25 30
 Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu Ala Leu
 35 40 45
 Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala Cys Trp
 50 55 60
 His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr Asp Gly
 65 70 75 80
 Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly Arg Cys
 85 90 95
 Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala Val Asn
 100 105 110
 Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp Leu Gly
 115 120 125
 Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His Gln Met
 130 135 140
 Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala Asp Cys
 145 150 155 160
 Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His Glu Glu
 165 170 175
 Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu Ser Glu
 180 185 190

Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg Trp Met
 195 200 205
 His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met Asn Asp Lys
 210 215 220
 Phe Pro Gly Phe Glu Gly Lys Val Asp Arg Trp Gln Ile Ile His Tyr
 225 230 235 240
 Tyr Tyr Pro Ser Thr Ile Cys Ile Asp Val Gly Val Ala Lys Ala Gly
 245 250 255
 Thr Gly Ala Gln Glu Gly Asp Arg Ser Gln Gly Val Asn Gly Tyr Val
 260 265 270
 Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Ser Ser His Tyr Phe Trp
 275 280 285
 Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr Thr Gln
 290 295 300
 Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp Met Leu
 305 310 315 320
 Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu Phe Tyr
 325 330 335
 Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile Leu Glu
 340 345 350
 Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr Phe Pro
 355 360 365
 Arg Ala Thr Pro Lys Pro Glu Ala
 370 375

<210> 413
 <211> 816
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(793)
 <223> RXN00658

<400> 413
 cattgacacc cacaggttta ccagcatcac ggaaagtttg gatggatttt tactccggcc 60
 acaacgtctg gctggaagct cagccacgtg ctttctggtc gtg cgc cac gac gag 115
 Val Arg His Asp Glu
 1 5
 cac tac cca gct gcg gca aac ctc att gct ttc gat aag gga tgg tcc 163
 His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe Asp Lys Gly Trp Ser
 10 15 20
 acc ctc atc gcc cct cag ctg gaa gat cca gag gcg gag gag ttc acc 211
 Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu Ala Glu Glu Phe Thr

25										30					35					
gcc	gga	ttc	ctc	acc	gaa	tac	cag	gac	aat	ctg	atc	act	gcg	ggc	atg	259				
Ala	Gly	Phe	Leu	Thr	Glu	Tyr	Gln	Asp	Asn	Leu	Ile	Thr	Ala	Gly	Met					
40				45				50												
gag	cac	cag	gcg	ctc	gcg	agc	ggc	ttc	ccg	gtg	ggg	cgt	cgc	ttc	aag	307				
Glu	His	Gln	Ala	Leu	Ala	Ser	Gly	Phe	Pro	Val	Gly	Arg	Arg	Phe	Lys					
55				60				65												
tcc	gat	att	gct	tta	cga	cgc	tgc	gat	gcg	gtg	acc	acc	cac	atc	ggc	355				
Ser	Asp	Ile	Ala	Leu	Arg	Arg	Cys	Asp	Ala	Val	Thr	Thr	His	Ile	Gly					
70				75				80				85								
cac	gaa	cac	tcc	gcc	gat	ggc	cac	tgg	agg	atc	tac	gta	ttc	gct	ggc	403				
His	Glu	His	Ser	Ala	Asp	Gly	His	Trp	Arg	Ile	Tyr	Val	Phe	Ala	Gly					
				90				95				100								
caa	gcc	acc	cca	caa	gat	tcc	gag	tct	gca	ctg	aac	aag	tgg	gcg	cag	451				
Gln	Ala	Thr	Pro	Gln	Asp	Ser	Glu	Ser	Ala	Leu	Asn	Lys	Trp	Ala	Gln					
105				110				115												
tgg	atg	gag	gaa	agc	gaa	gac	tca	cca	ctc	aac	cgc	ttc	acc	cca	gaa	499				
Trp	Met	Glu	Glu	Ser	Glu	Asp	Ser	Pro	Leu	Asn	Arg	Phe	Thr	Pro	Glu					
120				125				130												
gcc	ggc	gac	cgc	aac	gca	gtc	ttc	gat	atc	aag	gct	acc	tac	cag	cag	547				
Ala	Gly	Asp	Arg	Asn	Ala	Val	Phe	Asp	Ile	Lys	Ala	Thr	Tyr	Gln	Gln					
135				140				145												
cat	tac	cac	tcc	ttc	gac	ctg	ttc	gat	gcg	cca	gag	gtc	ttc	ttc	cca	595				
His	Tyr	His	Ser	Phe	Asp	Leu	Phe	Asp	Ala	Pro	Glu	Val	Phe	Phe	Pro					
150				155				160				165								
cga	gtt	gga	cca	tac	aag	ctg	caa	aac	ctc	gaa	aac	gtt	tgg	acc	gca	643				
Arg	Val	Gly	Pro	Tyr	Lys	Leu	Gln	Asn	Leu	Glu	Asn	Val	Trp	Thr	Ala					
				170				175				180								
ctg	gat	tcc	caa	gac	atc	ttt	gag	tcc	cgt	ggc	atc	agt	cgc	gat	ggc	691				
Leu	Asp	Ser	Gln	Asp	Ile	Phe	Glu	Ser	Arg	Gly	Ile	Ser	Arg	Asp	Gly					
185				190				195												
gca	att	gtt	gtc	gtt	cgc	cca	gac	cag	tac	gtc	gca	gca	gtc	ctc	cca	739				
Ala	Ile	Val	Val	Val	Arg	Pro	Asp	Gln	Tyr	Val	Ala	Ala	Val	Leu	Pro					
200				205				210												
ctc	gaa	gac	acc	gca	gca	ctg	gct	gag	ttc	ttc	aat	ggc	aat	ctg	ctt	787				
Leu	Glu	Asp	Thr	Ala	Ala	Leu	Ala	Glu	Phe	Phe	Asn	Gly	Asn	Leu	Leu					
215				220				225												
gag	cca	taaaccctaa	attctaggaa	cga											816					
Glu	Pro																			
230																				

<210> 414

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

Val Arg His Asp Glu His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe
 1 5 10 15
 Asp Lys Gly Trp Ser Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu
 20 25 30
 Ala Glu Glu Phe Thr Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu
 35 40 45
 Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val
 50 55 60
 Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val
 65 70 75 80
 Thr Thr His Ile Gly His Glu His Ser Ala Asp Gly His Trp Arg Ile
 85 90 95
 Tyr Val Phe Ala Gly Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu
 100 105 110
 Asn Lys Trp Ala Gln Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn
 115 120 125
 Arg Phe Thr Pro Glu Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys
 130 135 140
 Ala Thr Tyr Gln Gln His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro
 145 150 155 160
 Glu Val Phe Phe Pro Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu
 165 170 175
 Asn Val Trp Thr Ala Leu Asp Ser Gln Asp Ile Phe Glu Ser Arg Gly
 180 185 190
 Ile Ser Arg Asp Gly Ala Ile Val Val Val Arg Pro Asp Gln Tyr Val
 195 200 205
 Ala Ala Val Leu Pro Leu Glu Asp Thr Ala Ala Leu Ala Glu Phe Phe
 210 215 220
 Asn Gly Asn Leu Leu Glu Pro
 225 230

<210> 415

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> RXN00178

<400> 415

gcgaataatc cacggacggt cacagaagaa aacctcactg cgctgcttac cacagcgctc 60

 aacggcgacg atccagcaac tttgaattaa ggagaccaac atg act att tca gca 115
 Met Thr Ile Ser Ala

1

5

caa cag caa gca gtg gaa gaa gac ctt gta gag cgc gta ctc gca tct	163
Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu Arg Val Leu Ala Ser	
10 15 20	
ttt gat tcg tgt gaa aac cct cgc ctc aaa cta gtg atg aaa tcc ctg	211
Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu Val Met Lys Ser Leu	
25 30 35	
act gtg cat ctc cat gat ttc atc cgc gat gtt cga ctc act gaa gaa	259
Thr Val His Leu His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Glu	
40 45 50	
gag tgg aac tac gcc att gat ttc ctc acc aag gtt ggg cat atc acc	307
Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys Val Gly His Ile Thr	
55 60 65	
gac gat aag cgc caa gaa ttc gtg ttg ctc tct gac acc ttg ggt gca	355
Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala	
70 75 80 85	
tcc atg cag acc atc gct gtt aat aac gaa gca tat gaa gac gct acc	403
Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala Tyr Glu Asp Ala Thr	
90 95 100	
gaa gca aca gtc ttt ggc ccc ttc ttt gtc gat gat gcg cca ctg gtc	451
Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp Asp Ala Pro Leu Val	
105 110 115	
caa aac gga gat gac att gcc ttt ggc gca gtc ggc cag ccg gca tgg	499
Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val Gly Gln Pro Ala Trp	
120 125 130	
gtg gag gga acg gtc aaa gac act gaa gga aac ccc att ccc aat gca	547
Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn Pro Ile Pro Asn Ala	
135 140 145	
cgc att gaa gta tgg gaa tgc gat gaa gat gga ctt tat gat gtg caa	595
Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly Leu Tyr Asp Val Gln	
150 155 160 165	
tac gcc gat gag cgc agt gct gga cgc gca cac ctg tat tca gat gaa	643
Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His Leu Tyr Ser Asp Glu	
170 175 180	
aac ggc gaa tac cac ttc tgg gga cta act ccc gtg cca tat ccc atc	691
Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro Val Pro Tyr Pro Ile	
185 190 195	
cca cac gat ggt cca gta gga caa atg ctc caa gca gtt ggt cgt tcc	739
Pro His Asp Gly Pro Val Gly Gln Met Leu Gln Ala Val Gly Arg Ser	
200 205 210	
ccc gtt cgt tgc gcg cac cta cac ttc atg gtg act gcg cca gag aag	787
Pro Val Arg Cys Ala His Leu His Phe Met Val Thr Ala Pro Glu Lys	
215 220 225	
cga acc ttg gta acc cat atc ttc gtt gag ggc gat ccg cag cta gag	835
Arg Thr Leu Val Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu	
230 235 240 245	


```

atc ggc gat tcc gtg ttt ggc gtg aag gac tca ctg att aag aaa ttc      883
Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe
                250                255                260

gtt gag caa cct gca gga acc gca act cca gat ggt cgc gat gtg ggt      931
Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp Gly Arg Asp Val Gly
                265                270                275

gat caa acc tgg gca cgc aca cgt ttt gat att gtg ctc gcc ccc ggc      979
Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly
                280                285                290

aat gtc taagtagaag cagcaaaaaa cca      1008
Asn Val
                295

```

```

<210> 416
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 416
Met Thr Ile Ser Ala Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu
  1                5                10                15

Arg Val Leu Ala Ser Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu
                20                25                30

Val Met Lys Ser Leu Thr Val His Leu His Asp Phe Ile Arg Asp Val
                35                40                45

Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
  50                55                60

Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
  65                70                75                80

Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
                85                90                95

Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp
                100                105                110

Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val
                115                120                125

Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn
                130                135                140

Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly
  145                150                155                160

Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His
                165                170                175

Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro
                180                185                190

Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln

```

195						200						205					
Ala	Val	Gly	Arg	Ser	Pro	Val	Arg	Cys	Ala	His	Leu	His	Phe	Met	Val		
210						215					220						
Thr	Ala	Pro	Glu	Lys	Arg	Thr	Leu	Val	Thr	His	Ile	Phe	Val	Glu	Gly		
225					230					235				240			
Asp	Pro	Gln	Leu	Glu	Ile	Gly	Asp	Ser	Val	Phe	Gly	Val	Lys	Asp	Ser		
				245					250					255			
Leu	Ile	Lys	Lys	Phe	Val	Glu	Gln	Pro	Ala	Gly	Thr	Ala	Thr	Pro	Asp		
			260					265					270				
Gly	Arg	Asp	Val	Gly	Asp	Gln	Thr	Trp	Ala	Arg	Thr	Arg	Phe	Asp	Ile		
		275					280						285				
Val	Leu	Ala	Pro	Gly	Asn	Val											
	290						295										

<210> 417
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXN01461

<400> 417
 tcgactatga cgagaccggt gaaaacttcg cgcttggtta caagttcgac atcgtccttc 60
 gtggccgcaa cgccacccca tttgagtaaa gggttttgca atg att gat aca ggg 115
 Met Ile Asp Thr Gly
 1 5
 aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac 163
 Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn
 10 15 20
 gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc 211
 Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val
 25 30 35
 cac atc ggt ttg acc ctt gaa ggt gcg gag cat ctc gtg gag cca ggt 259
 His Ile Gly Leu Thr Leu Glu Gly Ala Glu His Leu Val Glu Pro Gly
 40 45 50
 tcg gaa ggc gcg gtg tcc ttt act gtt tcc gca act gat ggc aac ggc 307
 Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala Thr Asp Gly Asn Gly
 55 60 65
 gac ccc atc gcg gat gcc atg ttt gaa ctg tgg cag gcc gat cca gag 355
 Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp Gln Ala Asp Pro Glu
 70 75 80 85
 ggc atc cac aac tct gat ttg gat cca aac cgc aca gca cca gca acc 403
 Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg Thr Ala Pro Ala Thr
 90 95 100

gca gat ggc ttc cgc ggg ctt ggt cgc gcg atg gca aac gcg cag ggt 451
 Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met Ala Asn Ala Gln Gly
 105 110 115

gag gca acg ttc acc act ttg gtt ccg gga gca ttc gca gat gag gca 499
 Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala Phe Ala Asp Glu Ala
 120 125 130

cca cac ttc aag gtt ggt gtg ttc gcc cgt ggc atg ctg gag cgt ctg 547
 Pro His Phe Lys Val Gly Val Phe Ala Arg Gly Met Leu Glu Arg Leu
 135 140 145

tac act cgc gca tac ctg cca gac gcc gat ttg agc acc gac cca gtt 595
 Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu Ser Thr Asp Pro Val
 150 155 160 165

ttg gct gtg gtc cca gct gat cga cgt gac ctc ctg gtg gct caa aag 643
 Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu Leu Val Ala Gln Lys
 170 175 180

acc gat gat gga ttc cgc ttc gac atc act gtc cag gct gaa gac aat 691
 Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val Gln Ala Glu Asp Asn
 185 190 195

gaa acc cca ttt ttt gga ctc taaattgacc cgatctttat act 735
 Glu Thr Pro Phe Phe Gly Leu
 200

<210> 418

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

Met Ile Asp Thr Gly Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn
 1 5 10 15

Ile Ile Asp Gln Asn Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr
 20 25 30

Val Gly Pro Tyr Val His Ile Gly Leu Thr Leu Glu Gly Ala Glu His
 35 40 45

Leu Val Glu Pro Gly Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala
 50 55 60

Thr Asp Gly Asn Gly Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp
 65 70 75 80

Gln Ala Asp Pro Glu Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg
 85 90 95

Thr Ala Pro Ala Thr Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met
 100 105 110

Ala Asn Ala Gln Gly Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala
 115 120 125

Phe Ala Asp Glu Ala Pro His Phe Lys Val Gly Val Phe Ala Arg Gly

130 135 140

Met Leu Glu Arg Leu Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu
 145 150 155 160

Ser Thr Asp Pro Val Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu
 165 170 175

Leu Val Ala Gln Lys Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val
 180 185 190

Gln Ala Glu Asp Asn Glu Thr Pro Phe Phe Gly Leu
 195 200

<210> 419
 <211> 1584
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1561)
 <223> RXN01653

<400> 419

ttcattcagg gtgaatgctc tccttggttc agatgttcaa cgctccataa agtagaccgc 60

aatctagaca aagatgtcta ttttaattaa ggagcagaac atg gcc acg gcc gag 115
 Met Ala Thr Ala Glu
 1 5

aac aca aca cag gag aat cgg aaa atc ctg ttc aac gca ttt gat atg 163
 Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe Asn Ala Phe Asp Met
 10 15 20

aac tgc gtt gcg cat cag tcc cca gga ctg tgg aca cac ccg aag gat 211
 Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp Thr His Pro Lys Asp
 25 30 35

aag gcg cga gac tac aac act ctt gat tac tgg gtg cac ctt gcc aag 259
 Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp Val His Leu Ala Lys
 40 45 50

act ttg gag aag ggc ctt ttc gac ggc ctt ttc atc gca gat gtg ctt 307
 Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe Ile Ala Asp Val Leu
 55 60 65

gga act tac gat gtt tat ggt tct agt aat gaa gcg gcg ttg agc agt 355
 Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu Ala Ala Leu Ser Ser
 70 75 80 85

ggt gcg cag gtg cct gtc aat gat ccg atc ctt ctt gtt tct gcg atg 403
 Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu Leu Val Ser Ala Met
 90 95 100

gcc tat gcc aca aag aac ctc ggg ttt ggc att act gca ggt act gcc 451
 Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile Thr Ala Gly Thr Ala
 105 110 115

tat gag cac ccg tat cct ttt gcg cgg cgt ctg gcc aca ctt gat cac 499

Tyr	Glu	His	Pro	Tyr	Pro	Phe	Ala	Arg	Arg	Leu	Ala	Thr	Leu	Asp	His	
	120						125					130				
ctg	act	aat	ggg	cgt	gtg	ggg	tgg	aat	gtg	gtt	act	ggc	tat	ctt	ccc	547
Leu	Thr	Asn	Gly	Arg	Val	Gly	Trp	Asn	Val	Val	Thr	Gly	Tyr	Leu	Pro	
	135					140					145					
tct	gct	gct	caa	aac	atg	ggg	gac	acc	gat	cag	ctg	cca	cat	gat	gag	595
Ser	Ala	Ala	Gln	Asn	Met	Gly	Asp	Thr	Asp	Gln	Leu	Pro	His	Asp	Glu	
	150				155					160					165	
cgc	tat	gac	aaa	gca	gat	gaa	tac	ctg	gaa	gtg	atc	tac	aag	ctt	ctc	643
Arg	Tyr	Asp	Lys	Ala	Asp	Glu	Tyr	Leu	Glu	Val	Ile	Tyr	Lys	Leu	Leu	
				170					175					180		
gag	ggc	tcc	tgg	gaa	gac	gat	gct	gtt	caa	aac	aat	acg	gag	acg	agt	691
Glu	Gly	Ser	Trp	Glu	Asp	Asp	Ala	Val	Gln	Asn	Asn	Thr	Glu	Thr	Ser	
			185					190					195			
gtc	ttt	acg	gac	tcc	tcc	aaa	gtg	cac	gcc	att	aat	cat	cat	ggc	aag	739
Val	Phe	Thr	Asp	Ser	Ser	Lys	Val	His	Ala	Ile	Asn	His	His	Gly	Lys	
		200					205					210				
tac	ttt	gat	gtg	ccg	ggc	att	gcc	atc	act	gag	ccg	agt	gtg	cag	cgt	787
Tyr	Phe	Asp	Val	Pro	Gly	Ile	Ala	Ile	Thr	Glu	Pro	Ser	Val	Gln	Arg	
	215					220					225					
acg	ccg	gtg	atc	tac	cag	gcg	ggg	gca	tcg	ccg	cgc	gga	ttg	aaa	ttc	835
Thr	Pro	Val	Ile	Tyr	Gln	Ala	Gly	Ala	Ser	Pro	Arg	Gly	Leu	Lys	Phe	
	230				235					240					245	
gct	ggg	gag	aat	gca	gaa	gca	gtg	ttt	atc	aat	tcc	agc	acc	gtg	gag	883
Ala	Gly	Glu	Asn	Ala	Glu	Ala	Val	Phe	Ile	Asn	Ser	Ser	Thr	Val	Glu	
				250					255					260		
gca	atc	acc	aag	act	gtc	gca	aaa	att	cgc	gct	gct	gcg	gtc	gct	gcg	931
Ala	Ile	Thr	Lys	Thr	Val	Ala	Lys	Ile	Arg	Ala	Ala	Ala	Val	Ala	Ala	
			265					270					275			
gga	cgt	gat	cca	cat	gcg	gtg	aag	atc	ttt	gcg	atg	caa	acc	atc	atc	979
Gly	Arg	Asp	Pro	His	Ala	Val	Lys	Ile	Phe	Ala	Met	Gln	Thr	Ile	Ile	
		280					285					290				
act	ggg	gaa	aca	gaa	gca	gat	gcg	cag	gca	aag	ctg	gag	gaa	tac	agt	1027
Thr	Gly	Glu	Thr	Glu	Ala	Asp	Ala	Gln	Ala	Lys	Leu	Glu	Glu	Tyr	Ser	
	295					300					305					
cgc	tat	atc	gat	cct	gtc	ggg	ggg	ctg	acc	ttg	atg	tct	gga	tgg	acc	1075
Arg	Tyr	Ile	Asp	Pro	Val	Gly	Gly	Leu	Thr	Leu	Met	Ser	Gly	Trp	Thr	
	310				315					320					325	
ggc	gcg	gat	ctg	tcg	cag	tat	gac	ctg	gat	gaa	ccg	atc	acc	aat	att	1123
Gly	Ala	Asp	Leu	Ser	Gln	Tyr	Asp	Leu	Asp	Glu	Pro	Ile	Thr	Asn	Ile	
				330					335					340		
gag	tca	aac	gct	att	cag	tcc	act	gca	gcc	acc	att	agc	aac	ggc	acc	1171
Glu	Ser	Asn	Ala	Ile	Gln	Ser	Thr	Ala	Ala	Thr	Ile	Ser	Asn	Gly	Thr	
			345					350					355			
ggg	gaa	ggg	gcg	tgg	acg	gta	cgc	aaa	ctg	ggg	gag	gca	acc	ggc	atc	1219
Gly	Glu	Gly	Ala	Trp	Thr	Val	Arg	Lys	Leu	Gly	Glu	Ala	Thr	Gly	Ile	

360	365	370	
ggc ggc ttc gga cca gtg ctt gtg gga tct ggc gct aac gtt gcc gcg Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly Ala Asn Val Ala Ala 375 380 385			1267
gaa ctt gca cgc atc cag gat ctc agc gat gtt gat ggt ttc aac ctt Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val Asp Gly Phe Asn Leu 390 395 400 405			1315
gct tat gcc atc acc cca gga act ttt gaa gat gtc gtg gac ttt gtg Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp Val Val Asp Phe Val 410 415 420			1363
gtg cct gag ctg caa aaa ctt agc cgc tac aag acg gaa tac gcg ccg Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys Thr Glu Tyr Ala Pro 425 430 435			1411
ggt tcc ttg cgc aac aaa ttg ctc ggt aaa ggt gat cgc ctg gac gat Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly Asp Arg Leu Asp Asp 440 445 450			1459
acc cac cgc ggc gca agc tac cgc cta ggc gct cgg aac tcc acc gcc Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala Arg Asn Ser Thr Ala 455 460 465			1507
act att gat ctc agt tcc ata tcc gcc caa cta gtt tcc cag gga gcc Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu Val Ser Gln Gly Ala 470 475 480 485			1555
cac tca tgatctcacc gcaaacaatc atc His Ser			1584

<210> 420

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met	Ala	Thr	Ala	Glu	Asn	Thr	Thr	Gln	Glu	Asn	Arg	Lys	Ile	Leu	Phe	1	5	10	15
Asn	Ala	Phe	Asp	Met	Asn	Cys	Val	Ala	His	Gln	Ser	Pro	Gly	Leu	Trp	20	25	30	
Thr	His	Pro	Lys	Asp	Lys	Ala	Arg	Asp	Tyr	Asn	Thr	Leu	Asp	Tyr	Trp	35	40	45	
Val	His	Leu	Ala	Lys	Thr	Leu	Glu	Lys	Gly	Leu	Phe	Asp	Gly	Leu	Phe	50	55	60	
Ile	Ala	Asp	Val	Leu	Gly	Thr	Tyr	Asp	Val	Tyr	Gly	Ser	Ser	Asn	Glu	65	70	75	80
Ala	Ala	Leu	Ser	Ser	Gly	Ala	Gln	Val	Pro	Val	Asn	Asp	Pro	Ile	Leu	85	90	95	
Leu	Val	Ser	Ala	Met	Ala	Tyr	Ala	Thr	Lys	Asn	Leu	Gly	Phe	Gly	Ile	100	105	110	

Thr Ala Gly Thr Ala Tyr Glu His Pro Tyr Pro Phe Ala Arg Arg Leu
 115 120 125
 Ala Thr Leu Asp His Leu Thr Asn Gly Arg Val Gly Trp Asn Val Val
 130 135 140
 Thr Gly Tyr Leu Pro Ser Ala Ala Gln Asn Met Gly Asp Thr Asp Gln
 145 150 155 160
 Leu Pro His Asp Glu Arg Tyr Asp Lys Ala Asp Glu Tyr Leu Glu Val
 165 170 175
 Ile Tyr Lys Leu Leu Glu Gly Ser Trp Glu Asp Asp Ala Val Gln Asn
 180 185 190
 Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His Ala Ile
 195 200 205
 Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile Thr Glu
 210 215 220
 Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala Ser Pro
 225 230 235 240
 Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe Ile Asn
 245 250 255
 Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile Arg Ala
 260 265 270
 Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile Phe Ala
 275 280 285
 Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln Ala Lys
 290 295 300
 Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu Thr Leu
 305 310 315 320
 Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu Asp Glu
 325 330 335
 Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala Ala Thr
 340 345 350
 Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys Leu Gly
 355 360 365
 Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly
 370 375 380
 Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val
 385 390 395 400
 Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp
 405 410 415
 Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys
 420 425 430

Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly
 435 440 445

Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala
 450 455 460

Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu
 465 470 475 480

Val Ser Gln Gly Ala His Ser
 485

<210> 421
 <211> 702
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(679)
 <223> RXN02053

<400> 421
 aaccagccag aaactatctc caaaagctaa taaaaccctt gcactgacaa ataaggcgac 60

ctaccatgac tctgtttcca acacataaaa aggataaaaa atg tca ctt tca gtc 115
 Met Ser Leu Ser Val
 1 5

gtc gag gcg att acc aac cgc cgc gcc acc cgc aaa tac acc gat gaa 163
 Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg Lys Tyr Thr Asp Glu
 10 15 20

gct cct acc cct gag ctg atc gac aaa atc gtt gac ctt gcc ctg gag 211
 Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val Asp Leu Ala Leu Glu
 25 30 35

gca ccc agt gcg ttc aat gcg cag caa cgt gaa att gtt gtg att act 259
 Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu Ile Val Val Ile Thr
 40 45 50

gat ccc gca cag aag cag aag ctt tac gag gcc tcc cat cag aaa caa 307
 Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala Ser His Gln Lys Gln
 55 60 65

ttc ctc acc gca cct gta act ttc att gcg gtt gcc cgc gtg gaa aac 355
 Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val Ala Arg Val Glu Asn
 70 75 80 85

gag cct gag gat ttg gaa gag att ctt ggt acg gaa agg gct gaa cgt 403
 Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr Glu Arg Ala Glu Arg
 90 95 100

gtc gcg gga ttc atc aac ggt cgc agc att cag cag gca cgc gaa gca 451
 Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln Gln Ala Arg Glu Ala
 105 110 115

acg ttg agg gat gcc agc ctc gcg gcg gct ttt cta att ctg gct gcc 499
 Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe Leu Ile Leu Ala Ala
 120 125 130

cag gcg gag ggt ttg agt acc agc ccg act act ggt tgg gat gag gaa 547
 Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr Gly Trp Asp Glu Glu
 135 140 145

 aaa gtg aag gaa gca atc ggt ctc ggc ggg cgt gag gat cgt gca atc 595
 Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg Glu Asp Arg Ala Ile
 150 155 160 165

 gcc ctt gtt att gct acc gga ttc cct aat gaa cag ccg gag cac cct 643
 Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu Gln Pro Glu His Pro
 170 175 180

 ggt cgt ttg cag aat agg cgc atc gac aac agc tac taactctgcc 689
 Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser Tyr
 185 190

 agctcgcccg gac 702

<210> 422
 <211> 193
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 422
 Met Ser Leu Ser Val Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg
 1 5 10 15

 Lys Tyr Thr Asp Glu Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val
 20 25 30

 Asp Leu Ala Leu Glu Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu
 35 40 45

 Ile Val Val Ile Thr Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala
 50 55 60

 Ser His Gln Lys Gln Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val
 65 70 75 80

 Ala Arg Val Glu Asn Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr
 85 90 95

 Glu Arg Ala Glu Arg Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln
 100 105 110

 Gln Ala Arg Glu Ala Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe
 115 120 125

 Leu Ile Leu Ala Ala Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr
 130 135 140

 Gly Trp Asp Glu Glu Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg
 145 150 155 160

 Glu Asp Arg Ala Ile Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu
 165 170 175

 Gln Pro Glu His Pro Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser
 180 185 190

Tyr

```
<210> 423
<211> 1191
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1168)
<223> RXN00177
```

<400> 423															
ctattccaca gcagtgagcg ctgaacaact tcaaacacag attaagcagc tatcggatct 60															
acttcacctc aactcagttg tctggagcata ggagctaaaa atg tct tta cag ttc 115															
Met Ser Leu Gln Phe 5															
gat cat gaa acc ctc ggt caa cga gtt ctg ttc ggt tca ggt gag gcg 163															
Asp His Glu Thr Leu Gly Gln Arg Val Leu Phe Gly Ser Gly Glu Ala 20															
gcg caa aat ctc gcc gct gaa att agc cga ctc gat gcc aaa aac gtc 211															
Ala Gln Asn Leu Ala Ala Glu Ile Ser Arg Leu Asp Ala Lys Asn Val 35															
atg gtg gtt gcc ggt gat ttc gag ctt ccc atg gca cgg caa gta gca 259															
Met Val Val Ala Gly Asp Phe Glu Leu Pro Met Ala Arg Gln Val Ala 50															
gca gat att gat gtc aag gtg tgg cat tca aat gtc gtg atg cat gtg 307															
Ala Asp Ile Asp Val Lys Val Trp His Ser Asn Val Val Met His Val 65															
ccc atc gaa aca gca gaa gaa gca cgc agt gtt gcg aaa gaa aac gac 355															
Pro Ile Glu Thr Ala Glu Glu Ala Arg Ser Val Ala Lys Glu Asn Asp 85															
att gat gtt gtg gtg tgt gtg ggc ggt gga tcc aca aca ggt cta gct 403															
Ile Asp Val Val Val Cys Val Gly Gly Gly Ser Thr Thr Gly Leu Ala 100															
aaa gcg att gcc atg acc acc gca ttg ccg atc att gcg gta ccc act 451															
Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile Ile Ala Val Pro Thr 115															
act tat gca ggt tct gaa gca aca aat gtg tgg gga ttg acc gaa gcc 499															
Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp Gly Leu Thr Glu Ala 130															
gcg cgc aaa aca act ggt gtt gat aac aaa gtg ctg cca gtg aca gtt 547															
Ala Arg Lys Thr Thr Gly Val Asp Asn Lys Val Leu Pro Val Thr Val 145															
atc tac gat tca gcg tta acc atg tct ttg ccg gta gaa atg tcg gtt 595															
Ile Tyr Asp Ser Ala Leu Thr Met Ser Leu Pro Val Glu Met Ser Val 165															

gct tct ggt ctc aat ggt ttg gct cac tgc att gat tct ttg tgg gga	643
Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile Asp Ser Leu Trp Gly	
170 175 180	
ccg aag gcg gat ccc atc aat gcg gct atg gct gct gag gga att cga	691
Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala Ala Glu Gly Ile Arg	
185 190 195	
gca ctt tct gct ggc ctt ccc aag att gtg gca gat gct cag gac gta	739
Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala Asp Ala Gln Asp Val	
200 205 210	
gat ggt cgc gat gaa gcg ctc tac ggt gcc tac ctg gct gcg gtg tct	787
Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr Leu Ala Ala Val Ser	
215 220 225	
ttt gcc tct gct ggc tct ggt ctc cac cac aag atc tgc cac gtg ttg	835
Phe Ala Ser Ala Gly Ser Gly Leu His His Lys Ile Cys His Val Leu	
230 235 240 245	
ggt gga act ttt aac ctt cca cac gcg caa acc cat gca aca gta ctg	883
Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr His Ala Thr Val Leu	
250 255 260	
cct tat gtt ctt gcc ttc aac gcg cca tat gcg cca cag gca gaa caa	931
Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala Pro Gln Ala Glu Gln	
265 270 275	
cgc gca gcg gca gct ttc ggt tct gcg aca gca ctt gaa gga ttg caa	979
Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu Gln	
280 285 290	
cag ctg cgt gcc caa gtg gga gca cca cag cga cta tcc gat tac gga	1027
Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr Gly	
295 300 305	
ttc acc gca gca gga atc cca gag gca gtg gaa atc atc ttg gag aaa	1075
Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu Lys	
310 315 320 325	
gta ccg gcg aat aat cca cgg acg gtc aca gaa gaa aac ctc act gcg	1123
Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr Ala	
330 335 340	
ctg ctt acc aca gcg ctc aac ggc gac gat cca gca act ttg aat	1168
Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn	
345 350 355	
taaggagacc aacatgacta ttt	1191

<210> 424

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met	Ser	Leu	Gln	Phe	Asp	His	Glu	Thr	Leu	Gly	Gln	Arg	Val	Leu	Phe
1				5					10					15	

Gly Ser Gly Glu Ala Ala Gln Asn Leu Ala Ala Glu Ile Ser Arg Leu
 20 25 30
 Asp Ala Lys Asn Val Met Val Val Ala Gly Asp Phe Glu Leu Pro Met
 35 40 45
 Ala Arg Gln Val Ala Ala Asp Ile Asp Val Lys Val Trp His Ser Asn
 50 55 60
 Val Val Met His Val Pro Ile Glu Thr Ala Glu Glu Ala Arg Ser Val
 65 70 75 80
 Ala Lys Glu Asn Asp Ile Asp Val Val Val Cys Val Gly Gly Gly Ser
 85 90 95
 Thr Thr Gly Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile
 100 105 110
 Ile Ala Val Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp
 115 120 125
 Gly Leu Thr Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Asn Lys Val
 130 135 140
 Leu Pro Val Thr Val Ile Tyr Asp Ser Ala Leu Thr Met Ser Leu Pro
 145 150 155 160
 Val Glu Met Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile
 165 170 175
 Asp Ser Leu Trp Gly Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala
 180 185 190
 Ala Glu Gly Ile Arg Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala
 195 200 205
 Asp Ala Gln Asp Val Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr
 210 215 220
 Leu Ala Ala Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His His Lys
 225 230 235 240
 Ile Cys His Val Leu Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr
 245 250 255
 His Ala Thr Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala
 260 265 270
 Pro Gln Ala Glu Gln Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala
 275 280 285
 Leu Glu Gly Leu Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg
 290 295 300
 Leu Ser Asp Tyr Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu
 305 310 315 320
 Ile Ile Leu Glu Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu
 325 330 335
 Glu Asn Leu Thr Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro

340

345

350

Ala Thr Leu Asn
355

<210> 425
<211> 960
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(937)
<223> RXC00963

<400> 425
ctggctctga cggcgctcgac ttgttctgct tctctgatac accaatttttc gaggccctta 60
acctcgcacg tactttttact ccggaaggaa tctagaactt atg cgt ctt gca aca 115
Met Arg Leu Ala Thr
1 5
atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac 163
Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
10 15 20
acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag 211
Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln
25 30 35
gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg 259
Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
40 45 50
acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag 307
Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
55 60 65
att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc 355
Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
70 75 80 85
cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg 403
Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
90 95 100
ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag 451
Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
105 110 115
gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca 499
Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
120 125 130
cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct ggc tac gca 547
Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala Gly Tyr Ala
135 140 145
gtg atg aac gat tac acc acc cgc gat ttc cag tac gca gca cct gca 595
Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln Tyr Ala Ala Pro Ala

150	155	160	165	
aag act cca cag tgg	cac cag ggc aag tct ttg	gaa aag tcc gct ggc	643	
Lys Thr Pro Gln Trp	His Gln Gly Lys Ser Leu	Glu Lys Ser Ala Gly		
170	175	180		
ttc ggg cct tgg atg act acc cca gat tct ttt gag ttc ggc ggc gag	691			
Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe Glu Phe Gly Gly Glu				
185	190	195		
ctg gca acc tac ctc gag ggc gag aag gta cag tcc acc cct acc aat	739			
Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln Ser Thr Pro Thr Asn				
200	205	210		
gac ctg gtc ttt agc cca gaa aag ctc atc gaa tac atc acc cac atc	787			
Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu Tyr Ile Thr His Ile				
215	220	225		
tac cca ttg gat gct ggc gac gtc att gtc acc ggt acc cca ggc ggc	835			
Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr Gly Thr Pro Gly Gly				
230	235	240	245	
gtt ggc cac gca cgt aac cca cag cgc tac atc ggt gac ggc gaa acc	883			
Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile Gly Asp Gly Glu Thr				
250	255	260		
gta aag gtt gag att gcg ggc ctc ggc ttc att gaa aac aag acg gtg	931			
Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile Glu Asn Lys Thr Val				
265	270	275		
ttt gaa taaatgacaa ctttccacga tct	960			
Phe Glu				

<210> 426

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg	
1 5 10 15	
Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val	
20 25 30	
Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala	
35 40 45	
Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val	
50 55 60	
Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His	
65 70 75 80	
Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val	
85 90 95	
Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro	
100 105 110	

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
 115 120 125
 Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
 130 135 140
 Ile Ala Gly Tyr Ala Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln
 145 150 155 160
 Tyr Ala Ala Pro Ala Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu
 165 170 175
 Glu Lys Ser Ala Gly Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe
 180 185 190
 Glu Phe Gly Gly Glu Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln
 195 200 205
 Ser Thr Pro Thr Asn Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu
 210 215 220
 Tyr Ile Thr His Ile Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr
 225 230 235 240
 Gly Thr Pro Gly Gly Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile
 245 250 255
 Gly Asp Gly Glu Thr Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile
 260 265 270
 Glu Asn Lys Thr Val Phe Glu
 275

<210> 427
 <211> 1101
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1078)
 <223> RXN00299

<400> 427
 tgccatcggg ttggctattg attggaacaa gaaaggtgcc cagtctgttg caaagaagga 60
 atccatttcc gtctaatacgc taattgcgag gagtctttgc atg tct atc cca ctt 115
 Met Ser Ile Pro Leu 5
 1
 tca ctg att gat ttt gcc acc att ttt gag ggc gaa agg cct ggt gac 163
 Ser Leu Ile Asp Phe Ala Thr Ile Phe Glu Gly Glu Arg Pro Gly Asp 20
 10 15
 agc ttc aaa cga tca gtg gca ttg gcg caa aaa gct gaa ggt tta ggc 211
 Ser Phe Lys Arg Ser Val Ala Leu Ala Gln Lys Ala Glu Gly Leu Gly 35
 25 30
 ttc aag cgc att tgg tac gca gag cat cac aac atg gag agc att tct 259

Phe	Lys	Arg	Ile	Trp	Tyr	Ala	Glu	His	His	Asn	Met	Glu	Ser	Ile	Ser		
		40					45					50					
tca	gct	gct	cct	gca	gtg	ctt	att	tct	cac	atc	ggt	gcg	aac	acc	aag	307	
Ser	Ala	Ala	Pro	Ala	Val	Leu	Ile	Ser	His	Ile	Gly	Ala	Asn	Thr	Lys		
	55					60					65						
act	att	cgt	ctg	ggt	gcc	ggc	ggc	gtc	atg	ctg	ccc	aac	cac	tcc	cca	355	
Thr	Ile	Arg	Leu	Gly	Ala	Gly	Gly	Val	Met	Leu	Pro	Asn	His	Ser	Pro		
	70				75					80					85		
tat	gtc	atc	gct	gag	cag	ttc	ggc	acc	ttg	gcg	gag	ttg	tac	cca	gac	403	
Tyr	Val	Ile	Ala	Glu	Gln	Phe	Gly	Thr	Leu	Ala	Glu	Leu	Tyr	Pro	Asp		
				90					95					100			
cgc	atc	gac	ctc	ggc	ctg	ggc	cgt	gcc	cct	ggc	acg	gac	atg	aat	acc	451	
Arg	Ile	Asp	Leu	Gly	Leu	Gly	Arg	Ala	Pro	Gly	Thr	Asp	Met	Asn	Thr		
			105					110					115				
ttg	cgc	gct	tta	cga	cgc	gac	cct	cag	tcc	gcc	gag	aac	ttc	ccg	tcc	499	
Leu	Arg	Ala	Leu	Arg	Arg	Asp	Pro	Gln	Ser	Ala	Glu	Asn	Phe	Pro	Ser		
		120					125					130					
gac	gtt	gtc	gag	ctg	aac	tct	tac	ctc	acc	ggc	cgt	tcc	cgt	ctc	cca	547	
Asp	Val	Val	Glu	Leu	Asn	Ser	Tyr	Leu	Thr	Gly	Arg	Ser	Arg	Leu	Pro		
	135					140					145						
ggg	gtt	aac	gca	att	cca	ggc	aag	ggc	acc	aac	gta	ccg	ctg	tac	atc	595	
Gly	Val	Asn	Ala	Ile	Pro	Gly	Lys	Gly	Thr	Asn	Val	Pro	Leu	Tyr	Ile		
	150				155					160					165		
ttg	ggt	tca	tcc	ctc	ttt	ggt	gca	caa	ttg	gca	gca	cag	ttg	ggt	atg	643	
Leu	Gly	Ser	Ser	Leu	Phe	Gly	Ala	Gln	Leu	Ala	Ala	Gln	Leu	Gly	Met		
				170					175					180			
cct	tat	tcc	ttc	gca	tcc	cac	ttc	gca	cca	act	cac	ctt	gag	cac	gcg	691	
Pro	Tyr	Ser	Phe	Ala	Ser	His	Phe	Ala	Pro	Thr	His	Leu	Glu	His	Ala		
			185					190					195				
gtg	caa	acc	tac	cgg	gat	aac	tac	cag	cct	tca	gag	cag	cat	cct	gag	739	
Val	Gln	Thr	Tyr	Arg	Asp	Asn	Tyr	Gln	Pro	Ser	Glu	Gln	His	Pro	Glu		
		200				205						210					
cct	tat	gtc	att	gcg	gcc	gtc	aat	gtc	acc	gca	tct	gat	tcc	act	gaa	787	
Pro	Tyr	Val	Ile	Ala	Ala	Val	Asn	Val	Thr	Ala	Ser	Asp	Ser	Thr	Glu		
	215					220					225						
caa	gcc	cac	gat	gat	ttc	tac	aag	gta	gcg	cgt	gca	cgc	gtg	aag	aac	835	
Gln	Ala	His	Asp	Asp	Phe	Tyr	Lys	Val	Ala	Arg	Ala	Arg	Val	Lys	Asn		
	230				235					240					245		
atg	gca	ttg	cgt	ggc	cga	caa	gtt	act	gat	gag	caa	ctt	gat	gaa	ctc	883	
Met	Ala	Leu	Arg	Gly	Arg	Gln	Val	Thr	Asp	Glu	Gln	Leu	Asp	Glu	Leu		
				250					255					260			
atg	gat	tca	cca	gct	gct	cgc	caa	att	gtc	gac	atg	ctt	cac	tac	acc	931	
Met	Asp	Ser	Pro	Ala	Ala	Arg	Gln	Ile	Val	Asp	Met	Leu	His	Tyr	Thr		
			265					270					275				
gct	ata	ggc	act	gga	tcc	gaa	gtt	aaa	gaa	tac	cta	gac	ggt	ttt	gta	979	
Ala	Ile	Gly	Thr	Gly	Ser	Glu	Val	Lys	Glu	Tyr	Leu	Asp	Gly	Phe	Val		

280	285	290	
aag acg gca cag gct gat gaa ctg atg atc tcc ctg caa tcc ccc aac			1027
Lys Thr Ala Gln Ala Asp Glu Leu Met Ile Ser Leu Gln Ser Pro Asn			
295	300	305	
act gaa gca acc acg cgc aat atg gaa att ctt gcg gat gcg tgg att			1075
Thr Glu Ala Thr Thr Arg Asn Met Glu Ile Leu Ala Asp Ala Trp Ile			
310	315	320	325
aat tagtaccgat gggccggtag aca			1101
Asn			

<210> 428
 <211> 326
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 428
 Met Ser Ile Pro Leu Ser Leu Ile Asp Phe Ala Thr Ile Phe Glu Gly
 1 5 10 15
 Glu Arg Pro Gly Asp Ser Phe Lys Arg Ser Val Ala Leu Ala Gln Lys
 20 25 30
 Ala Glu Gly Leu Gly Phe Lys Arg Ile Trp Tyr Ala Glu His His Asn
 35 40 45
 Met Glu Ser Ile Ser Ser Ala Ala Pro Ala Val Leu Ile Ser His Ile
 50 55 60
 Gly Ala Asn Thr Lys Thr Ile Arg Leu Gly Ala Gly Gly Val Met Leu
 65 70 75 80
 Pro Asn His Ser Pro Tyr Val Ile Ala Glu Gln Phe Gly Thr Leu Ala
 85 90 95
 Glu Leu Tyr Pro Asp Arg Ile Asp Leu Gly Leu Gly Arg Ala Pro Gly
 100 105 110
 Thr Asp Met Asn Thr Leu Arg Ala Leu Arg Arg Asp Pro Gln Ser Ala
 115 120 125
 Glu Asn Phe Pro Ser Asp Val Val Glu Leu Asn Ser Tyr Leu Thr Gly
 130 135 140
 Arg Ser Arg Leu Pro Gly Val Asn Ala Ile Pro Gly Lys Gly Thr Asn
 145 150 155 160
 Val Pro Leu Tyr Ile Leu Gly Ser Ser Leu Phe Gly Ala Gln Leu Ala
 165 170 175
 Ala Gln Leu Gly Met Pro Tyr Ser Phe Ala Ser His Phe Ala Pro Thr
 180 185 190
 His Leu Glu His Ala Val Gln Thr Tyr Arg Asp Asn Tyr Gln Pro Ser
 195 200 205
 Glu Gln His Pro Glu Pro Tyr Val Ile Ala Ala Val Asn Val Thr Ala

```
<210> 429
<211> 784
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (18)..(761)
<223> FRXA00299
```

<400> 429																
gggtgccggc	ggcgggtcatg	ctg	ccc	aac	cac	tcc	cca	tat	gtc	atc	gct	gag		53		
	Met	Leu	Pro	Asn	His	Ser	Pro	Tyr	Val	Ile	Ala	Glu				
	1					5				10						
cag	ttc	ggc	acc	ttg	gcg	gag	ttg	tac	cca	gac	cgc	atc	gac	ctc	ggc	101
Gln	Phe	Gly	Thr	Leu	Ala	Glu	Leu	Tyr	Pro	Asp	Arg	Ile	Asp	Leu	Gly	
		15					20					25				
atg	ggc	cgt	gcc	cct	ggc	acg	gac	atg	aat	acc	ttg	cgc	gct	tta	cga	149
Met	Gly	Arg	Ala	Pro	Gly	Thr	Asp	Met	Asn	Thr	Leu	Arg	Ala	Leu	Arg	
	30					35					40					
cgc	gac	cct	cag	tcc	gcc	gag	aac	ttc	ccg	tcc	gac	gtt	gtc	gag	ctg	197
Arg	Asp	Pro	Gln	Ser	Ala	Glu	Asn	Phe	Pro	Ser	Asp	Val	Val	Glu	Leu	
	45				50					55					60	
aac	tct	tac	ctc	acc	ggc	cgt	tcc	cgt	ctc	cca	ggg	gtt	aac	gca	att	245
Asn	Ser	Tyr	Leu	Thr	Gly	Arg	Ser	Arg	Leu	Pro	Gly	Val	Asn	Ala	Ile	
				65					70					75		
cca	ggc	aag	ggc	acc	aac	gta	ccg	ctg	tac	atc	ttg	ggt	tca	tcc	ctc	293
Pro	Gly	Lys	Gly	Thr	Asn	Val	Pro	Leu	Tyr	Ile	Leu	Gly	Ser	Ser	Leu	
			80					85					90			
ttt	ggt	gca	caa	ttg	gca	gca	cag	ttg	ggt	atg	cct	tat	tcc	ttc	gca	341
Phe	Gly	Ala	Gln	Leu	Ala	Ala	Gln	Leu	Gly	Met	Pro	Tyr	Ser	Phe	Ala	

95					100					105						
tcc	cac	ttc	gca	cca	act	cac	ctt	gag	cac	gcg	gtg	caa	acc	tac	cgg	389
Ser	His	Phe	Ala	Pro	Thr	His	Leu	Glu	His	Ala	Val	Gln	Thr	Tyr	Arg	
110						115					120					
gat	aac	tac	cag	cct	tca	gag	cag	cat	cct	gag	cct	tat	gtc	att	gcg	437
Asp	Asn	Tyr	Gln	Pro	Ser	Glu	Gln	His	Pro	Glu	Pro	Tyr	Val	Ile	Ala	
125					130					135					140	
gcc	gtc	aat	gtc	acc	gca	tct	gat	tcc	act	gaa	caa	gcc	cac	gat	gat	485
Ala	Val	Asn	Val	Thr	Ala	Ser	Asp	Ser	Thr	Glu	Gln	Ala	His	Asp	Asp	
				145					150					155		
ttc	tac	aag	gta	gcg	cgt	gca	cgc	gtg	aag	aac	atg	gca	ttg	cgt	ggc	533
Phe	Tyr	Lys	Val	Ala	Arg	Ala	Arg	Val	Lys	Asn	Met	Ala	Leu	Arg	Gly	
		160						165					170			
cga	caa	gtt	act	gat	gag	caa	ctt	gat	gaa	ctc	atg	gat	tca	cca	gct	581
Arg	Gln	Val	Thr	Asp	Glu	Gln	Leu	Asp	Glu	Leu	Met	Asp	Ser	Pro	Ala	
		175					180					185				
gct	cgc	caa	att	gtc	gac	atg	ctt	cac	tac	acc	gct	ata	ggc	act	gga	629
Ala	Arg	Gln	Ile	Val	Asp	Met	Leu	His	Tyr	Thr	Ala	Ile	Gly	Thr	Gly	
	190					195					200					
tcc	gaa	gtt	aaa	gaa	tac	cta	gac	ggg	ttt	gta	aag	acg	gca	cag	gct	677
Ser	Glu	Val	Lys	Glu	Tyr	Leu	Asp	Gly	Phe	Val	Lys	Thr	Ala	Gln	Ala	
205					210					215					220	
gat	gaa	ctg	atg	atc	tcc	ctg	caa	tcc	ccc	aac	act	gaa	gca	acc	acg	725
Asp	Glu	Leu	Met	Ile	Ser	Leu	Gln	Ser	Pro	Asn	Thr	Glu	Ala	Thr	Thr	
				225					230					235		
cgc	aat	atg	gaa	att	ctt	gcg	gat	gcg	tgg	att	aat	tagtaccgat				771
Arg	Asn	Met	Glu	Ile	Leu	Ala	Asp	Ala	Trp	Ile	Asn					
		240					245									
gggcccggtag	aca															784

<210> 430

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Met	Leu	Pro	Asn	His	Ser	Pro	Tyr	Val	Ile	Ala	Glu	Gln	Phe	Gly	Thr
1				5					10					15	

Leu	Ala	Glu	Leu	Tyr	Pro	Asp	Arg	Ile	Asp	Leu	Gly	Met	Gly	Arg	Ala
		20						25					30		

Pro	Gly	Thr	Asp	Met	Asn	Thr	Leu	Arg	Ala	Leu	Arg	Arg	Asp	Pro	Gln
		35					40					45			

Ser	Ala	Glu	Asn	Phe	Pro	Ser	Asp	Val	Val	Glu	Leu	Asn	Ser	Tyr	Leu
	50					55					60				

Thr	Gly	Arg	Ser	Arg	Leu	Pro	Gly	Val	Asn	Ala	Ile	Pro	Gly	Lys	Gly
	65				70					75					80

```
<210> 431
<211> 825
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(802)  
<223> RXA00332
```

568

Ser Ile Glu Leu Ala Ile Gln Ala Glu Ala Gln Gly Phe Arg Gly Met
 40 45 50

tgg gtt cga gac gtt cca ctc gca gtt cct caa gga atc act gtt acc 307
 Trp Val Arg Asp Val Pro Leu Ala Val Pro Gln Gly Ile Thr Val Thr
 55 60 65

gat aaa cag gct acg tat tta gat gat cca ttc tta atg ctc ggt gcg 355
 Asp Lys Gln Ala Thr Tyr Leu Asp Asp Pro Phe Leu Met Leu Gly Ala
 70 75 80 85

atg gcc tct gtg acc tct aca atc gcg ctg ggc act gca gcg acc gtg 403
 Met Ala Ser Val Thr Ser Thr Ile Ala Leu Gly Thr Ala Ala Thr Val
 90 95 100

ctt cca ctc aga cat ccg cta cat gtg gcg aaa tcc gcg ctc acc ctt 451
 Leu Pro Leu Arg His Pro Leu His Val Ala Lys Ser Ala Leu Thr Leu
 105 110 115

gat cga ctc agc cac gga cgt ttc gtt tta ggc atc ggc tct ggc gac 499
 Asp Arg Leu Ser His Gly Arg Phe Val Leu Gly Ile Gly Ser Gly Asp
 120 125 130

agg cct gaa gaa ttc gag att ttt ggc aaa agc tta gac aat cga cgc 547
 Arg Pro Glu Glu Phe Glu Ile Phe Gly Lys Ser Leu Asp Asn Arg Arg
 135 140 145

gct gat att cag tct ggg tgg gca att ttg cgt gca gct ttg tcg ccg 595
 Ala Asp Ile Gln Ser Gly Trp Ala Ile Leu Arg Ala Ala Leu Ser Pro
 150 155 160 165

gat cct gcg atg cgg gcc gac ctt gaa ttt gcg cca acc acg cca cct 643
 Asp Pro Ala Met Arg Ala Asp Leu Glu Phe Ala Pro Thr Thr Pro Pro
 170 175 180

gaa gct cag atc ccc atg atc gct gta ggt tct gcc cga caa aca gtg 691
 Glu Ala Gln Ile Pro Met Ile Ala Val Gly Ser Ala Arg Gln Thr Val
 185 190 195

caa tgg atc gcc cga aac gcc gac gga tgg gca acc tac tac cgc ccc 739
 Gln Trp Ile Ala Arg Asn Ala Asp Gly Trp Ala Thr Tyr Tyr Arg Pro
 200 205 210

gct gaa gct caa gtc gga cgc ctc gat ctc tgg gac aaa gcc cgt ggt 787
 Ala Glu Ala Gln Val Gly Arg Leu Asp Leu Trp Asp Lys Ala Arg Gly
 215 220 225

ggc acc cgc cct tgt tgatttcctc catggggctc aac 825
 Gly Thr Arg Pro Cys
 230

<210> 432

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Ala Phe Asn Lys Ala Tyr Asp Ala Leu Arg Ala Pro Gln Ile Thr
 1 5 10 15

Leu Gly Leu Met Thr Pro Asn Gly Pro Glu Leu Gly Arg Ser Glu Met
 20 25 30
 Val Pro Thr Glu Asn Ser Ile Glu Leu Ala Ile Gln Ala Glu Ala Gln
 35 40 45
 Gly Phe Arg Gly Met Trp Val Arg Asp Val Pro Leu Ala Val Pro Gln
 50 55 60
 Gly Ile Thr Val Thr Asp Lys Gln Ala Thr Tyr Leu Asp Asp Pro Phe
 65 70 75 80
 Leu Met Leu Gly Ala Met Ala Ser Val Thr Ser Thr Ile Ala Leu Gly
 85 90 95
 Thr Ala Ala Thr Val Leu Pro Leu Arg His Pro Leu His Val Ala Lys
 100 105 110
 Ser Ala Leu Thr Leu Asp Arg Leu Ser His Gly Arg Phe Val Leu Gly
 115 120 125
 Ile Gly Ser Gly Asp Arg Pro Glu Glu Phe Glu Ile Phe Gly Lys Ser
 130 135 140
 Leu Asp Asn Arg Arg Ala Asp Ile Gln Ser Gly Trp Ala Ile Leu Arg
 145 150 155 160
 Ala Ala Leu Ser Pro Asp Pro Ala Met Arg Ala Asp Leu Glu Phe Ala
 165 170 175
 Pro Thr Thr Pro Pro Glu Ala Gln Ile Pro Met Ile Ala Val Gly Ser
 180 185 190
 Ala Arg Gln Thr Val Gln Trp Ile Ala Arg Asn Ala Asp Gly Trp Ala
 195 200 205
 Thr Tyr Tyr Arg Pro Ala Glu Ala Gln Val Gly Arg Leu Asp Leu Trp
 210 215 220
 Asp Lys Ala Arg Gly Gly Thr Arg Pro Cys
 225 230

<210> 433
 <211> 842
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(819)
 <223> RXA01838

<400> 433
 cag cac ctc tcc ggc ggc cgt gtt gac ctt atg atg ggc cgt ggc aac 48
 Gln His Leu Ser Gly Gly Arg Val Asp Leu Met Met Gly Arg Gly Asn
 1 5 10 15
 acc gga ccc gtt tac cca tgg ttt ggc aaa gac atc cac caa ggc atc 96
 Thr Gly Pro Val Tyr Pro Trp Phe Gly Lys Asp Ile His Gln Gly Ile
 20 25 30

cca cta gcg att gaa aac tac cac ctc ctg cgc cgc ctc tgg cgc gaa	144
Pro Leu Ala Ile Glu Asn Tyr His Leu Leu Arg Arg Leu Trp Arg Glu	
35 40 45	
gac gta gtc aac tgg cag ggc aaa ttc cgc aca ccg ttg cag gga tac	192
Asp Val Val Asn Trp Gln Gly Lys Phe Arg Thr Pro Leu Gln Gly Tyr	
50 55 60	
acc tct acc cca gca cca tta gac ggc gtt gca cca ttc gtc tgg cac	240
Thr Ser Thr Pro Ala Pro Leu Asp Gly Val Ala Pro Phe Val Trp His	
65 70 75 80	
ggc tcc atc cgc tcc acc gaa atc gca gag caa gca gcc ttc tat ggc	288
Gly Ser Ile Arg Ser Thr Glu Ile Ala Glu Gln Ala Ala Phe Tyr Gly	
85 90 95	
gac ggc ttc ttc cac aac aac atc ttc tgg aac aaa gag cac acc gcc	336
Asp Gly Phe Phe His Asn Asn Ile Phe Trp Asn Lys Glu His Thr Ala	
100 105 110	
caa atg gtc aac ctc tac cgc cag cgt ttc gaa cac tac gga cac ggc	384
Gln Met Val Asn Leu Tyr Arg Gln Arg Phe Glu His Tyr Gly His Gly	
115 120 125	
caa gca gac cag gcc atc gtg gga ctc ggt ggc caa gtc ttc atc ggc	432
Gln Ala Asp Gln Ala Ile Val Gly Leu Gly Gly Gln Val Phe Ile Gly	
130 135 140	
gat tct gaa gaa gaa gca aag aag acc ttc cgc ccc tac ttc gac aac	480
Asp Ser Glu Glu Glu Ala Lys Lys Thr Phe Arg Pro Tyr Phe Asp Asn	
145 150 155 160	
gcc cct gtc tac gga cac gga cca tca ctt gaa gat ttc tcc cgc ctg	528
Ala Pro Val Tyr Gly His Gly Pro Ser Leu Glu Asp Phe Ser Arg Leu	
165 170 175	
acc cca cta acc gtc ggt acc gct gag caa gtt atc gaa cgc acc atg	576
Thr Pro Leu Thr Val Gly Thr Ala Glu Gln Val Ile Glu Arg Thr Met	
180 185 190	
gaa ttc gcc gac tgg gta ggc gat tac cag cgc cag ctc ttc ctc atc	624
Glu Phe Ala Asp Trp Val Gly Asp Tyr Gln Arg Gln Leu Phe Leu Ile	
195 200 205	
gac cac gcc ggc ctg cca cta gaa atg gtc ctt gat cag atc gaa cgc	672
Asp His Ala Gly Leu Pro Leu Glu Met Val Leu Asp Gln Ile Glu Arg	
210 215 220	
ctc ggc cac gat gtc gtc cca gag gta cgc cgc cgc atg gag gag cgt	720
Leu Gly His Asp Val Val Pro Glu Val Arg Arg Arg Met Glu Glu Arg	
225 230 235 240	
cgc cca gac cac gtt ccc tcc aac cca cca acc cac cag agc ctg aag	768
Arg Pro Asp His Val Pro Ser Asn Pro Pro Thr His Gln Ser Leu Lys	
245 250 255	
gcc aac cga aac agc cct tac ttt cag atc aac cct ggt cag cca act	816
Ala Asn Arg Asn Ser Pro Tyr Phe Gln Ile Asn Pro Gly Gln Pro Thr	
260 265 270	

gag tagtttttct gaaactaagg aga
Glu

842

<210> 434

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Gln His Leu Ser Gly Gly Arg Val Asp Leu Met Met Gly Arg Gly Asn
1 5 10 15

Thr Gly Pro Val Tyr Pro Trp Phe Gly Lys Asp Ile His Gln Gly Ile
20 25 30

Pro Leu Ala Ile Glu Asn Tyr His Leu Leu Arg Arg Leu Trp Arg Glu
35 40 45

Asp Val Val Asn Trp Gln Gly Lys Phe Arg Thr Pro Leu Gln Gly Tyr
50 55 60

Thr Ser Thr Pro Ala Pro Leu Asp Gly Val Ala Pro Phe Val Trp His
65 70 75 80

Gly Ser Ile Arg Ser Thr Glu Ile Ala Glu Gln Ala Ala Phe Tyr Gly
85 90 95

Asp Gly Phe Phe His Asn Asn Ile Phe Trp Asn Lys Glu His Thr Ala
100 105 110

Gln Met Val Asn Leu Tyr Arg Gln Arg Phe Glu His Tyr Gly His Gly
115 120 125

Gln Ala Asp Gln Ala Ile Val Gly Leu Gly Gly Gln Val Phe Ile Gly
130 135 140

Asp Ser Glu Glu Glu Ala Lys Lys Thr Phe Arg Pro Tyr Phe Asp Asn
145 150 155 160

Ala Pro Val Tyr Gly His Gly Pro Ser Leu Glu Asp Phe Ser Arg Leu
165 170 175

Thr Pro Leu Thr Val Gly Thr Ala Glu Gln Val Ile Glu Arg Thr Met
180 185 190

Glu Phe Ala Asp Trp Val Gly Asp Tyr Gln Arg Gln Leu Phe Leu Ile
195 200 205

Asp His Ala Gly Leu Pro Leu Glu Met Val Leu Asp Gln Ile Glu Arg
210 215 220

Leu Gly His Asp Val Val Pro Glu Val Arg Arg Arg Met Glu Glu Arg
225 230 235 240

Arg Pro Asp His Val Pro Ser Asn Pro Pro Thr His Gln Ser Leu Lys
245 250 255

Ala Asn Arg Asn Ser Pro Tyr Phe Gln Ile Asn Pro Gly Gln Pro Thr
260 265 270

gaa aac cag atg ctt tac cca cca act gag aat ggc att cac gct tgg 643
 Glu Asn Gln Met Leu Tyr Pro Pro Thr Glu Asn Gly Ile His Ala Trp
 170 175 180
 gtt gca gtg ggt ggc agc cca gaa tca gtc gtg cgc gct gct aag tat 691
 Val Ala Val Gly Gly Ser Pro Glu Ser Val Val Arg Ala Ala Lys Tyr
 185 190 195
 cgt ttc ccg ttg atg ctt gcc atc atc ggc ggt gct cct gag cgt ttc 739
 Arg Phe Pro Leu Met Leu Ala Ile Ile Gly Gly Ala Pro Glu Arg Phe
 200 205 210
 cgc ccg tat gtg gat ctg tac aag cgt gcc aac gaa cag ttc ggg cag 787
 Arg Pro Tyr Val Asp Leu Tyr Lys Arg Ala Asn Glu Gln Phe Gly Gln
 215 220 225
 cct caa aag ccc att ggt gtg cac tcc cct gga ctc att gcg gca act 835
 Pro Gln Lys Pro Ile Gly Val His Ser Pro Gly Leu Ile Ala Ala Thr
 230 235 240 245
 gat gag gaa gcc cgt gag cta gca ctt aat gat tgg ttg gaa ctc caa 883
 Asp Glu Glu Ala Arg Glu Leu Ala Leu Asn Asp Trp Leu Glu Leu Gln
 250 255 260
 cgc aag atc ggt gct gaa cgc ggt tgg gct cct gcg gat gca atg cag 931
 Arg Lys Ile Gly Ala Glu Arg Gly Trp Ala Pro Ala Asp Ala Met Gln
 265 270 275
 ttt gaa cgc gaa atc gat cac ggt tcc tta tac atc ggt tcc cct gag 979
 Phe Glu Arg Glu Ile Asp His Gly Ser Leu Tyr Ile Gly Ser Pro Glu
 280 285 290
 acg gtc gca aag aag atc gcc aaa acc att tca gtg ctt gat ctt gat 1027
 Thr Val Ala Lys Lys Ile Ala Lys Thr Ile Ser Val Leu Asp Leu Asp
 295 300 305
 cgc ttt acc ctc aaa tac gcc agt ggc cag acc cct cat gag tac ttg 1075
 Arg Phe Thr Leu Lys Tyr Ala Ser Gly Gln Thr Pro His Glu Tyr Leu
 310 315 320 325
 ctg aag tcc att gag ttg tat ggc act gag gtt att ccg ctg gtg aag 1123
 Leu Lys Ser Ile Glu Leu Tyr Gly Thr Glu Val Ile Pro Leu Val Lys
 330 335 340
 gac atc ttg acc aag cag gct taagaaggct ttaggacatt ccc 1167
 Asp Ile Leu Thr Lys Gln Ala
 345

<210> 436

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 436

Met Lys Asn Val Ser Phe Gly Leu Asp Thr Phe Gly Asp Asn Ala Ile
 1 5 10 15

Asp Leu Gln Gly Asn Pro Val Ser Pro Ala Gln Thr Leu Arg Asn Ile
 20 25 30

Ile Asp Glu Ala Lys Met Ala Asp Lys Val Gly Val Asp Ile Ile Gly
 35 40 45
 Ile Gly Glu His His Arg Glu Glu Tyr Ser Val Ser Ala Pro Asp Ile
 50 55 60
 Val Met Thr Ala Ile Leu Ala Ser Thr Glu Arg Leu Lys Val Thr Ser
 65 70 75 80
 Ser Val Thr Val Leu Ser Ser Asp Asp Pro Val Arg Leu Phe Glu Arg
 85 90 95
 Tyr Ser Thr Met Asn Ala Leu Ser Asn Gly Arg Ala Glu Ile Thr Leu
 100 105 110
 Gly Arg Gly Ser Phe Ile Glu Ser Phe Pro Leu Phe Gly Phe Asp Leu
 115 120 125
 Gln Asp Tyr Glu Gln Leu Phe Ser Glu Arg Leu Asp Leu Phe Ala Lys
 130 135 140
 Ile Leu Glu Ala Asp Ser Arg Gly Gln Gly Val Thr Trp His Gly Glu
 145 150 155 160
 Thr Arg Ser Ala Leu Glu Asn Gln Met Leu Tyr Pro Pro Thr Glu Asn
 165 170 175
 Gly Ile His Ala Trp Val Ala Val Gly Gly Ser Pro Glu Ser Val Val
 180 185 190
 Arg Ala Ala Lys Tyr Arg Phe Pro Leu Met Leu Ala Ile Ile Gly Gly
 195 200 205
 Ala Pro Glu Arg Phe Arg Pro Tyr Val Asp Leu Tyr Lys Arg Ala Asn
 210 215 220
 Glu Gln Phe Gly Gln Pro Gln Lys Pro Ile Gly Val His Ser Pro Gly
 225 230 235 240
 Leu Ile Ala Ala Thr Asp Glu Glu Ala Arg Glu Leu Ala Leu Asn Asp
 245 250 255
 Trp Leu Glu Leu Gln Arg Lys Ile Gly Ala Glu Arg Gly Trp Ala Pro
 260 265 270
 Ala Asp Ala Met Gln Phe Glu Arg Glu Ile Asp His Gly Ser Leu Tyr
 275 280 285
 Ile Gly Ser Pro Glu Thr Val Ala Lys Lys Ile Ala Lys Thr Ile Ser
 290 295 300
 Val Leu Asp Leu Asp Arg Phe Thr Leu Lys Tyr Ala Ser Gly Gln Thr
 305 310 315 320
 Pro His Glu Tyr Leu Leu Lys Ser Ile Glu Leu Tyr Gly Thr Glu Val
 325 330 335
 Ile Pro Leu Val Lys Asp Ile Leu Thr Lys Gln Ala
 340 345

<210> 437
 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(703)
 <223> RXA01933

<400> 437

```

ctagaagcct taggcaagaa atttggttga gttttcgatc tctacgacgc gtcattctcaa 60
ttccacctag gcttggatgc aggttagaaa ggagccttcg atg tct aag act cgt 115
                                         Met Ser Lys Thr Arg
                                         1 5

act ttt ctg ttt gat ctt tat ggt gtt ctc atc aag gag cat ggt gcg 163
Thr Phe Leu Phe Asp Leu Tyr Gly Val Leu Ile Lys Glu His Gly Ala
          10          15          20

gcg cag ttt gag cgg gtt gcg cgt gcg gtg ggg gag ccg tcc aag aac 211
Ala Gln Phe Glu Arg Val Ala Arg Ala Val Gly Glu Pro Ser Lys Asn
          25          30          35

gac aag ctg cat gag gtt tat gag tcg ctt cgt ctg gat ctg gat gcc 259
Asp Lys Leu His Glu Val Tyr Glu Ser Leu Arg Leu Asp Leu Asp Ala
          40          45          50

ggc cgc gtg agt gag gtg aat tat tgg aat cag atc aaa cta ttg gtg 307
Gly Arg Val Ser Glu Val Asn Tyr Trp Asn Gln Ile Lys Leu Leu Val
          55          60          65

ggt ttg gag ttt ttg gat atc cag gag gtc atc gcg gct gac tac agg 355
Gly Leu Glu Phe Leu Asp Ile Gln Glu Val Ile Ala Ala Asp Tyr Arg
          70          75          80          85

ggc ctt tat gag cgt gat cag gac atg gtt gat tat gtg ttg tcg ttg 403
Gly Leu Tyr Glu Arg Asp Gln Asp Met Val Asp Tyr Val Leu Ser Leu
          90          95          100

aag gcg aaa ggc cac cgc atc gga att ttg tcg aat att ccg gag ggg 451
Lys Ala Lys Gly His Arg Ile Gly Ile Leu Ser Asn Ile Pro Glu Gly
          105          110          115

ttg gcc aag ctg ttg aag gag cac aat tcg gag tgg ctt gat cag ctt 499
Leu Ala Lys Leu Leu Lys Glu His Asn Ser Glu Trp Leu Asp Gln Leu
          120          125          130

gat gcg gtg act ttg tcg tgc gat att ggc gcg gcg aag ccg gag ccg 547
Asp Ala Val Thr Leu Ser Cys Asp Ile Gly Ala Ala Lys Pro Glu Pro
          135          140          145

aag tct ttc cat gtg gca ctt gag gcc ctt ggt gaa aaa gct gag gat 595
Lys Ser Phe His Val Ala Leu Glu Ala Leu Gly Glu Lys Ala Glu Asp
          150          155          160          165

gtg acc ttt att gat gat cgc gtg cgt aac att gag gca gcg cgc gaa 643
Val Thr Phe Ile Asp Asp Arg Val Arg Asn Ile Glu Ala Ala Arg Glu
          170          175          180

```

gaa ggt ctc agc aca att cac ttc act ggc tta gat tcc tta aaa gaa 691
 Glu Gly Leu Ser Thr Ile His Phe Thr Gly Leu Asp Ser Leu Lys Glu
 185 195 195

agc att cag gaa tgacacctca accactgatt ttg 726
 Ser Ile Gln Glu
 200

<210> 438

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Met Ser Lys Thr Arg Thr Phe Leu Phe Asp Leu Tyr Gly Val Leu Ile
 1 5 10 15

Lys Glu His Gly Ala Ala Gln Phe Glu Arg Val Ala Arg Ala Val Gly
 20 25 30

Glu Pro Ser Lys Asn Asp Lys Leu His Glu Val Tyr Glu Ser Leu Arg
 35 40 45

Leu Asp Leu Asp Ala Gly Arg Val Ser Glu Val Asn Tyr Trp Asn Gln
 50 55 60

Ile Lys Leu Leu Val Gly Leu Glu Phe Leu Asp Ile Gln Glu Val Ile
 65 70 75 80

Ala Ala Asp Tyr Arg Gly Leu Tyr Glu Arg Asp Gln Asp Met Val Asp
 85 90 95

Tyr Val Leu Ser Leu Lys Ala Lys Gly His Arg Ile Gly Ile Leu Ser
 100 105 110

Asn Ile Pro Glu Gly Leu Ala Lys Leu Leu Lys Glu His Asn Ser Glu
 115 120 125

Trp Leu Asp Gln Leu Asp Ala Val Thr Leu Ser Cys Asp Ile Gly Ala
 130 135 140

Ala Lys Pro Glu Pro Lys Ser Phe His Val Ala Leu Glu Ala Leu Gly
 145 150 155 160

Glu Lys Ala Glu Asp Val Thr Phe Ile Asp Asp Arg Val Arg Asn Ile
 165 170 175

Glu Ala Ala Arg Glu Glu Gly Leu Ser Thr Ile His Phe Thr Gly Leu
 180 185 190

Asp Ser Leu Lys Glu Ser Ile Gln Glu
 195 200

<210> 439

<211> 1039

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1039)

<223> RXA02351

<400> 439

```

tgacacttta cagactgggt ttcaactaat gacaccgaaa gaaatacacc tcaacctttt 60

tgcttttcggt gccgggcacc acgcggcggc gtggcgagcg gtg gag gga agc gtc 115
                               Val Glu Gly Ser Val
                               1           5

gaa aag ctg ggt tta att tcc tgg tgg gag gaa ctc gcg cgc acc gct 163
Glu Lys Leu Gly Leu Ile Ser Trp Trp Glu Glu Leu Ala Arg Thr Ala
                        10                15                20

gag cgg ggc aag ctg gat gcg gtc ttt ttg gcc gat ggg cag gcg att 211
Glu Arg Gly Lys Leu Asp Ala Val Phe Leu Ala Asp Gly Gln Ala Ile
                        25                30                35

aat ccg gtc ggt ctg gag aat ggg ccg ggc tgg ttt ttg gag ccg gtg 259
Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp Phe Leu Glu Pro Val
                        40                45                50

acc gcg ttg act gcg atg gcg ccg gcg acg aac aat att ggg ttg atc 307
Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn Asn Ile Gly Leu Ile
                        55                60                65

agc aca att tcc agt acg ttt tgg cag ccg ttt cat gcg gcg ccg atg 355
Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe His Ala Ala Arg Met
                        70                75                80                85

atc gcc agc ttg gat cat att tcg ggt ggg cgt gct gga atc aat gtg 403
Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg Ala Gly Ile Asn Val
                        90                95                100

gtg aca tcg atg acc gat gcg gag gcg cgt aac cac ggg atg gat gcg 451
Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn His Gly Met Asp Ala
                        105                110                115

ttg ccg ggt cac gat gtt cgc tat gcg cgc gct gcg gaa ttt att gaa 499
Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala Ala Glu Phe Ile Glu
                        120                125                130

acc atc act gcg ctg tgg gat tct tgg cct gcg gaa agt ttg gtg atg 547
Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala Glu Ser Leu Val Met
                        135                140                145

gat cgt gct gga aaa ttt gcg gac tcc tcg ctc att aaa tct atc gat 595
Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu Ile Lys Ser Ile Asp
                        150                155                160                165

cat gat ggt gag ttc ttc caa gtc gct ggt ccg ctg aat atc ccc agt 643
His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro Leu Asn Ile Pro Ser
                        170                175                180

cct ccg cag ggt cga ccc gta ctt ttt cag gct gga tcc tca ccg caa 691
Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala Gly Ser Ser Pro Gln
                        185                190                195

gga ccg gaa atc gct gcg aaa tac gcc gag gca att tac tct gtg gcg 739

```

Gly	Arg	Glu	Ile	Ala	Ala	Lys	Tyr	Ala	Glu	Ala	Ile	Tyr	Ser	Val	Ala		
		200					205					210					
tgg	gat	ttg	gag	caa	gcg	caa	gat	tat	cgc	tct	gat	att	cat	gct	cgt	787	
Trp	Asp	Leu	Glu	Gln	Ala	Gln	Asp	Tyr	Arg	Ser	Asp	Ile	His	Ala	Arg		
	215					220					225						
gcc	act	gcc	cag	ggg	gcg	gag	ccc	atg	ccg	gtg	ctt	cct	ggt	ttg	gtg	835	
Ala	Thr	Ala	Gln	Gly	Arg	Glu	Pro	Met	Pro	Val	Leu	Pro	Gly	Leu	Val		
230					235					240					245		
act	ttt	gtt	ggc	acg	acc	gtg	gaa	gaa	gcg	cgt	gca	aaa	cag	cag	gct	883	
Thr	Phe	Val	Gly	Thr	Thr	Val	Glu	Glu	Ala	Arg	Ala	Lys	Gln	Gln	Ala		
			250						255					260			
ctt	aat	gcg	ttg	ctg	ccg	gtc	aaa	gac	tca	cta	aat	cag	ttg	agt	ttc	931	
Leu	Asn	Ala	Leu	Leu	Pro	Val	Lys	Asp	Ser	Leu	Asn	Gln	Leu	Ser	Phe		
		265						270					275				
ttt	gtg	ggg	caa	gat	tgc	tcg	acg	tgg	gat	ttg	gat	gca	cct	ccc	cca	979	
Phe	Val	Gly	Gln	Asp	Cys	Ser	Thr	Trp	Asp	Leu	Asp	Ala	Pro	Pro	Pro		
	280						285					290					
cca	ctg	cca	ccg	cta	gaa	gag	ttt	tcc	ggg	cct	aaa	ggc	agg	tac	gaa	1027	
Pro	Leu	Pro	Pro	Leu	Glu	Glu	Phe	Ser	Gly	Pro	Lys	Gly	Arg	Tyr	Glu		
	295					300					305						
acg	gtc	ctg	cgg													1039	
Thr	Val	Leu	Arg														
310																	

<210> 440
 <211> 313
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 440
 Val Glu Gly Ser Val Glu Lys Leu Gly Leu Ile Ser Trp Trp Glu Glu
 1 5 10 15
 Leu Ala Arg Thr Ala Glu Arg Gly Lys Leu Asp Ala Val Phe Leu Ala
 20 25 30
 Asp Gly Gln Ala Ile Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp
 35 40 45
 Phe Leu Glu Pro Val Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn
 50 55 60
 Asn Ile Gly Leu Ile Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe
 65 70 75 80
 His Ala Ala Arg Met Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg
 85 90 95
 Ala Gly Ile Asn Val Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn
 100 105 110
 His Gly Met Asp Ala Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala
 115 120 125

Ala Glu Phe Ile Glu Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala
 130 135 140

Glu Ser Leu Val Met Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu
 145 150 155 160

Ile Lys Ser Ile Asp His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro
 165 170 175

Leu Asn Ile Pro Ser Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala
 180 185 190

Gly Ser Ser Pro Gln Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala
 195 200 205

BGI-128CPPC
 Phe Tyr Ser Val Ala Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser
 210 215 220

Asp Ile His Ala Arg Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val
 225 230 235 240

Leu Pro Gly Leu Val Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg
 245 250 255

Ala Lys Gln Gln Ala Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu
 260 265 270

Asn Gln Leu Ser Phe Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu
 275 280 285 290

Asp Ala Pro Pro Pro Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro
 295 300 305

Lys Gly Arg Tyr Glu Thr Val Leu Arg
 310

BGI-128CPPC 315 Arg

?